

09/757443

[illegible]

Query Match	18.2%	Score 27	16.1	Length 7
Best Local Similarity	100.0%	Prod No. 1	100.0%	
Matches	21	Conservative	0%	Mismatches 0%
QY	7	Kp 8		
QI	1	Kp 7		

RESIDUE 23	NAME	STATUS	PROT.	% AA.
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QY	8 PR 9				
TD	11				
	7 PR 8				
REQUIT 22					
FA54_CALV.					
IID	FA44_CALV	SIAM-AMU.	URL:	9 AA.	
AC	041859.				
01	01-NW-1995 (Ref. 32. (checked)				
01	01-NW-1995 (Ref. 32. Last sequence update)				
01	01-NW-1995 (Ref. 32. Last annotation update)				
05	Calliphora vomitoria 4.				
06	Calliphora vomitoria (Blue Blowfly).				
08	Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota.				
08	Neoptera: Ephemeroptera: Diptera: Brachycera: Muscomorpha: Dipteroidea: Pterygota.				
08	Calliphoridae: Calliphoridae.				
0X	NCBI_TaxID=27494				
KN	111				
PP	SEQUENCE.				
PP	75556 Therapeutic function.				
RX	MEDLINE=92196171 PubMed 19435951				
KA	Dove H., Johnson A.H., Stewell J.W., Scott A.G., Orchard I.,				
KA	Rehfeld J.F., Thorpe A.J.				
RT	"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2				
RT	neuropeptides (designated calliphenkafamides) from the blowfly				
RI	Calliphora vomitoria."				
RI	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992)				
CC	1. SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)				
	FAMILY.				
ER	PIS: 041978; 041979.				
ER	Next sequence: A0401160.				
SW	SWD: 055				
	9. AMPLIFICATION.				











RE TISSUE: Placenta;  
 RX MEDLINE 22494955; PubMed 12506452;  
 RA FUJIMOTO, B., KOTY, B., SOUSA, N.M., DALLA, R., DALLA, R. & DALLA, R. (1994)  
 RA MURPHY, J.P., BECKERS, J., F.M. (1994)  
 FT Isolation and partial characterization of three fragments associated  
 RI glycoproteins from the cow placenta.

RE Ref. reported: bcy: 641199-206 (2003)  
 CC -1- FUNCTION: This protease which is involved in participating in  
 CC intracellular degradation and turnover of proteins has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds, preferentially cleaves after Arg, Lys and His in  
 CC small molecule substrates (thus different from carboxypeptidase Y in  
 CC addition to being an endopeptidase, see e.g. Fujimoto et al. 1994)  
 CC -1- ACTIVITY: Liberating C-terminal peptide  
 CC -1- SUBUNIT: dimer of a heavy chain and a light chain (not linked  
 CC by a disulfide bond (by similarity))  
 CC -1- SUBCELLULAR LOCATION: Lysosomal (by similarity)  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11;  
 CC (entry: P000169); SH3 domain.  
 CC PROSITE: P00040; THIOLEPROTEINASE; PARTIAL;  
 CC PROSITE: P00040; THIOLEPROTEINASE; PARTIAL;  
 KW Hydrolyses: small protease; lysosomal;  
 RI N-TER 10 10  
 SQ SEQUENCE 10 AA: 1177 MW: 87676.066 Da; pI: 4.1

Query Match: 16.2%; Score 2: DB 1; Length 10;  
 Best Local Similarity 100.0%; Proj. No. 104;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

SV 1 AP 2  
 11  
 14 7 AP 8

RESULT 40  
 COXL RAB1  
 ID COXLLRAB1 STANDARD PRI: 10 AA.  
 AC P00442  
 DI 01-07-1994 (Ref. 30, Created)  
 DT 01-07-1994 (Ref. 30, Last sequence update)  
 DE 16 FEB 2003 (Ref. 40, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII (EC 1.9.3.1) (Fragment)  
 CS Oxidoreductase (rainbow trout) (Rainbow trout)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Proteocephali; Cyprinidae; Salmoniformes; Salmonidae; Cyprinidae;  
 CC NCBI TaxID: 8022;  
 RN 11  
 RE SEQUENCE  
 RX MEDLINE 54241150; PubMed 8181460;  
 RA Freund R., Kadochach B.  
 FT Identification of tissue-specific isoforms of cytochromes VI and VIII  
 RI of cytochrome c oxidase isolated from rainbow trout.

RE Eur. J. Biochem. 221:1111-1116 (1994)  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferricytochrome c + 0(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrion; inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VI/8 FAMILY.  
 RX P00442: S4453;  
 KW Oxidoreductase; inner membrane; Mitochondrion;  
 RI N-TER 10 10  
 SQ SEQUENCE 10 AA: 1174 MW: 47064.042 Da; pI: 4.1

Query Match: 16.2%; Score 2: DB 1; Length 10;  
 Best Local Similarity 100.0%; Proj. No. 104;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 QK 4  
 11  
 14 7 QK 9

RESULT 47  
 COXL RAB1  
 ID COXLRAB1 STANDARD PRI: 10 AA.  
 AC P00442  
 DI 01-07-1994 (Ref. 32, Created)  
 DT 01-07-1994 (Ref. 32, Last sequence update)  
 DE 26 FEB 2003 (Ref. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII, mitochondrial (EC 1.9.3.1)  
 DE (Fragment)  
 CS Oxidoreductase (Rabbit)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Muridae; Murinae; Rattus.  
 CC NCBI TaxID: 10116;  
 RN 11  
 RE SEQUENCE  
 RX STRAIN Wistar; Tissue: Liver;  
 RX MEDLINE 9542429; PubMed 7601105;  
 RA Scheidegger H., Niggli V., Hallack W., Brandt U., von Jagow G.  
 FT Cytochrome c oxidase in developing rat heart. Enzymic properties and  
 RI amino-terminal sequences suggest identity of the fetal heart and the  
 RI adult liver isoform.  
 RE Eur. J. Biochem. 230:235-241 (1995).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferricytochrome c + 0(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrion;  
 FT N-TER 10 10  
 SQ SEQUENCE 10 AA: 1219 MW: 69708.771 Da; pI: 4.1

Query Match: 16.2%; Score 2: DB 1; Length 10;  
 Best Local Similarity 100.0%; Proj. No. 104;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 QK 4  
 11  
 14 7 QK 4

RESULT 48  
 COXL RAB1  
 ID COXLRAB1 STANDARD PRI: 10 AA.  
 AC P00442  
 DI 01-07-1994 (Ref. 30, Created)  
 DT 01-07-1994 (Ref. 30, Last sequence update)  
 DE 26 FEB 2003 (Ref. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
 DE (Fragment)  
 CS Oxidoreductase (Rabbit)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CC NCBI TaxID: 9986;  
 RN 11  
 RE SEQUENCE  
 RX Freund R., Kadochach B.  
 RA Submitted (MAR 1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferricytochrome c + 0(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 KW Oxidoreductase; Mitochondrion;

01 SEQ ID# 10 10 1027 MW: 264265000.000 (1994)  
 02 SEQUENCE 10 AA: 1027 MW: 264265000.000 (1994)  
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 05 Best Local Similarity 100.0% Ident. No. 1004  
 06 Matches 21 Conservative 0 Mismatches 0 Gaps 0  
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01 MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 02 THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 03 CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 04 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOTT.  
 05 INTERPRO: IP0002191; FIBRINOGEN.  
 06 PROSITE: PS00554; FIBRIN A3 (DOMAIN: PARTIAL).  
 07 KW: Based on: Clotting Plasma.  
 08 FT: RESIDUE 1 10 FIBRINOPEPTIDE B.  
 09 NON TER 10  
 10 SEQUENCE 10 AA: 1097 MW: 942620000.000 (1994) CRC64:  
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 12 Query Match 18.2% Score 21 DB 11 Length 10  
 13 Best Local Similarity 100.0% Ident. No. 1004  
 14 Matches 21 Conservative 0 Mismatches 0 Gaps 0  
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DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadotrophin-releasing hormone I (GHRH I)  
 DE (GHRH I)  
 DE Petromyzon latrans (Sea lamprey)  
 DE Eukaryota; Metazoa; Chordata; Vertebrata; Hyperostei  
 DE Petromyzontiformes; Petromyzontidae; Petromyzon  
 DE NCBI\_TaxID: 7757;  
 DE [1]  
 DE SEQUENCE  
 DE TISSUE: Brain;  
 DE MEDLINE: 8636192; PubMed: 9514604;  
 DE Sherwood N.M., Sewer S.A., Marshall E.K., Fliser B.A., Brownstein M.D.,  
 DE "Primary structure of gonadotropin-releasing hormone from lamprey  
 DE brain". J. Biol. Chem. 261:4812-4815(1986).  
 DE CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
 DE the secretion of both luteinizing and follicle-stimulating  
 DE hormones.  
 DE CC -!- SUBCELLULAR LOCATION: Secreted.  
 DE CC -!- SIMILARITY: Belongs to the GNRH family.  
 DE DR 11K: AC:412; RHMG5.  
 DE DR InterPro: IPR002012; GNRH.  
 DE DR Pfam: PF00446; GNRH; 1.  
 DE DR PROSITE: PS00473; GNRH; 1.  
 DE KW Hormone; Amidation; Hypothalamus; Pyrolidone carboxylic acid.  
 DE FT MOD\_RES 10 1 PYROLIDONE CARBOXYLIC ACID.  
 DE FT MOD\_RES 10 10 AMIDATION.  
 DE SEQUENCE 10 AA: 1244 MW: 28456.2975; CAS: 69614;  
 DE Query Match 38.2%; Score 2; DB 1; Length 10;  
 DE Best Local Similarity 100.0%; Pred. No. le+04;  
 DE Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DE QY 7 KP 4  
 DE DB 1  
 DE 4 KP 9  
 DE RESULT 44  
 DE GNRH\_PETMA STANDARD: PROT: 10 AA.  
 DE AC P30448;  
 DE DT 01-JUL-1993 (Rel. 26, Created)  
 DE DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DE DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE DE Gonadotrophin-releasing hormone III (GHRH-III)  
 DE (GHRH-III)  
 DE Petromyzon latrans (Sea lamprey)  
 DE Eukaryota; Metazoa; Chordata; Vertebrata; Hyperostei  
 DE Petromyzontiformes; Petromyzontidae; Petromyzon  
 DE NCBI\_TaxID: 7757;  
 DE [1]  
 DE SEQUENCE  
 DE TISSUE: Brain;  
 DE MEDLINE: 9317831; PubMed: 8443174;  
 DE Sherwood S.A., Chiana Y.-C., Lovaas S., Shalton D.W.,  
 DE "Primary structure and biological activity of a third gonadotrope  
 DE releasing hormone from lamprey brain".  
 DE Endocrinology 132:1125-1132(1994).  
 DE CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
 DE the secretion of both luteinizing and follicle-stimulating  
 DE hormones.  
 DE CC -!- SUBCELLULAR LOCATION: Secreted.  
 DE CC -!- SIMILARITY: Belongs to the GNRH family.  
 DE DR InterPro: IPR002012; GNRH.  
 DE DR Pfam: PF00446; GNRH; 1.  
 DE DR PROSITE: PS00473; GNRH; 1.  
 DE KW Hormone; Amidation; Hypothalamus; Pyrolidone carboxylic acid.  
 DE FT MOD\_RES 10 1 PYROLIDONE CARBOXYLIC ACID.  
 DE FT MOD\_RES 10 10 AMIDATION.  
 DE SEQUENCE 10 AA: 1277 MW: 28466.2766; CAS: 69614;  
 DE Query Match 38.2%; Score 2; DB 1; Length 10;

DE Best Local Similarity 100.0%; Pred. No. le+04;  
 DE Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DE QY 7 KP 8  
 DE DB 1  
 DE 8 KP 9  
 DE RESULT 44  
 DE LPK2\_LOCM1 STANDARD: PROT: 10 AA.  
 DE ID LPK2\_LOCM1  
 DE AC P41488;  
 DE DT 01-NOV-1995 (Rel. 32, Created)  
 DE DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE DE Locustapyrokinin 2 (LOM-PK-2) (EXPRL-amide).  
 DE Locusta migratoria (Migratory locust).  
 DE CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 DE CC Acridoidea; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 DE CC Acrididae; Acrididae; Cediopodinae; Locusta.  
 DE CC NCBI\_TaxID: 7004;  
 DE RN [1]  
 DE SEQUENCE  
 DE TISSUE: Brain;  
 DE MEDLINE: 94094539; PubMed: 7503606;  
 DE Schoofs L., Holman G.M., Nachman K., Proost P., van Damme J.,  
 DE "Isolation, identification and synthesis of locustapyrokinin II from  
 DE Locusta migratoria, another member of the EXPRL-amide peptide  
 DE family." J.  
 DE Comp. Biochem. Physiol. 106C:103-109(1993).  
 DE CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC  
 DE ACTIVITY).  
 DE CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DE DR InterPro: IPR01484; Pyrokinin.  
 DE DR PROSITE: PS00539; PYROKININ; 1.  
 DE KW Neuropeptide; Amidation; Pyrokinin; Pyrolidone carboxylic acid.  
 DE FT MOD\_RES 1 1 PYROLIDONE CARBOXYLIC ACID.  
 DE FT MOD\_RES 10 10 AMIDATION.  
 DE SEQUENCE 10 AA: 1145 MW: 2464271A9D1B772 CRC64;  
 DE Query Match 18.2%; Score 2; DB 1; Length 10;  
 DE Best Local Similarity 100.0%; Pred. No. le+04;  
 DE Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DE QY 8 KP 9  
 DE DB 1  
 DE 8 KP 9  
 DE RESULT 45  
 DE MP2\_MTCOC STANDARD: PROT: 10 AA.  
 DE ID MP2\_MTCOC  
 DE AC P81533;  
 DE DT 15-JUL-1999 (Rel. 38, Created)  
 DE DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE DE MP2 protein (Fragment).  
 DE CC Microplitis orellatae (braconid wasp)  
 DE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 DE CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidae;  
 DE CC Braconidae; Microgasterinae; Microplitis.  
 DE CC NCBI\_TaxID: 99573;  
 DE RN [1]  
 DE SEQUENCE  
 DE TISSUE: Larva;  
 DE RA Takahashi M., Qiu X. D., J. J.  
 DE Submitted (06-1998) to the SWISS-PROT data bank.  
 DE CC -!- ISSUE SPECIFICITY: SALIVARY GLANDS.  
 DE CC -!- DEVELOPMENTAL STAGE: LARVAL.  
 DE FT N-TER 10 10  
 DE SEQUENCE 10 AA: 1255 MW: FE4FD9336C41AFA CRC64;



RX MEDLINE 84204263; PubMed-2452451;  
 RA "Galanin (Mr. Katsoulis S.; Schmidt W.E.; Chum L.;  
 FT "[Galanin] Substance P and neuropeptide A from chicken small intestine";  
 RL Regl. Pept. 20:171-180(1988).  
 CC FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC 1. SUBCELLULAR LOCATION: Secreted  
 CC 1. SIMILARITY: BELONGS TO THE TACHYKININ FAMILY  
 DR PIR: JN0624; JN0624.  
 DR Gasteiger: PR002040; tachykinin.  
 DR PIR: PR202; tachykinin.  
 DR PROSITE: PS00257; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT M02 RES 10 10 AMIDATION  
 SQ SEQUENCE 10 AA: KAVDAGDQVQPKA; (Ref.1)

Query Match 18.2%; Score 2; DR 1; E-value 10;  
 Best Local Similarity 100.0%; Pred. No. gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

CY 4 K1 5  
 LU 2 K1 4

RESULT 1  
 LK1 GREEN  
 ID TACHYKININ STANDARD; 187; 18 AA.  
 AC P42763.  
 DI 01 FEB 1990 (Ref. 32; Created)  
 DT 01 FEB 1990 (Ref. 32; Last sequence added)  
 TI 15 SEP 2004 (Ref. 42; Last annotation update)  
 FE Trichistatachykinin I.  
 OS Trichostema angustifolius.  
 CC Eukaryotic; Metazoa; Echinura; Xenuroidea; Trichodina; Drosophila.  
 OX N01 TaxId 6432.  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE: Ventral nerve cord.  
 RX MEDLINE 94236558; PubMed-8475470;  
 RA Ikeda T.; Mitsuoka H.; Nomoto K.; Kobata E.; Marukawa Y.  
 RT "Two novel tachykinin-related neuropeptides in the central nervous  
 KT Drosophila angustifolius";  
 RI Peptide. Biophys. Res. Commun. 192:1-7 (1993)  
 DI FUNCTION CONTRACTILE ACTION IN THE INVERTEBRATE MUSCLE  
 CC MUSCLE OF THE ANIMAL.  
 CC 1. SUBCELLULAR LOCATION: Secreted  
 CC 1. SIMILARITY: SOME SIMILARITY TO TACHYKININ  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT M02 RES 10 10 AMIDATION  
 SQ SEQUENCE 10 AA: YLWVDSQDQAW; (Ref.1)

Query Match 18.2%; Score 2; DR 1; E-value 10;  
 Best Local Similarity 100.0%; Pred. No. gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

CY 2 K2 4  
 LU 1  
 LU 2 K2 4

Search completed: September 30, 2003; 10:26:04  
 Run time: 7.25 secs



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an problem - problem search, using a model:

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File: US-05-787-443-12

Period score: 11

Sequence: I AKQKTMKPKRS 11

Scoring table: class 09, 09-01-01

Sealed: 83.525 sec, 258.52604 revs./min.

W. S. L. 120

total number of  $n$ 's satisfying chosen properties. For

Mining in the 1930s, 1940s, and 1950s 8

Max L. 2m 103 50g 15

and "early bird" breakfasts.

nat. abuse

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1: sp archea: *

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2: sp. bacteria:

2 : sp fungi : \*

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1. stemand 1

**THE**

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Proc. No. 15, the number of

Prod. No. is the number of rejections produced by having to leave a 5000-gram bag of equal to the size of the bag containing particles  $L$ . It is determined by dividing the number of rejections by the bag size.

Result No.	Score	Query *		Length	DB	ID	Description
		Match	%				
1	3	27.3	6	9	Q58630		Q58630: bacteriophage
2	3	27.3	6	9	Q58683		Q58683: bacteriophage
3	4	27.3	9	7	Q58626		Q58626: bacteriophage
4	3	27.3	7	7	Q58625		Q58625: bacteriophage
5	4	27.3	12	2	Q47345		Q47345: bacteriophage
6	2	27.3	11	8	Q58684		Q58684: bacteriophage
7	2	27.3	12	2	Q55579		Q55579: bacteriophage
8	3	27.3	13	12	Q65461		Q65461: bacteriophage
9	3	27.3	14	2	P71177		P71177: bacteriophage
10	3	27.3	14	2	Q81362		Q81362: bacteriophage
11	3	27.3	14	10	Q94512		Q94512: bacteriophage
12	3	27.3	14	15	Q50253		Q50253: bacteriophage
13	3	27.3	14	15	Q10229		Q10229: bacteriophage
14	3	27.3	14	15	Q10252		Q10252: bacteriophage
15	3	27.3	14	15	Q16274		Q16274: bacteriophage
16	3	27.3	14	15	Q16273		Q16273: bacteriophage













OS Human immunodeficiency virus 1.  
 OC VIRUSES; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garboglio A.R., Di Caro A., Pulciani S., Montella F., Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RI virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U99851; AAC26091.1;  
 DK InterPro: IPR000428; Env\_GP41.  
 DB Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1591 MW: 15874719(450566) Ck664;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 DB 2 PER 4

## RESULT 15

Q0244  
 AC Q0244; PRELIMINARY; PRI: 14 AA;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DI 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DI 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC VIRUSES; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garboglio A.R., Di Caro A., Pulciani S., Montella F., Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RI virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U99851; AAC26091.1;  
 DK InterPro: IPR000428; Env\_GP41.  
 DB Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1733 MW: 15874690(450566) Ck64;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 DB 2 PER 4

## RESULT 16

Q0245  
 AC Q0245; PRELIMINARY; PRI: 14 AA;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DI 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DI 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC VIRUSES; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garboglio A.R., Di Caro A., Pulciani S., Montella F., Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RI virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U99851; AAC26091.1;  
 DK InterPro: IPR000428; Env\_GP41.  
 DB Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1591 MW: 15874719(450566) Ck664;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 DB 2 PER 4

OS Human immunodeficiency virus 1.  
 OC VIRUSES; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garboglio A.R., Di Caro A., Pulciani S., Montella F., Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RI virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U99851; AAC26091.1;  
 DK InterPro: IPR000428; Env\_GP41.  
 DB Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1591 MW: 15874719(450566) Ck664;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 DB 2 PER 4

## RESULT 17

Q0245  
 AC Q0245; PRELIMINARY; PRI: 14 AA;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DI 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DI 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC VIRUSES; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garboglio A.R., Di Caro A., Pulciani S., Montella F., Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RI virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U99851; AAC26091.1;  
 DK InterPro: IPR000428; Env\_GP41.  
 DB Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1591 MW: 15874719(450566) Ck664;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 DB 2 PER 4

## RESULT 18

Q0229  
 AC Q0229; PRELIMINARY; PRI: 14 AA;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DI 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DI 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC VIRUSES; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garboglio A.R., Di Caro A., Pulciani S., Montella F., Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RI virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U99851; AAC26091.1;  
 DK InterPro: IPR000428; Env\_GP41.  
 DB Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1591 MW: 15874719(450566) Ck664;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 DB 2 PER 4



OC Viruses; Retroviral viruses; Retroviridae; Lentivirus  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:98216723; PubMed:9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RP EMBL: U09849; AAC26085.1;  
 DR InterPro: IPR000428; Env\_GP41.  
 DK Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA: 1691 MW: 156750.945; DB 15: Length 14;  
 Query Match 27.8% Score 3; DB 15: Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PER 10  
 DB [1]  
 CD 2 PER 4

RESULT 19  
 ID 010226 PRELIMINARY; PRT: 14 AA.  
 AC 010226;  
 DT 01-JUN-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:98216723; PubMed:9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RP EMBL: U09849; AAC26085.1;  
 DR InterPro: IPR000428; Env\_GP41.  
 DK Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA: 1721 MW: 162750.945; DB 15: Length 14;  
 Query Match 27.8% Score 3; DB 15: Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PER 10  
 DB [1]  
 CD 2 PER 4

RESULT 20  
 ID 010227 PRELIMINARY; PRT: 14 AA.  
 AC 010227;  
 DT 01-JUN-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:98216723; PubMed:9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RP EMBL: U09849; AAC26085.1;  
 DR InterPro: IPR000428; Env\_GP41.  
 DK Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA: 1721 MW: 162750.945; DB 15: Length 14;  
 Query Match 27.8% Score 3; DB 15: Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PER 10  
 DB [1]  
 CD 2 PER 4

OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:98216723; PubMed:9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RP EMBL: U09849; AAC26085.1;  
 DR InterPro: IPR000428; Env\_GP41.  
 DK Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA: 1691 MW: 156747.190450566; DB 15: Length 14;  
 Query Match 27.8% Score 3; DB 15: Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PER 10  
 DB [1]  
 CD 2 PER 4

RESULT 21  
 ID 010226 PRELIMINARY; PRT: 14 AA.  
 AC 010226;  
 DT 01-JUN-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:98216723; PubMed:9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RP EMBL: U09849; AAC26085.1;  
 DR InterPro: IPR000428; Env\_GP41.  
 DK Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA: 1691 MW: 156747.190450566; DB 15: Length 14;  
 Query Match 27.8% Score 3; DB 15: Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PER 10  
 DB [1]  
 CD 2 PER 4

RESULT 22  
 ID 054298 PRELIMINARY; PRT: 15 AA.  
 AC 054298;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE RNA polymerase alpha subunit (Fragment).  
 GN RPOA.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.

CX NCBI\_TaxID 6024  
 RN 111  
 RP SEQUENCE FROM N.A.  
 SC STRAIN-112  
 RX MEDLINE 9818810; PubMed-9520474  
 RA Holsinger K.E., Holmes O., Andersson P.  
 RT "VIRULENCE OF ANTIBIOTIC RESISTANT *Salmonella typhimurium*."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:1949-1953(1998)  
 RR EMBL AJ224240; CAA11204.1  
 FT NNN\_TFR 15  
 SQ SEQUENCE 15 AA: 1720 MW: 16.61 kDa; 15.66 MW: 16.61 kDa; 15.66 MW: 16.61 kDa

Query Match 27.98; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 7 KIR 9

30 10 KIR 12

RESULT 23

Q95660

ID Q95660 PRELIMINARY; PRO; 15 AA.

DI 01-MAY-1996 (TrEMBLrel. 13, Created)

DI 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)

DI 01-JUN-2003 (TrEMBLrel. 14, Last annotation update)

DE Various sensitive acetylactate synthase latent mutant (E14.11.3.18)

DS (Fragment)

OS Serratia marcescens

OC Bacterioidetes; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Serratia

CX NCBI\_TaxID 615

RN 111

RP SEQUENCE

RX MEDLINE 9428439; PubMed-8507655

RA Yoon H., Kim S.S.

RT "Identification and characterization of the *acvA* gene, which encodes an acetylactate synthase from *Serratia marcescens* ATCC 35061."

RL Biochem. Biophys. Acta 1157:174-184(1993)

RR EMBL X61253; CAA11204.1

SQ SEQUENCE 15 AA: 1615 MW: 16.61 kDa; 15.66 MW: 16.61 kDa; 15.66 MW: 16.61 kDa

Query Match 27.98; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKQ 3

30 1 AKQ 12

RESULT 24

Q95642

ID Q95642 PRELIMINARY; PRO; 15 AA.

DI 01-MAY-1996 (TrEMBLrel. 13, Created)

DI 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)

DI 01-JUN-2003 (TrEMBLrel. 14, Last annotation update)

DE 40S ribosomal protein S2 homolog (Fructose)

OS Mycobacterium bovis

OC Bacterioidetes; Proteobacteria; Actinobacteriales; Actinomycetales

OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium

CX NCBI\_TaxID 1745

RN 111

RP SEQUENCE

RX MEDLINE 94209453; PubMed-8405414

RA Chato N., Kimura M., Hoshino Y., Yamashita T.

RT "Isolation and amino acid sequence of the 40S ribosomal protein S2"

RL From *Mycobacterium bovis* HCG."

RR EMBL X61253; CAA11204.1

SQ SEQUENCE 15 AA: 1726 MW: 43.02 kDa; 15.66 MW: 16.61 kDa; 15.66 MW: 16.61 kDa

Query Match 27.98; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KIR 7

30 4 KIR 9

RESULT 25

Q95660

ID Q95660 PRELIMINARY; PRO; 15 AA.

DI 01-MAY-1996 (TrEMBLrel. 13, Created)

DI 01-MAY-1996 (TrEMBLrel. 13, Last sequence update)

DI 01-DEC-2003 (TrEMBLrel. 14, Last annotation update)

DE Light-harvesting complex 1 alpha polypeptide (Fragment)

OS Rhodospirillum rubrum

OC Bacterioidetes; Proteobacteria; Rhodospirillales; Rhodospirillales

OC Rhodospirillaceae; Rhodospirillum

CX NCBI\_TaxID 1061

RN 111

RP SEQUENCE FROM N.A.

RX MEDLINE 92244963; PubMed-1563629

RA Richter P., Brand M., Drews G.

RT "Characterization of LH1- and LH2- Rhodobacter capsulatus putative mutants."

RL J. Bacteriol. 174:3030-3041(1992)

RR EMBL S97552; AAC60406.1

SQ SEQUENCE 15 AA: 2054 MW: 35.15 kDa; 15.66 MW: 16.61 kDa; 15.66 MW: 16.61 kDa

Query Match 27.98; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KIR 10

30 4 KIR 12

RESULT 26

Q46013

ID Q46013 PRELIMINARY; PRO; 15 AA.

DI 01-MAY-1996 (TrEMBLrel. 13, Created)

DI 01-MAY-1996 (TrEMBLrel. 13, Last sequence update)

DI 01-MAR-2002 (TrEMBLrel. 2, Last annotation update)

DE Leader peptidase

OS Caulobacter crescentus

OC Bacterioidetes; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteriaceae; Caulobacter

CX NCBI\_TaxID 155892

RN 111

RP SEQUENCE FROM N.A.

RX MEDLINE 94266743; PubMed-8268653

RA Carlsberg J.C., Madsen J., Ely S.

RT "Regulation of *Caulobacter crescentus* *llyA* gene expression."

RL J. Bacteriol. 176:4765-4774(1994)

RR EMBL X25317; AAA24046.1

SQ SEQUENCE 15 AA: 1760 MW: 46.94 kDa; 15.66 MW: 16.61 kDa; 15.66 MW: 16.61 kDa

Query Match 27.98; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KIR 6

30 3 KIR 5

RESULT 27



[illegible]

```

Q7      5 MK 7
LB      1 MK 2

RESULT 34
C9K362
ID      Q9R5Z2      PRELIMINARY      FRT      R AA
AC      9R5Z2
DT      01-MAY-2002 (TEMPORARY, Created)
DE      01-MAY-2002 (TEMPORARY, Last sequence update)
DE      01-JUN-2002 (TEMPORARY, Last annotation update)
DE      31-000, 1A product of C9R5 (Fragment).
OS      Shigella dysenteriae.
OC      Bacterial Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Shigella
OX      NCBI_TaxID=622
RN      111
RP      SEQUENCE
RX      MEDLINE=92085248; PubMed 15609240
KA      Polard P, Popp S F, Chaudier M, Payet C
FT      2B gene expression of bacterial insertion sequence IS911.*
PI      2B. Mol. Biol. 222:465-477(1994)
FT      K-N-TER
SU      SEQUENCE      R AA: 902 MW, FEZMAF5586AE336 CRC64;

Query Match      18.2% Score 21 Db 21 Length 8;
Best Local Similarity 100.0% Prod. No. 8.3e-05;
Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps

Q7      6 MK 7
LB      1 MK 2

RESULT 35
C9Z560
ID      C9Z560      PRELIMINARY      FRT      R AA
AC      0Z560
DT      01-JAN-1998 (TEMPORARY, Created)
DE      01-JAN-1998 (TEMPORARY, Last sequence update)
DE      01-DEC-2001 (TEMPORARY, Last annotation update)
LE      Phosphoglycerate kinase (Frequent).
OS      E. coli.
OC      Bacterial Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia
OX      NCBI_TaxID=562
RN      11
RP      SEQUENCE FROM N A
RX      MEDLINE 99446199, PubMed 13207173
KA      Brissotier JC, Sauer J
FT      The YnfP gene in Escherichia coli W118 is separated from the rest of
FT      the Ynf operon by insertion of 155 elements.*
PI      DNA Seq. 9:163-188(1998)
OS      E. coli.
OX      NCBI_TaxID=562
RN      1
RP      SEQUENCE      R AA: 1000 MW, 4A50FEB044140D04 CRC64;
RX      K-N-TER
FT      1
SU      SEQUENCE      R AA: 1000 MW, 4A50FEB044140D04 CRC64;

Query Match      18.2% Score 21 Db 21 Length 8;
Best Local Similarity 100.0% Prod. No. 8.3e-05;
Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps

Q7      1 AK 2
LB      2 AK 3

```

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ID   Q56258          PRELIMINARY:          PRT:          8 AA.
AC   Q56258.1
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DI   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE   G1: DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   N11H (Fragment).
GN   N11H.
OS   Synchococcus sp. (strain POC 4801 / R6 1) (cyanobacterium)
OC   Bacteria; Cyanobacteria; Chroococcales; Cyanophyceae
CX   NCBI_TaxID: 41431
LN   111
DR   EMBL: X04609; CAA24278.1; -
FT   NON_TER
RP   SEQUENCE FROM N.A.
RC   STRAIN: R6 1
RX   MEDLINE: 99251261; PubMed: 10217599.
RA   Huang L., Lin R.F., Chu M.K., Chen H.K.
RT   "Genetization and expression of nitrogen fixation genes in the aerobic
RT   nitrogen fixing unicellular cyanobacterium Synchococcus sp. strain
RT   R6-1."
RI   Microbiology 145:743-751(1999).
DR   EMBL: AF001780; AAC33369.1; -
FT   NON_TER
RP   SEQUENCE 8 AA: 985 MW; F16854C1A041C406:R6764;
SC   QUERY Match
      18.2% Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%; Pred. No. 8.4e-05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   2 KQ 3
DB   11
      2 KQ 3

RESULT 37
Q939E0          PRELIMINARY:          PRT:          8 AA.
AC   Q939E0.1
DT   01-MAY-2000 (TrEMBLrel. 19, Created)
DI   01-MAY-2000 (TrEMBLrel. 19, Last sequence update)
DE   01-MAY-2000 (TrEMBLrel. 19, Last annotation update)
DE   Stage V spotolation protein E (Fragment).
GN   SpvE.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX   NCBI_TaxID: 1423;
LN   111
DR   EMBL: X64258; CAA45556.1; -
FT   NON_TER
RP   SEQUENCE 8 AA: 853 MW; E575A1A3321H1A6:R6C64;
SC   QUERY Match
      18.2% Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%; Pred. No. 8.4e-05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   4 KI 5
DB   11
      5 KI 6

RESULT 40
Q93SP2          PRELIMINARY:          PRT:          8 AA.
AC   Q93SP2.1
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DI   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Quaternary ammonium compound-resistance protein QacEdelta1
DE   (Fragment).
GN   QACDELTA1.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
CX   NCBI_TaxID: 287;
LN   111
DR   EMBL: X64258; CAA45556.1; -
FT   NON_TER
RP   SEQUENCE FROM N.A.

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ID   Q56246          PRELIMINARY:          PRT:          8 AA.
AC   Q56246.1
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DI   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Thermophilic proton ATPase epsilon subunit amino terminal (fragment).
GN   N11H.
OS   Synchococcus sp. (strain POC 4801 / R6 1) (cyanobacterium)
OC   Bacteria; Cyanobacteria; Chroococcales; Cyanophyceae
CX   NCBI_TaxID: 41431
LN   111
DR   EMBL: X04609; CAA24278.1; -
FT   NON_TER
RP   SEQUENCE FROM N.A.
RC   STRAIN: R6 1
RX   MEDLINE: 99251261; PubMed: 10217599.
RA   Huang L., Lin R.F., Chu M.K., Chen H.K.
RT   "Genetization and expression of nitrogen fixation genes in the aerobic
RT   nitrogen fixing unicellular cyanobacterium Synchococcus sp. strain
RT   R6-1."
RI   Microbiology 145:743-751(1999).
DR   EMBL: AF001780; AAC33369.1; -
FT   NON_TER
RP   SEQUENCE 8 AA: 985 MW; F16854C1A041C406:R6764;
SC   QUERY Match
      18.2% Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%; Pred. No. 8.4e-05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   2 KQ 3
DB   11
      2 KQ 3

RESULT 37
Q939E0          PRELIMINARY:          PRT:          8 AA.
AC   Q939E0.1
DT   01-MAY-2000 (TrEMBLrel. 21, Created)
DI   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   B64G protein (Fragment).
GN   B64G.
OS   Lactobacillus collinoides.
OC   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC   Lactobacillus.
CX   NCBI_TaxID: 43950;
LN   111
DR   EMBL: A120774; CAG31093.1; -
FT   NON_TER
RP   SEQUENCE FROM N.A.
RC   STRAIN: LMG 18853;
RA   Sackaquet N., Goulet K., Laplace J.M., Authier Y.
RT   "Characterisation of the Gal galactarase B64 protein of Lactobacillus
RT   collinoides."
RI   FEMS Microbiol. Lett. 03:05(0).
DR   EMBL: A120774; CAG31093.1; -
FT   NON_TER
RP   SEQUENCE 8 AA: 862 MW; E5A5A506A81A6:R6C64;
SC   QUERY Match
      18.2% Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%; Pred. No. 8.4e-05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   10 RS 11
DB   11
      7 RS 9

RESULT 38
Q56246          PRELIMINARY:          PRT:          8 AA.
AC   Q56246.1
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DI   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Thermophilic proton ATPase epsilon subunit amino terminal (fragment).
GN   N11H.
OS   Synchococcus sp. (strain POC 4801 / R6 1) (cyanobacterium)
OC   Bacteria; Cyanobacteria; Chroococcales; Cyanophyceae
CX   NCBI_TaxID: 41431
LN   111
DR   EMBL: X04609; CAA24278.1; -
FT   NON_TER
RP   SEQUENCE FROM N.A.

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31 1 MK 2
RESULT 47
Q15900
ID Q15900 PRELIMINARY: PRI: 8 AA.
AC Q15900
DT 01-NOV-1999 (FIREBLREL: 01, Created)
DT 01-NOV-1999 (FIREBLREL: 01, Last sequence update)
DT 01-NOV-1999 (FIREBLREL: 01, Last annotation update)
DE Runt/820t/MTG8 protein (Fragment)
SN Runt/820t/MTG8
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606
RN 111
RP SEQUENCE FROM N.A. PubMed 7919424
RA MEDLINE=95002916; PubMed 7919424;
RA Figue J.E., Galabi F.
RA "Alternative, out-of-frame run1/MTG8 transcripts are encoded by the
RT derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
M2."
KI B5004 8412115-2121(1994)
DR EMBL: S74092; AAA14144.1
FT NON-TER 1
SQ SEQUENCE 8 AA: 1667 MW: 20F414044B17244B CRC64:
Query Match 18.2% Score 21 DB 4: Length 8:
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MK 10
DB 1
7 RS 7

RESULT 48
Q15898
ID Q15898 PRELIMINARY: PRI: 8 AA.
AC Q15898
DT 01-NOV-1996 (FIREBLREL: 01, Created)
DT 01-NOV-1996 (FIREBLREL: 01, Last sequence update)
DT 01-DEC-2001 (FIREBLREL: 19, Last annotation update)
DE (Clone XPA11b) (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606
RN 111
RP SEQUENCE FROM N.A.
RA Lee C.C., Yaddan A., Weinert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.L., Chinault C.A., Balout A., Lindsay E.A., Zhao Z., Y.
RA "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RI Hum. Mol. Genet. 9:10-0(1995)
DR EMBL: 152078; AAA74888.1
FT NON-TER 1
SQ SEQUENCE 8 AA: 946 MW: 44A1140477B458B CRC64:
Query Match 18.2% Score 21 DB 4: Length 8:
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RS 11
DB 1
7 RS 8

RESULT 49
Q15888
ID Q15888 PRELIMINARY: PRI: 8 AA.
AC Q15888

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247	3	27.3	9	3	US-09-082-797-5	Sequence 5, Appl	320	3	27.3	9	4	US-09-229-037-6	Sequence 6, Appl
248	3	27.3	9	3	US-09-082-797-6	Sequence 6, Appl	321	3	27.3	9	4	US-09-311-784A-267	Sequence 267, Appl
249	3	27.3	9	3	US-09-082-797-7	Sequence 7, Appl	322	3	27.3	9	4	US-08-929-847-10	Sequence 10, Appl
250	3	27.3	9	3	US-09-082-797-8	Sequence 8, Appl	323	3	27.3	9	4	US-09-839-542B-503	Sequence 503, Appl
251	3	27.3	9	3	US-09-082-797-9	Sequence 9, Appl	324	3	27.3	9	4	US-09-839-542B-3074	Sequence 3074, Appl
252	3	27.3	9	3	US-09-082-797-13	Sequence 13, Appl	325	3	27.3	9	4	US-09-839-542B-3076	Sequence 3076, Appl
253	3	27.3	9	3	US-09-082-797-14	Sequence 14, Appl	326	3	27.3	9	4	US-09-839-542B-3119	Sequence 3119, Appl
254	3	27.3	9	3	US-09-082-797-15	Sequence 15, Appl	327	3	27.3	9	4	US-09-839-542B-3121	Sequence 3121, Appl
255	3	27.3	9	3	US-09-082-797-16	Sequence 16, Appl	328	3	27.3	9	4	US-09-839-542B-3164	Sequence 3164, Appl
256	3	27.3	9	3	US-09-082-797-17	Sequence 17, Appl	329	3	27.3	9	4	US-09-839-542B-3166	Sequence 3166, Appl
257	3	27.3	9	3	US-09-139-832-178	Sequence 178, Appl	330	3	27.3	9	4	US-09-839-542B-3209	Sequence 3209, Appl
258	3	27.3	9	3	US-09-139-832-29	Sequence 29, Appl	331	3	27.3	9	4	US-09-839-542B-3211	Sequence 3211, Appl
259	3	27.3	9	3	US-09-139-832-4	Sequence 4, Appl	332	3	27.3	9	4	US-09-839-542B-3254	Sequence 3254, Appl
260	3	27.3	9	3	US-09-225-622-9	Sequence 9, Appl	333	3	27.3	9	4	US-09-839-542B-3256	Sequence 3256, Appl
261	3	27.3	9	3	US-09-112-206-25	Sequence 221, Appl	334	3	27.3	9	4	US-09-839-542B-3302	Sequence 3302, Appl
262	3	27.3	9	3	US-09-112-206-222	Sequence 222, Appl	335	3	27.3	9	4	US-08-926-9-4-178	Sequence 178, Appl
263	3	27.3	9	3	US-09-112-206-22	Sequence 22, Appl	336	3	27.3	9	5	PCT-US93-11781-5	Sequence 5, Appl
264	3	27.3	9	3	US-09-112-206-224	Sequence 224, Appl	337	3	27.3	9	5	PCT-US94-01258-58	Sequence 58, Appl
265	3	27.3	9	3	US-09-112-206-225	Sequence 225, Appl	338	3	27.3	9	5	PCT-US94-09798-9	Sequence 9, Appl
266	3	27.3	9	3	US-09-112-206-226	Sequence 226, Appl	339	3	27.3	9	5	PCT-US95-00147-20	Sequence 20, Appl
267	3	27.3	9	3	US-09-112-206-227	Sequence 227, Appl	340	3	27.3	9	5	PCT-US95-00147-26	Sequence 26, Appl
268	3	27.3	9	3	US-09-177-245-4	Sequence 47, Appl	341	3	27.3	9	5	PCT-US95-02478-12	Sequence 12, Appl
269	3	27.3	9	3	US-09-263-975-33	Sequence 33, Appl	342	3	27.3	9	5	PCT-US95-11235-58	Sequence 58, Appl
270	3	27.3	9	3	US-09-131-643-31	Sequence 31, Appl	343	3	27.3	9	5	PCT-US95-11235-58	Sequence 58, Appl
271	3	27.3	9	3	US-09-476-482-19	Sequence 19, Appl	344	3	27.3	10	1	US-07-666-719-7	Sequence 7, Appl
272	3	27.3	9	3	US-09-504-413-9	Sequence 9, Appl	345	3	27.3	10	1	US-07-754-540-1	Sequence 1, Appl
273	3	27.3	9	3	US-09-502-603-44	Sequence 44, Appl	346	3	27.3	10	1	US-08-128-971H-5	Sequence 5, Appl
274	3	27.3	9	3	US-09-518-045-41	Sequence 41, Appl	347	3	27.3	10	1	US-08-139-034-4	Sequence 4, Appl
275	3	27.3	9	3	US-08-278-865-4	Sequence 4, Appl	348	3	27.3	10	1	US-08-115-171-4	Sequence 4, Appl
276	3	27.3	9	3	US-09-492-543-32	Sequence 32, Appl	349	3	27.3	10	1	US-08-370-648-7	Sequence 7, Appl
277	3	27.3	9	4	US-09-492-543-58	Sequence 58, Appl	350	3	27.3	10	1	US-08-212-190A-9	Sequence 9, Appl
278	3	27.3	9	4	US-09-492-543-71	Sequence 71, Appl	351	3	27.3	10	1	US-08-462-917-9	Sequence 9, Appl
279	3	27.3	9	4	US-09-492-543-113	Sequence 113, Appl	352	3	27.3	10	1	US-08-300-386A-54	Sequence 54, Appl
280	3	27.3	9	4	US-09-492-543-114	Sequence 114, Appl	353	3	27.3	10	1	US-08-190-801-1	Sequence 1, Appl
281	3	27.3	9	4	US-09-492-543-172	Sequence 172, Appl	354	3	27.3	10	1	US-08-704-170-41	Sequence 41, Appl
282	3	27.3	9	4	US-08-505-265-29	Sequence 29, Appl	355	3	27.3	10	2	US-08-531-662B-7	Sequence 7, Appl
283	3	27.3	9	4	US-09-187-859-503	Sequence 503, Appl	356	3	27.3	10	2	US-08-764-640-60	Sequence 60, Appl
284	3	27.3	9	4	US-09-187-859-504	Sequence 504, Appl	357	3	27.3	10	2	US-08-602-864-1	Sequence 1, Appl
285	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	358	3	27.3	10	2	US-08-556-597-86	Sequence 86, Appl
286	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	359	3	27.3	10	2	US-08-556-597-98	Sequence 98, Appl
287	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	360	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
288	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	361	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
289	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	362	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
290	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	363	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
291	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	364	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
292	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	365	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
293	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	366	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
294	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	367	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
295	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	368	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
296	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	369	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
297	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	370	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
298	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	371	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
299	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	372	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
300	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	373	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
301	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	374	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
302	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	375	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
303	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	376	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
304	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	377	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
305	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	378	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
306	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	379	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
307	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	380	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
308	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	381	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
309	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	382	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
310	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	383	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
311	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	384	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
312	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	385	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
313	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	386	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
314	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	387	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
315	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	388	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
316	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	389	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
317	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	390	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
318	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	391	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl
319	3	27.3	9	4	US-09-187-859-576	Sequence 576, Appl	392	3	27.3	10	2	US-08-556-597-141	Sequence 141, Appl

443	3	27.3	10	3	US-08-085-449-6	Sequence 6, Appl 1	466	4	27.3	10	6	5171838-8	Patent No. 5171838
444	3	27.3	10	3	US-09-114-921-62	Sequence 12, Appl 1	467	3	27.3	10	6	5179097-17	Patent No. 5179097
445	3	27.3	10	3	US-09-113-921-63	Sequence 13, Appl 1	468	3	27.3	10	6	5204096-31	Patent No. 5204096
446	3	27.3	10	3	US-09-486-442-11	Sequence 11, Appl 1	469	3	27.3	11	1	US-07-666-719-18	Sequence 18, Appl 1
447	3	27.3	10	3	US-08-843-574-5	Sequence 5, Appl 1	470	3	27.3	11	1	US-07-755-161A-9	Sequence 9, Appl 1
448	3	27.3	10	3	US-09-315-344-66	Sequence 5, Appl 1	471	3	27.3	11	1	US-07-841-474-9	Sequence 9, Appl 1
449	3	27.3	10	3	US-09-320-904-20	Sequence 4, Appl 1	472	3	27.3	11	1	US-08-646-538-1	Sequence 1, Appl 1
450	3	27.3	10	3	US-09-253-945-22	Sequence 12, Appl 1	473	3	27.3	11	1	US-08-197-795-5	Sequence 5, Appl 1
451	3	27.3	10	3	US-09-263-975-34	Sequence 14, Appl 1	474	3	27.3	11	1	US-08-128-971B-15	Sequence 15, Appl 1
452	3	27.3	10	3	US-09-116-704-60	Sequence 1, Appl 1	475	3	27.3	11	1	US-08-476-875-3	Sequence 3, Appl 1
453	3	27.3	10	3	US-09-152-942-26	Sequence 2, Appl 1	476	3	27.3	11	1	US-08-318-935-3	Sequence 3, Appl 1
454	3	27.3	10	3	US-09-151-649-42	Sequence 5, Appl 1	477	3	27.3	11	1	US-08-483-932-3	Sequence 3, Appl 1
455	3	27.3	10	3	US-08-133-964-30	Sequence 1, Appl 1	478	3	27.3	11	1	US-08-256-771-32	Sequence 32, Appl 1
456	3	27.3	10	3	US-09-534-433-1	Sequence 1, Appl 1	479	3	27.3	11	1	US-08-462-977-10	Sequence 10, Appl 1
457	3	27.3	10	3	US-08-278-805-3	Sequence 1, Appl 1	480	3	27.3	11	1	US-08-483-140-4	Sequence 3, Appl 1
458	3	27.3	10	3	US-09-017-634A-1	Sequence 6, Appl 1	481	3	27.3	11	1	US-08-323-531-32	Sequence 32, Appl 1
459	3	27.3	10	3	US-09-167-869-677	Sequence 5, Appl 1	482	3	27.3	11	1	US-08-548-540-145	Sequence 145, Appl 1
460	3	27.3	10	3	US-09-167-869-678	Sequence 6, Appl 1	483	3	27.3	11	1	US-08-548-540-160	Sequence 160, Appl 1
461	3	27.3	10	3	US-09-167-869-679	Sequence 7, Appl 1	484	3	27.3	11	1	US-08-198-094-32	Sequence 32, Appl 1
462	3	27.3	10	3	US-09-167-869-680	Sequence 8, Appl 1	485	3	27.3	11	1	US-08-732-970-2	Sequence 2, Appl 1
463	3	27.3	10	3	US-09-167-869-681	Sequence 9, Appl 1	486	3	27.3	11	1	US-08-381-984-32	Sequence 12, Appl 1
464	3	27.3	10	3	US-09-167-869-682	Sequence 10, Appl 1	487	3	27.3	11	1	US-08-669-721-16	Sequence 16, Appl 1
465	3	27.3	10	3	US-09-167-869-683	Sequence 11, Appl 1	488	3	27.3	11	1	US-08-485-938A-3	Sequence 3, Appl 1
466	3	27.3	10	3	US-09-167-869-684	Sequence 12, Appl 1	489	3	27.3	11	1	US-08-464-182A-11	Sequence 11, Appl 1
467	3	27.3	10	3	US-09-167-869-685	Sequence 13, Appl 1	490	3	27.3	11	1	US-08-464-182A-12	Sequence 12, Appl 1
468	3	27.3	10	3	US-09-167-869-686	Sequence 14, Appl 1	491	3	27.3	11	1	US-08-693-274A-3	Sequence 3, Appl 1
469	3	27.3	10	3	US-09-167-869-687	Sequence 15, Appl 1	492	3	27.3	11	1	US-08-693-274A-4	Sequence 4, Appl 1
470	3	27.3	10	3	US-09-167-869-688	Sequence 16, Appl 1	493	3	27.3	11	1	US-08-693-274A-5	Sequence 5, Appl 1
471	3	27.3	10	3	US-09-167-869-689	Sequence 17, Appl 1	494	3	27.3	11	1	US-08-693-274A-6	Sequence 6, Appl 1
472	3	27.3	10	3	US-09-167-869-690	Sequence 18, Appl 1	495	3	27.3	11	1	US-08-693-274A-7	Sequence 7, Appl 1
473	3	27.3	10	3	US-09-167-869-691	Sequence 19, Appl 1	496	3	27.3	11	1	US-08-693-274A-8	Sequence 8, Appl 1
474	3	27.3	10	3	US-09-167-869-692	Sequence 20, Appl 1	497	3	27.3	11	1	US-08-693-274A-9	Sequence 9, Appl 1
475	3	27.3	10	3	US-09-167-869-693	Sequence 21, Appl 1	498	3	27.3	11	1	US-08-693-274A-10	Sequence 10, Appl 1
476	3	27.3	10	3	US-09-167-869-694	Sequence 22, Appl 1	499	3	27.3	11	1	US-08-693-274A-11	Sequence 11, Appl 1
477	3	27.3	10	3	US-09-167-869-695	Sequence 23, Appl 1	500	3	27.3	11	1	US-08-693-274A-12	Sequence 12, Appl 1
478	3	27.3	10	3	US-09-167-869-696	Sequence 24, Appl 1	501	3	27.3	11	1	US-08-693-274A-13	Sequence 13, Appl 1
479	3	27.3	10	3	US-09-167-869-697	Sequence 25, Appl 1	502	3	27.3	11	1	US-08-693-274A-14	Sequence 14, Appl 1
480	3	27.3	10	3	US-09-167-869-698	Sequence 26, Appl 1	503	3	27.3	11	1	US-08-693-274A-15	Sequence 15, Appl 1
481	3	27.3	10	3	US-09-167-869-699	Sequence 27, Appl 1	504	3	27.3	11	1	US-08-693-274A-16	Sequence 16, Appl 1
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485	3	27.3	10	3	US-09-167-869-703	Sequence 31, Appl 1	508	3	27.3	11	1	US-08-693-274A-20	Sequence 20, Appl 1
486	3	27.3	10	3	US-09-167-869-704	Sequence 32, Appl 1	509	3	27.3	11	1	US-08-693-274A-21	Sequence 21, Appl 1
487	3	27.3	10	3	US-09-167-869-705	Sequence 33, Appl 1	510	3	27.3	11	1	US-08-693-274A-22	Sequence 22, Appl 1
488	3	27.3	10	3	US-09-167-869-706	Sequence 34, Appl 1	511	3	27.3	11	1	US-08-693-274A-23	Sequence 23, Appl 1
489	3	27.3	10	3	US-09-167-869-707	Sequence 35, Appl 1	512	3	27.3	11	1	US-08-693-274A-24	Sequence 24, Appl 1
490	3	27.3	10	3	US-09-167-869-708	Sequence 36, Appl 1	513	3	27.3	11	1	US-08-693-274A-25	Sequence 25, Appl 1
491	3	27.3	10	3	US-09-167-869-709	Sequence 37, Appl 1	514	3	27.3	11	1	US-08-693-274A-26	Sequence 26, Appl 1
492	3	27.3	10	3	US-09-167-869-710	Sequence 38, Appl 1	515	3	27.3	11	1	US-08-693-274A-27	Sequence 27, Appl 1
493	3	27.3	10	3	US-09-167-869-711	Sequence 39, Appl 1	516	3	27.3	11	1	US-08-693-274A-28	Sequence 28, Appl 1
494	3	27.3	10	3	US-09-167-869-712	Sequence 40, Appl 1	517	3	27.3	11	1	US-08-693-274A-29	Sequence 29, Appl 1
495	3	27.3	10	3	US-09-167-869-713	Sequence 41, Appl 1	518	3	27.3	11	1	US-08-693-274A-30	Sequence 30, Appl 1
496	3	27.3	10	3	US-09-167-869-714	Sequence 42, Appl 1	519	3	27.3	11	1	US-08-693-274A-31	Sequence 31, Appl 1
497	3	27.3	10	3	US-09-167-869-715	Sequence 43, Appl 1	520	3	27.3	11	1	US-08-693-274A-32	Sequence 32, Appl 1
498	3	27.3	10	3	US-09-167-869-716	Sequence 44, Appl 1	521	3	27.3	11	1	US-08-693-274A-33	Sequence 33, Appl 1
499	3	27.3	10	3	US-09-167-869-717	Sequence 45, Appl 1	522	3	27.3	11	1	US-08-693-274A-34	Sequence 34, Appl 1
500	3	27.3	10	3	US-09-167-869-718	Sequence 46, Appl 1	523	3	27.3	11	1	US-08-693-274A-35	Sequence 35, Appl 1

## ALIGNMENTS

## RESULT 1

: Sequence 65, Application US/595431  
 : Patent No. 595431  
 : GENERAL INFORMATION:  
 : APPLICANT: Stevens, Richard L.  
 : APPLICANT: Huang, Chifu  
 : TITLE OF INVENTION: FAST CELL PROTEASE PEPTIDE  
 : TITLE OF INVENTION: INHIBITORS  
 : NUMBER OF SEQUENCES: 65  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: M&L Groenfield & Sacks, P.C.  
 : STREET: 603 Atlantic Avenue  
 : CITY: Boston  
 : STATE: MA  
 : COUNTRY: U.S.A.  
 : ZIP: 02210-2211  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ for Windows Version 2.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/016,366A  
 : FILING DATE: January 30, 1998  
 : CLASSIFICATION: 53C  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 60/037,090  
 : FILING DATE: 05 FEB 1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Plummer, Elizabeth R.  
 : REGISTRATION NUMBER: 36,637  
 : REFERENCE/DOCKET NUMBER: B0801/7093



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1  LENGTH: 8
2  SEQ ID NO: 8
3  LENGTH: 8
4  TYPE: PR1
5  ORGANISM: Artificial Sequence
6  FEATURE:
7  NAME/KEY: SITE
8  LOCATION: (1)
9  OTHER INFORMATION: THIS IS D-LYSINE
10 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: ANALOG OF
11 OTHER INFORMATION: NEUROTENSIN
12 US 09 484 423 7

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Query Match: 36.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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Q7 7 KRR 10
11
12 1 KRR 4

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RESULT 8
US 09 484 423 7
1 Sequence 7, Application US/0944423
2 Patent No. 6264941
3 GENERAL INFORMATION:
4 APPLICANT: Achillevu, Samuel
5 APPLICANT: Rajagopalan, Radhavan
6 APPLICANT: Bouda, Joseph E.
7 TITLE OF INVENTION: NOVEL INDOXYANINE DYES
8 FILE REFERENCE: DNA STRING
9 CURRENT APPLICATION NUMBER: US/09/44423
10 NUMBER OF SEQ ID NOS: 8
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO: 7
13 LENGTH: 8
14 TYPE: PR1
15 FEATURE:
16 NAME/KEY: SITE
17 LOCATION: (1)
18 OTHER INFORMATION: THIS IS D-LYSINE
19 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: ANALOG OF
20 OTHER INFORMATION: NEUROTENSIN
21 US 09 484 423 7

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Query Match: 36.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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Q7 7 KRR 10
11
12 1 KRR 4

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RESULT 7
US 09 425 769 6
1 Sequence 8, Application US/09425769
2 Patent No. 6264948
3 GENERAL INFORMATION:
4 APPLICANT: Achillevu, Samuel
5 APPLICANT: Bouda, Joseph E.
6 APPLICANT: Rajagopalan, Radhavan
7 TITLE OF INVENTION: NOVEL CYANINE AND XANTHENE DYE FOR BIOMEDICAL APPLICATIONS
8 FILE REFERENCE: 1998-206
9 CURRENT APPLICATION NUMBER: US/09/425769
10 NUMBER OF SEQ ID NOS: 8
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO: 8
13 LENGTH: 8
14 TYPE: PR1
15 FEATURE:
16 NAME/KEY: SITE
17 LOCATION: (1)
18 OTHER INFORMATION: THIS IS D-LYSINE
19 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: ANALOG OF
20 OTHER INFORMATION: NEUROTENSIN
21 US 09 484 423 7

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1  LENGTH: 8
2  SEQ ID NO: 8
3  LENGTH: 8
4  TYPE: PR1
5  ORGANISM: Artificial Sequence
6  FEATURE:
7  NAME/KEY: SITE
8  LOCATION: (1)
9  OTHER INFORMATION: THIS IS D-LYSINE
10 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: ANALOG OF
11 OTHER INFORMATION: NEUROTENSIN
12 US 09 425 769 6

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Query Match: 36.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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Q7 7 KRR 10
11
12 1 KRR 4

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RESULT 8
US 09 436 170 7
1 Sequence 7, Application US/09436170
2 Patent No. 6264949
3 GENERAL INFORMATION:
4 APPLICANT: Achillevu, Samuel
5 APPLICANT: Rajagopalan, Radhavan
6 APPLICANT: Bouda, Joseph E.
7 TITLE OF INVENTION: NOVEL INDOXYANINE DYES
8 FILE REFERENCE: DNA STRING
9 CURRENT APPLICATION NUMBER: US/09/436170
10 CURRENT FILING DATE: 2000-08-10
11 NUMBER OF SEQ ID NOS: 8
12 SOFTWARE: Patent In Ver. 2.1
13 SEQ ID NO: 7
14 LENGTH: 8
15 TYPE: PR1
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 NAME/KEY: SITE
19 LOCATION: (1)
20 OTHER INFORMATION: THIS IS D-LYSINE
21 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: ANALOG OF
22 OTHER INFORMATION: NEUROTENSIN
23 US 09 646 170 7

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Query Match: 36.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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Q7 7 KRR 10
11
12 1 KRR 4

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RESULT 9
US 09 646 170 7
1 Sequence 7, Application US/09646170
2 Patent No. 6264920
3 GENERAL INFORMATION:
4 APPLICANT: Achillevu, Samuel
5 APPLICANT: Rajagopalan, Radhavan
6 APPLICANT: Bouda, Joseph E.
7 TITLE OF INVENTION: Durable Indocyanine Dyes For Biomedical Applications
8 FILE REFERENCE: 1998-206
9 CURRENT APPLICATION NUMBER: US/09/646170
10 CURRENT FILING DATE: 2000-08-10
11 NUMBER OF SEQ ID NOS: 8
12 SOFTWARE: Patent In Ver. 2.1
13 SEQ ID NO: 7
14 LENGTH: 8
15 TYPE: PR1
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 NAME/KEY: SITE
19 LOCATION: (1)
20 OTHER INFORMATION: THIS IS D-LYSINE
21 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: ANALOG OF
22 OTHER INFORMATION: NEUROTENSIN
23 US 09 646 170 7

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SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 7
LENGTH: 6
TYPE: IRT Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: EHS IS D-LYSINE.
OTHER INFORMATION: NEUTROENIN
US 09-547 544 7

Query Match: 36.4% Score 4: 100.0% Seq ID NO: 7
Best Local Similarity 100.0% Pred. No. 1.2e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPR 10
DB 1 KPR 4

RESULT 10
US 08 141 324 6
Sequence 6, Application US/08141324
Patent No. 5475097
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Poteempa, Jan S.
APPLICANT: Bart, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-Specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Greenlee and Wagner, P.C.
STREET: 5470 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1994
CLASSIFICATION: 4.45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Donna M.
REGISTRATION NUMBER: 43,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANEGNESS: single
TOPOLOGY: linear
MUTABLE TYPE: peptide
HYDROPHILIC: NO
US 08 141-324 6

Query Match: 36.4% Score 4: 100.0% Seq ID NO: 6
Best Local Similarity 100.0% Pred. No. 1.2e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPR 10
DB 1 KPR 4

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III,
5 KPR 8

RESULT 11
US 08 541 902 6
Sequence 6, Application US/08541902
Patent No. 5757620
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Poteempa, Jan S.
APPLICANT: Bart, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-Specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Greenlee and Wagner, P.C.
STREET: 5470 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,902
FILING DATE:
CLASSIFICATION: 4.45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Donna M.
REGISTRATION NUMBER: 43,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANEGNESS: single
TOPOLOGY: linear
MUTABLE TYPE: peptide
HYDROPHILIC: NO
US 08 541-902 6

Query Match: 36.4% Score 4: 100.0% Seq ID NO: 6
Best Local Similarity 100.0% Pred. No. 1.2e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPR 10
DB 5 KPR 9

RESULT 12
US 08 546 554 52
Sequence 52, Application US/08655456
Patent No. 5965536
GENERAL INFORMATION:
APPLICANT: Cohen, Allen B.
APPLICANT: Miller, Edmund J.
APPLICANT: Kardowska, Anna
APPLICANT: Bayashi, Shinichiro
APPLICANT: Tattler, Ronald R.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXc INTERCRINE

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1 TITLE OF INVENTION: MOLECULES  
 2 NUMBER OF SEQUENCES: 58  
 3 CORRESPONDENCE ADDRESS:  
 4 ADDRESSEE: Arnold, White & Burke  
 5 STREET: P.O. Box 4433  
 6 CITY: Houston  
 7 STATE: Texas  
 8 COUNTRY: USA  
 9 ZIP: 77210  
 10  
 11 COMPUTER READABLE FORM:  
 12 MEDIUM TYPE: Floppy disk  
 13 COMPUTER: IBM PC compatible  
 14 OPERATING SYSTEM: PC DOS/MS DOS  
 15 SOFTWARE: Patent in Release #1.0, Version #1.30  
 16  
 17 CURRENT APPLICATION DATA:  
 18 APPLICATION NUMBER: US/08/665,472  
 19 FILING DATE: 14 JUN 1996  
 20 CLASSIFICATION: 530  
 21 PRIORITY APPLICATION DATA:  
 22 APPLICATION NUMBER: PCT/US95/12245  
 23 FILING DATE: 15 DEC 1993  
 24 ATTORNEY/AGENT INFORMATION:  
 25 NAME: Kitchell, Barbara S.  
 26 REGISTRATION NUMBER: 33,928  
 27 REFERENCE/DOCKET NUMBER: USN:020  
 28 TELECOMMUNICATION INFORMATION:  
 29 TELEPHONE: 512/474-7577  
 30 TELEFAX: 512/474-7577  
 31 INFORMATION FOR SEQ ID NO: 52:  
 32 SEQUENCE CHARACTERISTICS:  
 33 LENGTH: 12 amino acids  
 34 TYPE: amino acid  
 35 STRANDEDNESS:  
 36 TOPOLGY: Linear  
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 38 US 08-665,564 52  
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1 TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEGRADING ENZYME  
 2 FILE REFERENCE: 1422-468P  
 3 CURRENT APPLICATION NUMBER: US/09/404,832  
 4 CURRENT FILING DATE: 1998-12-21  
 5 NUMBER OF SEQ ID NOS: 17  
 6 SOFTWARE: Patent In Ver. 2.0  
 7 SEQ ID NO 4  
 8 LENGTH: 12  
 9 TYPE: PRT  
 10 ORGANISM: Artificial Sequence  
 11 FEATURE:  
 12 OTHER INFORMATION: Xaa = N pyrrolidyl leucine  
 13 FEATURE:  
 14 OTHER INFORMATION: Description of Artificial Sequence: Reiterations  
 15 OTHER INFORMATION: manufactured by peptide technologies, Inc.  
 16 US 09-202-832-4

Query Match: 36.4% Score 4: 0b 4: Length 12:  
 Best Local Similarity 100.0% Pred. No. 1,2a-02:  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 7 PPRS 10  
 1111  
 DB 5 PPRS 8

RESULT 15  
 US-09-650-438-52  
 1 Sequence 52: Application US/09/504,438  
 2 Patent No. 6456639  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Miller, Edmund J.  
 5 TITLE OF INVENTION: PEPTIDE INHIBITING CELL GROWTH INHIBITORS  
 6 NUMBER OF SEQUENCES: 58  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Arnold, White & Durkee  
 9 STREET: P.O. Box 4433  
 10 CITY: Houston  
 11 STATE: Texas  
 12 COUNTRY: USA  
 13 ZIP: 77210  
 14 COMPUTER READABLE FORM:  
 15 MEDIUM TYPE: Floppy disk  
 16 COMPUTER: IBM PC compatible  
 17 OPERATING SYSTEM: PC-DOS/MS-DOS  
 18 SOFTWARE: Patent In Ver. 2.0, Version 4.1.0  
 19 CURRENT APPLICATION DATA:  
 20 APPLICATION NUMBER: US/09/504,438  
 21 FILING DATE: 29-Aug-2000  
 22 CLASSIFICATION: C08K6/20

PRI-9 APPLICATION DATA:  
 1 APPLICATION NUMBER: 09/605,117  
 2 FILING DATE: <Unknown>  
 3 ATTORNEY/AGENT INFORMATION:  
 4 NAME: Kitchell, Barbara S.  
 5 REGISTRATION NUMBER: 31,928  
 6 REFERENCE/DOCKET NUMBER: 0755-020  
 7 TELECOMMUNICATION INFORMATION:  
 8 TELEPHONE: 512/418-3500  
 9 TELEFAX: 512/474-7577  
 10 INFORMATION FOR SEQ ID NO: 52:  
 11 SEQUENCE CHARACTERISTICS:  
 12 LENGTH: 12 amino acids  
 13 TYPE: amino acid  
 14 STRANDEDNESS: <Unknown>  
 15 TOPOLOGY: linear  
 16 SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US 09-650-438-52  
 Query Match: 36.4% Score 4: 0b 4: Length 12:  
 Best Local Similarity 100.0% Pred. No. 1,2a-02:  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 PPRS 11  
 1111  
 DB 3 PPRS 6  
 RESULT 17  
 PCT US93-12245-52  
 1 Sequence 52: Application PCT/US93/12245  
 2 GENERAL INFORMATION:  
 3 APPLICANT: Cohen, Allen B.  
 4 APPLICANT: Miller, Edmund J.  
 5 APPLICANT: KUPCANSKA, Anna  
 6 APPLICANT: HAYASHI, Shinichiro  
 7 APPLICANT: JOTTLE, Ronald R.  
 8 TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXC  
 9 TITLE OF INVENTION: INTERFERING MOLECULES  
 10 NUMBER OF SEQUENCES: 58  
 11 CORRESPONDENCE ADDRESS:  
 12 ADDRESSEE: Arnold, White & Durkee  
 13 STREET: P.O. Box 4433  
 14 CITY: Houston  
 15 STATE: Texas  
 16 COUNTRY: USA  
 17 ZIP: 77210  
 18 COMPUTER READABLE FORM:  
 19 MEDIUM TYPE: Floppy disk  
 20 COMPUTER: IBM PC compatible  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
 22 SOFTWARE: WordPerfect 5.1  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: PCT/US93/12245  
 25 FILING DATE: Concurrently herewith  
 26 CLASSIFICATION:  
 27 ATTORNEY/AGENT INFORMATION:  
 28 NAME: Kitchell, Barbara S.  
 29 REGISTRATION NUMBER: 31,928  
 30 REFERENCE/DOCKET NUMBER: C1FN016PCT  
 31 TELECOMMUNICATION INFORMATION:  
 32 TELEPHONE: (512) 320-7250  
 33 TELEFAX: (713) 789-2679  
 34 TELEX: 79-0924  
 35 INFORMATION FOR SEQ ID NO: 52:  
 36 SEQUENCE CHARACTERISTICS:  
 37 LENGTH: 12 amino acids  
 38 TYPE: amino acid  
 39 STRANDEDNESS: single  
 40 TOPOLOGY: linear  
 41 MOLECULE TYPE: peptide  
 42 PCT US93-12245-52

Query Match: 36.4% Score 4: 0b 5: Length 12:  
 Best Local Similarity 100.0% Pred. No. 1,2a-02:  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 PPRS 11  
 1111  
 DB 3 PPRS 6

RESULT 18  
 US-07-714-540-8  
 1 Sequence 6: Application US/97/714542  
 2 Patent No. 5262521  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Almquist, Ronald G.  
 5 APPLICANT: Toll, Lawrence  
 6 TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING  
 7 TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF  
 8 NUMBER OF SEQUENCES: 13  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: Irell & Manella

STREET: 545 Modettefield Road, Suite 200  
 CITY: Malibu Park  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90265  
 COM-01116 RELEASABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version # 1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/01/11,540  
 FILING DATE: 19910607  
 CLASSIFICATION: 514  
 AGENCY/AGENT INFORMATION:  
 NAME: Reed, Dianne E.  
 REGISTRATION NUMBER: 41,492  
 REFERENCE/DRAWN NUMBER: 8500,550,000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE NO: 415-427-2259  
 TELEFAX NO: 415-427-2951  
 TELEX: 796141  
 INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: AMIN-ACID  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MEDIUM TYPE: protein  
 US-09-787-443-12

Query Match: 36.4% Score 47 DB 1 Length 13  
 Best local Similarity: 100.0% Prd. No. 1 4e-02  
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 6 KPRR 9

RESULT 19  
 US-09-787-443-12  
 Sequence 117, Application US/04428400  
 Patent No. 5,246,64  
 GENERAL INFORMATION:  
 APPLICANT: BRUNN, Nicholas S.  
 TITLE OF INVENTION: BRAIN-ENHANCING COMPOSITIONS  
 TITLE OF INVENTION: BRAIN-ENHANCING COMPOSITIONS  
 NUMBER OF INVENTION: PUBLISHED BY US/04428400  
 NUMBER OF SEQUENCES: 107  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brunns, Dianne, S.  
 STREET: P.O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22115-1404  
 COM-01116 RELEASABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version # 1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/48,466  
 FILING DATE: 27-APR 1995  
 CLASSIFICATION: 514  
 AGENCY/AGENT INFORMATION:  
 NAME: Baumgister, Mary Kat  
 REGISTRATION NUMBER: 26,254  
 REFERENCE/DRAWN NUMBER: G067,4 180  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 FEATURES:  
 NAME/KEY: Modified site  
 LOCATION: 1  
 OTHER INFORMATION: /code "Position 1 p-Glu"  
 FEATURES:  
 NAME/KEY: Modified site  
 LOCATION: 1  
 OTHER INFORMATION: /code "Position 13 Leu-OH"  
 US-09-787-443-12

Query Match: 36.4% Score 47 DB 1 Length 13  
 Best local Similarity: 100.0% Prd. No. 1 4e-02  
 Matches: 4: Conservative 0: Mismatches 0: Gaps 0

35 7 KPRR 10  
 36 11  
 6 KPRR 9

RESULT 20  
 US-09-787-443-12  
 Sequence 117, Application US/08747147  
 Patent No. 5,945,034  
 GENERAL INFORMATION:  
 APPLICANT: YEN, Richard C.K.  
 TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
 NUMBER OF SEQUENCES: 184  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, 8th Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/747,147  
 FILING DATE: 12 NOV 1998  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/212,546  
 FILING DATE: 14 MAR 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/069,931  
 FILING DATE: 01 JUN 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/959,560  
 FILING DATE: 13 OCT 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/641,720  
 FILING DATE: 15 JAN 1991  
 AGENCY/AGENT INFORMATION:  
 NAME: Apple, Randolph L.  
 REGISTRATION NUMBER: 45,429  
 REFERENCE/DRAWN NUMBER: G16197-00084005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415 576-7200  
 INFORMATION FOR SEQ ID NO: 117:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Not relevant

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FEATURES: not relevant
NAME/KEY: Modified-site
DETECTION: 1
OTHER INFORMATION: /product "P-Glu"
US-08-747-137-117

Query Match: 36.4%, Score: 1, ID: 1, Length: 13
Best Local Similarity: 100.0%, Pred. No. 1.3e+02
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY: 7 KRR 10
ID: 11
6 KRR 9

RESULT 23
US-08-747-299A
Sequence 1, Application US/08747299A
Patent No. 5952454
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,299A
FILING DATE: 21 JUL 1997
CLASSIFICATION: 540
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/02153
FILING DATE: 21 FEB 1995
ATTORNEY/AGENT INFORMATION:
NAME: Jeffrey S. Boone
REGISTRATION NUMBER: 29284
REFERENCE/DCKET NUMBER: Mergatw 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 654-4156
TELEFAX: (314) 654-8065
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
STRANDNESS: not relevant
POLARITY: not relevant
FEATURE TYPE: internal
FEATURE:
NAME/KEY: Modified-site
DETECTION: 1
OTHER INFORMATION: /product "P-Glu"
US-08-747-299A 1

Query Match: 36.4%, Score: 1, ID: 1, Length: 13
Best Local Similarity: 100.0%, Pred. No. 1.3e+02
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY: 7 KRR 10
ID: 11
6 KRR 9

RESULT 24
US-08-747-254A 1
Sequence 1, Application US/08747254A
Patent No. 6194486
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

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RESULT 22
US-08-817-869 6
Sequence 6, Application US/08817869
Patent No. 6501970
GENERAL INFORMATION:
APPLICANT: STRASSER, CATHERINE D.
APPLICANT: CASARDO, MARGARET A.
APPLICANT: MAWELL, DOUGLAS J.
TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM H. NUTBOLS IN
STREET: 121 EAST LINCOLN AVENUE
CITY: RAINWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07069-1900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/345,017
FILING DATE: 27 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: NICHOLSON, WILLIAM H.
REGISTRATION NUMBER: 25,147
REFERENCE/DCKET NUMBER: 19419Y PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-1348
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDNESS: single
POLARITY: linear
MOLECULE TYPE: peptide
US-08-817-869-6

Query Match: 36.4%, Score: 4, ID: 3, Length: 13
Best Local Similarity: 100.0%, Pred. No. 1.3e+02
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY: 2 KRR 1
ID: 11
9 KRR 12

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```

1  SOFTWARE: Patent In Release #14, Ver. 0.0.1
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/09/787-443-12
4  FILING DATE:
5  CLASSIFICATION:
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: 09/787-443
8  FILING DATE:
9  ATTORNEY/AGENT INFORMATION:
10 NAME: Jeffrey S. Boone
11 REGISTRATION NUMBER: 29294
12 REFERENCE/ID # KEY NUMBER: 6063 W. 18
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: 1 (314) 654-8956
15 TELEFAX: 1 (314) 654-3156
16 INFORMATION FOR SEQ ID NO: 1:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 13 amino acids
19 TYPE: amino acid
20 STRANDNESS: not relevant
21 FEATURE: not relevant
22 MOLECULE TYPE: peptide
23 FRAGMENT TYPE: internal
24 FEATURE:
25 NAME/KEY: Modified site
26 LOCATION: 1
27 OTHER INFORMATION: /product: "PYROGLUTAMATE"
US-09-787-443-12

```

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Query Match: 96.4%; Score 4; DB 1; Length 13;
Best Local Similarity: 100.0%; Pred. No. 1.3e-02;
Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

```

```

47 7 KRR 10
111
112 6 KRR 9

```

```

RESULT 24
US-09-787-443-12
1  Sequence: Application US/09/289-693-1
2  Patent No. 6214794
3  GENERAL INFORMATION:
4  APPLICANT: Richardson, Elliott
5  APPLICANT: Casack, Bernadette Marie
6  APPLICANT: Egan, Yuan-Ping
7  APPLICANT: McSwicker, Daniel J.
8  APPLICANT: Fard, Abdul
9  APPLICANT: Taylor, Beth Marie
10 APPLICANT: Boudreau, M. and
11 FILE REFERENCE: 07/09/041003
12 TITLE OF INVENTION: NO. 1387001-1
13 CURRENT APPLICATION NUMBER: US/09/289-693-1
14 EARLIER FILING DATE: 1999-04-09
15 EARLIER APPLICATION NUMBER: US 60/114,117
16 EARLIER FILING DATE: 1998-12-14
17 EARLIER APPLICATION NUMBER: US 60/298,119
18 EARLIER FILING DATE: 1998-08-27
19 EARLIER APPLICATION NUMBER: US 60/066,100
20 EARLIER FILING DATE: 1998-07-09
21 EARLIER APPLICATION NUMBER: US 60/061,000
22 EARLIER FILING DATE: 1998-04-20
23 NUMBER OF SEQ ID NOS: 30
24 SOFTWARE: FASTSEQ for Windows Version 4
25 SEQ ID NO: 1
26 LENGTH: 13
27 TYPE: PSI
28 ORGANISM: Artificial Sequence
29 FEATURE:
30 OTHER INFORMATION: N: Synthesized by Genentech for L.A.
31 FEATURE:
32 NAME/KEY: SITE
33 LOCATION: (1)-(11)

```

```

1  OTHER INFORMATION: Xaa - pyrrolidone carboxylic acid
2  US-09-289-693-1
3  Query Match: 96.4%; Score 4; DB 3; Length 13;
4  Best Local Similarity: 100.0%; Pred. No. 1.3e-02;
5  Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
6  QY 7 KRR 10
7  11
8  6 KRR 9
9  RESULT 25
10 US-09-355-869-2
11 Sequence: Application US/09/355-869-2
12 Patent No. 6332663
13 GENERAL INFORMATION:
14 APPLICANT: Regent, Gene Therapeutic
15 TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF MALIGNANT
16 TITLE OF INVENTION: HUMAN TUMORS
17 FILE REFERENCE: 1608, 614
18 CURRENT APPLICATION NUMBER: US/09/355-869-2
19 EARLIER FILING DATE: 1999-09-04
20 EARLIER APPLICATION NUMBER: PCT/US95/01964
21 EARLIER FILING DATE: 1996-02-04
22 EARLIER APPLICATION NUMBER: EP 97200247.6
23 EARLIER FILING DATE: 1997-02-04
24 NUMBER OF SEQ ID NOS: 4
25 SOFTWARE: Patent In Ver. 2.0
26 SEQ ID NO: 2
27 LENGTH: 14
28 TYPE: PSI
29 ORGANISM: Homo sapiens
30 FEATURE:
31 NAME/KEY: SITE
32 LOCATION: (1)
33 OTHER INFORMATION: This site is pyroglutamate.
US-09-355-869-2

```

```

Query Match: 96.4%; Score 4; DB 4; Length 13;
Best Local Similarity: 100.0%; Pred. No. 1.3e-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

```

QY 7 KRR 10
11
112 6 KRR 9

```

```

RESULT 26
US-09-355-869-2
1  Sequence: Application US/09/355-869-2
2  Patent No. 6344551
3  GENERAL INFORMATION:
4  APPLICANT: Craid, A. Grey
5  APPLICANT: Griffin, David
6  APPLICANT: Oliveira, Baldomero M.
7  APPLICANT: Watkins, Maren
8  APPLICANT: Riley, David R.
9  APPLICANT: Imperial, Julia
10 APPLICANT: Cruz, Lourdes J.
11 APPLICANT: Wagstaff, John D.
12 APPLICANT: Layer, Richard L.
13 APPLICANT: Jones, Robert M.
14 APPLICANT: McCabe, R. Tyron
15 APPLICANT: Cognetix, Inc.
16 APPLICANT: University of Utah Research Foundation
17 APPLICANT: Salk Institute
18 TITLE OF INVENTION: Controlling
19 FILE REFERENCE: Controlling
20 CURRENT APPLICATION NUMBER: US/09/355-869-2
21 EARLIER FILING DATE: 2003-06-29
22 EARLIER APPLICATION NUMBER: US 09/420,797
23 EARLIER FILING DATE: 1999-10-19

```

1 PRIOR APPLICATION NUMBER: US 60/126,561  
 2 PRIOR FILING DATE: 1999-04-23  
 3 PRIOR APPLICATION NUMBER: US 60/126,561  
 4 PRIOR FILING DATE: 1999-04-09  
 5 PRIOR APPLICATION NUMBER: US 60/105,015  
 6 PRIOR FILING DATE: 1998-10-20  
 7 NUMBER OF SEQ ID NOS: 13  
 8 SOFTWARE: PatentIn Ver. 2.0  
 9 SEQ ID NO 8  
 10 LENGTH: 13  
 11 TYPE: PRT  
 12 ORGANISM: Bos sp.  
 13 FEATURES:  
 14 NAME/KEY: PEPTIDE  
 15 LOCATION: (1)  
 16 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 17 US-09-605-991-B

Query Match 36.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.1e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0

QY 7 KPRR 10  
 111  
 12 6 KPRR 9

RESULT 2/  
 US-09-420-797-B

1 Sequence 8, Application US/09420797-B  
 2 Patent No. 6525221  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldozero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Jolita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.  
 16 APPLICANT: University of Utah Research Foundation  
 17 APPLICANT: Salk Institute  
 18 TITLE OF INVENTION: Conculakin-G, Analogs Thereof and Uses Thereof  
 19 FILE REFERENCE: Conculakin-G  
 20 CURRENT APPLICATION NUMBER: US 60/126,561  
 21 PRIOR FILING DATE: 1999-04-23  
 22 PRIOR APPLICATION NUMBER: US 60/126,561  
 23 PRIOR FILING DATE: 1999-04-23  
 24 PRIOR APPLICATION NUMBER: US 60/126,561  
 25 PRIOR FILING DATE: 1999-04-23  
 26 PRIOR APPLICATION NUMBER: US 60/126,561  
 27 PRIOR FILING DATE: 1999-04-23  
 28 NUMBER OF SEQ ID NOS: 13  
 29 SOFTWARE: PatentIn Ver. 2.0  
 30 SEQ ID NO 8  
 31 LENGTH: 13  
 32 TYPE: PRT  
 33 ORGANISM: Bos sp.  
 34 FEATURES:  
 35 NAME/KEY: PEPTIDE  
 36 LOCATION: (1)  
 37 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 38 US-09-420-797-B

Query Match 36.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.1e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0

QY 7 KPRR 10  
 111  
 12 6 KPRR 9

RESULT 2/  
 US-09-420-797-B

1 Sequence 8, Application US/09420797-B  
 2 Patent No. 6525221  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldozero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Jolita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.  
 16 APPLICANT: University of Utah Research Foundation  
 17 APPLICANT: Salk Institute  
 18 TITLE OF INVENTION: Conculakin-G, Analogs Thereof and Uses Thereof  
 19 FILE REFERENCE: Conculakin-G  
 20 CURRENT APPLICATION NUMBER: US 60/126,561  
 21 PRIOR FILING DATE: 1999-04-23  
 22 PRIOR APPLICATION NUMBER: US 60/126,561  
 23 PRIOR FILING DATE: 1999-04-23  
 24 PRIOR APPLICATION NUMBER: US 60/126,561  
 25 PRIOR FILING DATE: 1999-04-23  
 26 PRIOR APPLICATION NUMBER: US 60/126,561  
 27 PRIOR FILING DATE: 1999-04-23  
 28 NUMBER OF SEQ ID NOS: 13  
 29 SOFTWARE: PatentIn Ver. 2.0  
 30 SEQ ID NO 8  
 31 LENGTH: 13  
 32 TYPE: PRT  
 33 ORGANISM: Bos sp.  
 34 FEATURES:  
 35 NAME/KEY: PEPTIDE  
 36 LOCATION: (1)  
 37 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 38 US-09-420-797-B

Query Match 36.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.1e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0

QY 7 KPRR 10

DB 1111  
 6 KPRR 9  
 RESULT 2/  
 US-09-605-991-B

1 Sequence 8, Application US/09605991  
 2 Patent No. 6525221  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldozero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Jolita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.  
 16 APPLICANT: University of Utah Research Foundation  
 17 APPLICANT: Salk Institute  
 18 TITLE OF INVENTION: Conculakin-G, Analogs Thereof and Uses Thereof  
 19 FILE REFERENCE: Conculakin-G  
 20 CURRENT APPLICATION NUMBER: US 60/126,561  
 21 PRIOR FILING DATE: 2000-06-29  
 22 PRIOR APPLICATION NUMBER: US/09420797-B  
 23 PRIOR FILING DATE: 1999-10-19  
 24 PRIOR APPLICATION NUMBER: US 60/136,661  
 25 PRIOR FILING DATE: 1999-04-23  
 26 PRIOR APPLICATION NUMBER: US 60/126,561  
 27 PRIOR FILING DATE: 1999-04-09  
 28 PRIOR APPLICATION NUMBER: US 60/105,015  
 29 PRIOR FILING DATE: 1998-10-20  
 30 NUMBER OF SEQ ID NOS: 13  
 31 SOFTWARE: PatentIn Ver. 2.0  
 32 SEQ ID NO 8  
 33 LENGTH: 13  
 34 TYPE: PRT  
 35 ORGANISM: Bos sp.  
 36 FEATURES:  
 37 NAME/KEY: PEPTIDE  
 38 LOCATION: (1)  
 39 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 40 US-09-605-991-B

Query Match 35.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.1e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 KPRR 10  
 111  
 12 6 KPRR 9

RESULT 2/  
 US-09-609-544-B

1 Sequence 8, Application US/09609544  
 2 Patent No. 6525221  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldozero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Jolita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.  
 16 APPLICANT: University of Utah Research Foundation  
 17 APPLICANT: Salk Institute  
 18 TITLE OF INVENTION: Conculakin-G, Analogs Thereof and Uses Thereof  
 19 FILE REFERENCE: Conculakin-G  
 20 CURRENT APPLICATION NUMBER: US 60/126,561  
 21 PRIOR FILING DATE: 1999-04-23  
 22 PRIOR APPLICATION NUMBER: US 60/126,561  
 23 PRIOR FILING DATE: 1999-04-23  
 24 PRIOR APPLICATION NUMBER: US 60/126,561  
 25 PRIOR FILING DATE: 1999-04-23  
 26 PRIOR APPLICATION NUMBER: US 60/126,561  
 27 PRIOR FILING DATE: 1999-04-23  
 28 NUMBER OF SEQ ID NOS: 13  
 29 SOFTWARE: PatentIn Ver. 2.0  
 30 SEQ ID NO 8  
 31 LENGTH: 13  
 32 TYPE: PRT  
 33 ORGANISM: Bos sp.  
 34 FEATURES:  
 35 NAME/KEY: PEPTIDE  
 36 LOCATION: (1)  
 37 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 38 US-09-609-544-B

QY 7 KPRR 10

```

1 APPLICANT: University of Utah Research Foundation
2 APPLICANT: Salk Institute
3 TITLE OF INVENTION: Contulakin-C, Analogs thereof and Uses Thereof
4 FILE REFERENCE: Contulakin-G CIP
5 CURRENT APPLICATION NUMBER: US/09/09,594
6 CURRENT FILING DATE: 2000-06-15
7 EARLIER APPLICATION NUMBER: US 60/133,661
8 EARLIER FILING DATE: 1999-04-23
9 EARLIER APPLICATION NUMBER: US 60/128,167
10 EARLIER FILING DATE: 1999-04-09
11 EARLIER APPLICATION NUMBER: US 10/105,115
12 EARLIER FILING DATE: 1998-10-20
13 EARLIER APPLICATION NUMBER: US 09/420,737
14 EARLIER FILING DATE: 1999-10-29
15 EARLIER APPLICATION NUMBER: US 09/
16 EARLIER FILING DATE: 2000-05-24
17 NUMBER OF SEQ ID NOS: 13
18 SOFTWARE: PatentIn Ver. 2.0
19 SEQ ID NO: 1
20 LENGTH: 13
21 TYPE: LRP
22 ORGANISM: H.S. SP.
23 FEATURE:
24 NAME/KEY: PEPTIDE
25 LOCATION: (1)
26 OTHER INFORMATION: Xaa at residue 1 is pyro D.
27 US 09 609 594 #

```

```

Query Match: 36.4% Score 4: DB 4: Length 13;
Best Local Similarity: 100.0% Pred. No. 1.4e-02;
Matches 4: Conservative 0: Mismatches 0: Gaps 0;

```

```

CY 7 KRR 10
III
DL 7 KRR 10

```

```

RESULT 41
US-09-787-443-12
1 Sequence 4: Application: US/09/0955272
2 Patent No. 562269
3 GENERAL INFORMATION:
4 APPLICANT: Kumar, Kamesh
5 APPLICANT: Sharma, Ajay
6 APPLICANT: M.
7 APPLICANT: Khoury-Christianson, Anastasia
8 TITLE OF INVENTION: Production of Therapeutic Peptides in Transgenic Animals as a Fusion with Hemoglobin
9 NUMBER OF SEQUENCES: 12
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: PENNIE & EMMONS
12 STREET: 1155 Avenue of the Americas
13 CITY: New York
14 STATE: NY
15 COUNTRY: USA
16 ZIP: 10036-2711
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 OPERATING SYSTEM: IBM PC compatible
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/255,272
23 FILING DATE:
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Cotuzzi, Laura A.
27 REGISTRATION NUMBER: 30742
28 REFERENCE/DOCKET NUMBER: 5794 092
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (212) 793-9090
31 TELEFAX: (212) 659-9741/8864
32 INFORMATION FOR SEQ ID NO: 4:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 14 amino acids
35 TYPE: amino acid
36 TOPOLOGY: unknown
37 MOLECULE TYPE: peptide
38 HYPOTHETICAL: NO
39 ANTI-SENSE: NO
40 US-08-255-272 4

```

```

Query Match: 36.4% Score 4: DB 1: Length 14;
Best Local Similarity: 100.0% Pred. No. 1.4e-02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

```

```

CY 7 KRR 10
III
DL 7 KRR 10

```

```

RESULT 42
US-07-420 937 2

```

```

1 SEQUENCE CHARACTERISTICS:
2 LENGTH: 13 amino acids
3 TYPE: amino acid
4 STRANDEDNESS: Single
5 TOPOLOGY: Linear
6 MOLECULE TYPE: peptide
7 PCT-US95-14577-6

```

```

Query Match: 36.4% Score 4: DB 5: Length 13;
Best Local Similarity: 100.0% Pred. No. 1.4e-02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

```

```

CY 2 KRR 5
III
DL 9 KRR 12

```

```

RESULT 41
US-09-255-272-4
1 Sequence 4: Application: US/09/255272
2 Patent No. 562269
3 GENERAL INFORMATION:
4 APPLICANT: Kumar, Kamesh
5 APPLICANT: Sharma, Ajay
6 APPLICANT: M.
7 APPLICANT: Khoury-Christianson, Anastasia
8 TITLE OF INVENTION: Production of Therapeutic Peptides in Transgenic Animals as a Fusion with Hemoglobin
9 NUMBER OF SEQUENCES: 12
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: PENNIE & EMMONS
12 STREET: 1155 Avenue of the Americas
13 CITY: New York
14 STATE: NY
15 COUNTRY: USA
16 ZIP: 10036-2711
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 OPERATING SYSTEM: IBM PC compatible
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/255,272
23 FILING DATE:
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Cotuzzi, Laura A.
27 REGISTRATION NUMBER: 30742
28 REFERENCE/DOCKET NUMBER: 5794 092
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (212) 793-9090
31 TELEFAX: (212) 659-9741/8864
32 INFORMATION FOR SEQ ID NO: 4:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 14 amino acids
35 TYPE: amino acid
36 TOPOLOGY: unknown
37 MOLECULE TYPE: peptide
38 HYPOTHETICAL: NO
39 ANTI-SENSE: NO
40 US-08-255-272 4

```

```

1 Sequence 2, Application US/07920597
2 Patent No. 5447915
3 GENERAL INFORMATION:
4 APPLICANT: Schreiber, Stuart
5 APPLICANT: Burakoff, Steven
6 TITLE OF INVENTION: Terminally-Blocked Anticatalytic Peptides
7 NUMBER OF SEQUENCES: 12
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Allgretti & Wilcoff, Ltd
10 STREET: 10 South Wacker Drive, Suite 600
11 CITY: Chicago
12 STATE: IL
13 COUNTRY: USA
14 ZIP: 60606
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.2
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/07/920,597
22 FILING DATE: 19920828
23 CLASSIFICATION: 514
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: WO/92/0591/01142
26 FILING DATE: 28 FEB 1991
27 ATTORNEY/AGENT INFORMATION:
28 NAME: No. 5447915nan, Kevin E
29 REGISTRATION NUMBER: 45,604
30 REFERENCE/PACKET NUMBER: 41,174-E
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 312-715-1000
33 TELEFAX: 312-715-1234
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 9 amino acids
37 TYPE: amino acid
38 STANDARDS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41 US 07-920-597-2
42
43 Query Match 27.5% Score 3, DR 1, Length 8;
44 Best Local Similarity 100.0%, Pct. No. 2, 50.0%
45 Matches 3: Conservative 0: Mismatches 0: Gaps 0:
46
47 QY 7 KPR 3
48 DB 6 KPR 6
49
50 RESULT 14
51 US-08-178-570-51
52 Sequence 3, Application US/07920597
53 Patent No. 5447915
54 GENERAL INFORMATION:
55 APPLICANT: Schreiber, Stuart
56 APPLICANT: Burakoff, Steven
57 TITLE OF INVENTION: Terminally-Blocked Anticatalytic Peptides
58 NUMBER OF SEQUENCES: 12
59 CORRESPONDENCE ADDRESS:
60 ADDRESSEE: Allgretti & Wilcoff, Ltd
61 STREET: 10 South Wacker Drive, Suite 600
62 CITY: Chicago
63 STATE: IL
64 COUNTRY: USA
65 ZIP: 60606
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC-DOS/MS-DOS
70 SOFTWARE: PatentIn Release #1.0, Version #1.2
71 CURRENT APPLICATION DATA:
72 APPLICATION NUMBER: US/07/920,597
73 FILING DATE: 19920828
74 CLASSIFICATION: 514
75 PRIOR APPLICATION DATA:
76 APPLICATION NUMBER: WO/92/0591/01142
77 FILING DATE: 28 FEB 1991
78 ATTORNEY/AGENT INFORMATION:
79 NAME: No. 5447915nan, Kevin E
80 REGISTRATION NUMBER: 45,604
81 REFERENCE/PACKET NUMBER: 41,174-E
82 TELECOMMUNICATION INFORMATION:
83 TELEPHONE: 312-715-1000
84 TELEFAX: 312-715-1234
85 INFORMATION FOR SEQ ID NO: 2:
86 SEQUENCE CHARACTERISTICS:
87 LENGTH: 9 amino acids
88 TYPE: amino acid
89 STANDARDS: single
90 TOPOLOGY: linear
91 MOLECULE TYPE: peptide
92 US 07-920-597-2

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/07/920,597
3 FILING DATE: 19920828
4 CLASSIFICATION: 514
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: WO/92/0591/01142
7 FILING DATE: 28 FEB 1991
8 ATTORNEY/AGENT INFORMATION:
9 NAME: No. 5447915nan, Kevin E
10 REGISTRATION NUMBER: 45,604
11 REFERENCE/PACKET NUMBER: 41,174-E
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 312-715-1000
14 TELEFAX: 312-715-1234
15 INFORMATION FOR SEQ ID NO: 3:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 8 amino acids
18 TYPE: amino acid
19 STANDARDS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 US 07-920-597-4
23
24 Query Match 27.5% Score 3, DR 1, Length 8;
25 Best Local Similarity 100.0%, Pct. No. 2, 50.0%
26 Matches 3: Conservative 0: Mismatches 0: Gaps 0:
27
28 QY 7 KPR 9
29 DB 4 KPR 6
30
31 RESULT 34
32 US-08-178-570-51
33 Sequence 51, Application US/08178570
34 Patent No. 5542157
35 GENERAL INFORMATION:
36 APPLICANT: Lewis G. Cardley
37 APPLICANT: Zhou Song Yang
38 TITLE OF INVENTION: Substrate Specificity of Protein Kinases
39 NUMBER OF SEQUENCES: 77
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: LAHVE & JACKFIELD
42 STREET: 60 STATE STREET, SUITE 510
43 CITY: BOSTON
44 STATE: MASSACHUSETTS
45 COUNTRY: USA
46 ZIP: 02109-1575
47 COMPUTER READABLE FORM:
48 MEDIUM TYPE: Floppy disk
49 COMPUTER: IBM PC compatible
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: ASCII text
52 CURRENT APPLICATION DATA:
53 APPLICATION NUMBER: US/08/178,570
54 FILING DATE: JANUARY 7, 1994
55 CLASSIFICATION: 435
56 ATTORNEY/AGENT INFORMATION:
57 NAME: DOUGELL, GIGLIO, A. JR.
58 REGISTRATION NUMBER: 33,593
59 REFERENCE/PACKET NUMBER: BB1-004
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (617) 227-7400
62 TELEFAX: (617) 227-5941
63 INFORMATION FOR SEQ ID NO: 51:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 8 amino acids
66 TYPE: amino acid
67 TOPOLOGY: linear
68 MOLECULE TYPE: peptide
69 FRAGMENT TYPE: internal
70 US-08-178-570-51

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Query Match: 27.5% Sequence: 20.1% Identity: 8%  
 Best Local Similarity: 100.0% From: 20.1%  
 Matches: 31 Conservative 0 Mismatches 0 Indels 0

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

Query Match: 27.5% Sequence: 20.1% Identity: 8%  
 Best Local Similarity: 100.0% From: 20.1%  
 Matches: 31 Conservative 0 Mismatches 0 Indels 0

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

Query Match: 27.5% Sequence: 20.1% Identity: 8%  
 Best Local Similarity: 100.0% From: 20.1%  
 Matches: 31 Conservative 0 Mismatches 0 Indels 0

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/09-787-443-12  
 2 Patent No. 5,667,745  
 3 GENERAL INFORMATION  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHLOROFORM BLENDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 3000 K Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS  
 16 SOFTWARE: IBM PC compatible  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 425  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Godt, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/25-768  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5400  
 26 TELEFAX: (202) 672-5455  
 27 TEXT: 004196  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: Linear  
 33 TOPOLOGY: Linear  
 34 MODIFIER TYPE: peptide  
 35 US-09-787-443-12

CV 1 KIR 3  
 DL 1 KIR 3

Result 6:  
 US 09-787-443-12



ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 568222men D.  
 REGISTRATION NUMBER: 40,946  
 REFERENCE/Docket NUMBER: 100,946  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-9864  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-09 370-626 4

Query Match: 27.3% Score: 4.1 E-11 Length: 8  
 Best Local Similarity: 100.0% Ident: 100.0%  
 Matches: 3/3 Conservative 0/0 Mismatches 0/0 Indels 0/0 Gaps 0/0

QY 8 PER 10  
 20 5 PER 7

RESULT 4:  
 US-08 102-748-25  
 Sequence 25, Application US/08/02748  
 Patent No. 6,746,766  
 GENERAL INFORMATION:  
 APPLICANT: Seidel, Christoph, Withayach, Eugene, Best, Ken  
 APPLICANT: Bayer, Hubert, Jung, Guenther, Gerhardt, Vincent, J., Hans  
 TITLE OF INVENTION: BCV Peptide Anticancer And Related  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fette & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York City  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 0.6 KB, 1.44 MB  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: Wordperfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/102,748  
 FILING DATE: 6 AUG 1994  
 CLASSIFICATION: A24  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 42 26 01 A 0  
 FILING DATE: 7-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 42 40 98 A 2  
 FILING DATE: 5-DEC 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isail, Christine H.  
 REGISTRATION NUMBER: 34,254  
 REFERENCE/Docket NUMBER: 100,946  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 SCANDENESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08 102-748-25

Query Match: 27.3% Score: 4.1 E-11 Length: 8  
 Best Local Similarity: 100.0% Ident: 100.0%  
 Matches: 3/3 Conservative 0/0 Mismatches 0/0 Indels 0/0 Gaps 0/0

Best Local Similarity: 100.0% Ident: 100.0%  
 Matches: 3/3 Conservative 0/0 Mismatches 0/0 Indels 0/0 Gaps 0/0

QY 8 PER 10  
 20 6 PER 5

RESULT 4:  
 US-08 714-484-10  
 Sequence 10, Application US/08/71484  
 Patent No. 5,679,642  
 GENERAL INFORMATION:  
 APPLICANT: Goodbody, Anne  
 TITLE OF INVENTION: PEPTIDE-CELLULOSER CONJUGATES  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fette & Lynch  
 STREET: Suite 500, 900 K Street, N.W.  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/714,484  
 FILING DATE: 13-SEP-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/202,178  
 FILING DATE: 25-FEB-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,766  
 REFERENCE/Docket NUMBER: 56777/290/ALLE  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5490  
 TELEFAX: (202) 672-5499  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-714-484-10

Query Match: 27.3% Score: 4.1 E-11 Length: 8  
 Best Local Similarity: 100.0% Ident: 100.0%  
 Matches: 3/3 Conservative 0/0 Mismatches 0/0 Indels 0/0 Gaps 0/0

QY 7 PER 5  
 20 2 PER 4

RESULT 40  
 US-08-754-170-45  
 Sequence 45, Application US/08/754170  
 Patent No. 570,626  
 GENERAL INFORMATION:  
 APPLICANT: Leivas, Acetone  
 APPLICANT: Takenawa, Yoshi  
 APPLICANT: Ehresmann, Glenn  
 TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
 NUMBER OF SEQUENCES: 121  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: KODAK, Robert & Carson  
 STREET: 21 No. 370/626th Fiquetod Street, Suite 500

1 CITY: Los Angeles  
2 STATE: California  
3 COUNTRY: U.S.A.  
4 ZIP: 90012  
5 COMPUTER READABLE FORM:  
6 MEDIUM TYPE: Floppy disk  
7 COMPUTER: IBM PC compatible  
8 OPERATING SYSTEM: PC DOS/MS DOS  
9 SOFTWARE: Patent in Release #10, Version #1.0  
10 CURRENT APPLICATION DATA:  
11 APPLICATION NUMBER: US/08/74,443  
12 FILING DATE:  
13 CLASSIFICATION: 424  
14 PREP APPLICATION DATA:  
15 APPLICATION NUMBER: US 08/02,850  
16 FILING DATE: 11 MAR 1994  
17 ATTORNEY/AGENT INFORMATION:  
18 NAME: Spitzals, John P.  
19 REGISTRATION NUMBER: 29,215  
20 REFERENCE/CRACKET NUMBER: 1929 443  
21 TELECOMMUNICATION INFORMATION:  
22 TELEPHONE: (213) 977-1001  
23 TELEFAX: (213) 977-1003  
24 INFORMATION FOR SEQ ID NO: 45:  
25 SEQUENCE CHARACTERISTICS:  
26 LENGTH: 8 amino acids  
27 TYPE: amino acid  
28 TOPLOGY: linear  
29 MEDIUM TYPE: peptide  
30 US-08-74 443-45

Query Match: 27.8% Score 5: DB 1: Length 8;  
Best Local Similarity: 100.0% Pred. No. 2.5e-05;  
Matches 3: Conservative 0; Mismatches 0; Gaps 0;

QY 8 QRT 40  
DB 111  
19% 3

RESULT 42  
US-08-594-447  
1 Sequence 55, Application US/08/59447  
2 Patent No. 571216  
3 GENERAL INFORMATION:  
4 APPLICANT: Rott, Toritt  
5 APPLICANT: Rappaport, Eugene W  
6 APPLICANT: Voloshin, Andri F  
7 TITLE OF INVENTION: METHOD FOR DETECTING AND TREATING  
8 TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES  
9 NUMBER OF SEQUENCES: 75  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: MORRISON & MORRISON  
12 STREET: 2000 Pennsylvania Avenue, NW  
13 CITY: Washington  
14 STATE: DC  
15 COUNTRY: USA  
16 ZIP: 20006-1888  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Floppy disk  
19 COMPUTER: IBM PC compatible  
20 OPERATING SYSTEM: PC-DOS/MS DOS  
21 SOFTWARE: Patent in Release #1.0, Version #1.0  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/08/594-447  
24 FILING DATE: 31 JAN 1996  
25 CLASSIFICATION: 425  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: Marshback, Kate H  
28 REGISTRATION NUMBER: 29,959  
29 REFERENCE/CRACKET NUMBER: 22550 2002-21  
30 TELECOMMUNICATION INFORMATION:

1 TELEPHONE: (202) 887-1500  
2 TELEFAX: (202) 622-0188  
3 TELE: 90-45 to MRSNEPERSWSH  
4 INFORMATION FOR SEQ ID NO: 5:  
5 SEQUENCE CHARACTERISTICS:  
6 LENGTH: 8 amino acids  
7 TYPE: amino acid  
8 STRANGENESS: Single  
9 TOPLOGY: linear  
10 MEDIUM TYPE: peptide  
11 FEATURES:  
12 NAME/KEY: Peptide  
13 LOCATION: 1-8  
14 OTHER INFORMATION / detail: 100 72-1  
15 US-08-594-447-5

Query Match: 27.8% Score 3: DB 1: Length 8;  
Best Local Similarity: 100.0% Pred. No. 2.5e-05;  
Matches 3: Conservative 0; Mismatches 0; Indels 0;

QY 5 QRT 5  
DB 111  
2 QRT 4

RESULT 42  
US-08-259-550A-55  
1 Sequence 55, Application US/08/259550A  
2 Patent No. 5716892  
3 GENERAL INFORMATION:  
4 APPLICANT: Gamble, David F  
5 APPLICANT: Gull, Ronald G  
6 TITLE OF INVENTION: Anti Inflammatory Peptides  
7 NUMBER OF SEQUENCES: 91  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: PENNIE & FERNANIS  
10 STREET: 1155 Avenue of the Americas  
11 CITY: New York  
12 STATE: New York  
13 COUNTRY: U.S.A.  
14 ZIP: 10036-2711  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Floppy disk  
17 COMPUTER: IBM PC compatible  
18 OPERATING SYSTEM: PC-DOS/MS DOS  
19 SOFTWARE: Patent in Release #1.0, Version #1.25  
20 CURRENT APPLICATION DATA:  
21 APPLICATION NUMBER: US/08/259,550A  
22 FILING DATE: 16 JUN 1994  
23 CLASSIFICATION: 514  
24 ATTORNEY/AGENT INFORMATION:  
25 NAME: Misonick, Stephen  
26 REGISTRATION NUMBER: 18,872  
27 REFERENCE/CRACKET NUMBER: 7142 021  
28 TELECOMMUNICATION INFORMATION:  
29 TELEPHONE: (212) 790-9040  
30 TELEFAX: (212) 869-8864/9741  
31 TELE: 60241 PENNIE  
32 INFORMATION FOR SEQ ID NO: 55:  
33 SEQUENCE CHARACTERISTICS:  
34 LENGTH: 8 amino acids  
35 TYPE: amino acid  
36 TOPLOGY: unknown  
37 MEDIUM TYPE: Peptide  
38 HYDROTICAL: NO  
39 ANTI-SENSE: NO  
40 US-08-259-550A-55

Query Match: 27.8% Score 5: DB 1: Length 8;  
Best Local Similarity: 100.0% Pred. No. 2.5e-05;  
Matches 3: Conservative 0; Mismatches 0; Indels 0;

QY 9 QRT 9

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1  111
2  0 K55 R
3
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STRANEGENESS:
TOPLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: P01104
LOCATION: 1-18
OTHER INFORMATION: /note="His Galb1, peak11; N-terminus"
DS: 69, 274A, 2

Query Match:
Best Local Similarity: 100.0%; Pred. No. 2, 50455;
Matches: 3; Conserved: 0; Mismatches: 0; Indels:
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RESIST 49  
 US 02-555,283-10  
 : Sequence ID, Applicant ID, QS/28955283  
 : Patent No. 5866544  
 : SERIAL INFORMATION

APPLICANT: POLARIS ATCOG  
 TITLE OF INVENTION: PEPTIDE-CHLATOR CONJUGATES  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: POLARIS & LACROIX  
 STREET: SUITE 500, 4000 K STREET, N.W.  
 CITY: WASHINGTON, D.C.  
 COUNTRY: USA  
 TEL: 202/675-5119  
 COMPUTER-READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: PatentIn Release 1.1.0, Version 11.10  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/755,264  
 FILING DATE:

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1  ENTER APPLICATION DATA:
2  APPLICATION NUMBER: 15 08/115.464
3  FILING DATE: 23 SEP 1976
4  APPLICATION NUMBER: US 052,178
5  FILING DATE: 20 FEB 1974
6  ATTORNEY/AGENT INFORMATION:
7  NAME: BOYD, Stephen A
8  ATTORNEY'S NUMBER: 29,748
9  ADDRESS: 5210881 NUMBER: 1611296/ALIE
10 TELEPHONE: 642-5309
11 TELEFAX: 642-5309
12 INDEX: 642-5309
13 INFORMATION FOR SEQUENCING:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 8 entries
16 TYPE: continuous
17 PUBLICATION:
18 PUBLICATION TYPE: journal
19 NO. 955, 642-5309

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Best local similarity	100.0%					
Matches	5	Conservative	0	Mismatches	0	Indels
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Q	14					
	2 KRF 4					
QV	14					
Q	2					

Sequence 45, Application US/00/4596.E  
 Patent No. 5903157  
 GENERAL INFORMATION:  
 APPLICANT: GUENTERICH, F. Peter  
 APPLICANT: GSD, Zeyu  
 APPLICANT: SANDHU, Punam  
 APPLICANT: GILLAM, Elizabeth M.  
 TITLE OF INVENTION: EXPRESSION AND PRODUCTION OF  
 TITLE OF INVENTION: HUMAN  
 TITLE OF INVENTION: PSYCHOPEPTIDE  
 NUMBER OF SEQUENCES: 08  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NEEDLE & RESINWORKS, INC.  
 STREET: Suite 1200, 127 Peachtree Street, N.W.  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30303 1811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 CIPHER: 10M PC compatible  
 OPERATING SYSTEM: PC/DOS/MS-DOS  
 SOFTWARE: Patent in Release #10, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/787,443  
 FILING DATE: February 10, 1994  
 CLASSIFICATION: 455  
 AGENCY/AGENT INFORMATION:  
 NAME: Elizabeth Solby  
 REGISTRATION NUMBER: 02,206  
 REFERENCE/DESKET NUMBER: 22,000,000  
 INFORMATION INFORMATION:  
 REFERENCE: (494) 688 9770  
 REFERENCE: (494) 688 9869  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 Molecule type: peptide  
 HYDROPHOBICITY: N  
 FRAGMENT TYPE: N-terminal  
 PS: 09-194-001-1

Query Match: 27.98% Sequence: 100% Identity: 100%  
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 Matches: 8/8 Conservative: 8/8 Non-conservative: 0/0

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 3. Ape 4

Search completed: September 30, 2003, 11:06:49  
 Job time: 14.937808s

Genome version 5.1.6  
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EM protein - protein search, using sw model

Run on: September 30, 2003, 10:10:00 : Search time 21.8 seconds  
(with 4.4 sec read in)  
77.415 Minutes over all queries/seq

File: US-09-787-443-12

Perfect score: 11

Sequence: 1 ASGTMKRRS 11

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Sequences: 56894 seqs, 15140744 residues

Word size: 3

Total number of hits satisfying chosen parameters: 68367

Maximum DB seq length: 8

Maximum DB seq length: 15

FAST processing: listing first 500 summaries

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and is derived by analysis of the data in the database.

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100	3	27.3	8	15	US-10-006-869-503	Sequence 503, Appl	173	3	27.3	9	11	US-09-876-904A-523	Sequence 523, Appl
101	3	27.3	8	15	US-10-006-869-504	Sequence 504, Appl	174	3	27.3	9	11	US-09-922-226-88	Sequence 88, Appl
102	3	27.3	8	15	US-10-006-869-507	Sequence 507, Appl	175	3	27.3	9	11	US-09-952-680A-60	Sequence 60, Appl
103	3	27.3	8	15	US-10-006-869-507A	Sequence 507A, Appl	176	3	27.3	9	11	US-09-897-848-6	Sequence 6, Appl
104	3	27.3	8	15	US-10-006-869-512A	Sequence 512A, Appl	177	3	27.3	9	11	US-09-907-969-444	Sequence 444, Appl
105	3	27.3	8	15	US-10-006-869-512B	Sequence 512B, Appl	178	3	27.3	9	12	US-09-932-165-22	Sequence 22, Appl
106	3	27.3	8	15	US-10-006-869-516	Sequence 516, Appl	179	3	27.3	9	12	US-09-932-165-22	Sequence 433, Appl
107	3	27.3	8	15	US-10-006-869-516A	Sequence 516A, Appl	180	3	27.3	9	12	US-09-932-165-636	Sequence 636, Appl
108	3	27.3	8	15	US-10-006-869-5206	Sequence 5206, Appl	181	3	27.3	9	12	US-09-932-165-817	Sequence 817, Appl
109	3	27.3	8	15	US-10-006-869-5208	Sequence 5208, Appl	182	3	27.3	9	12	US-09-932-165-842	Sequence 842, Appl
110	3	27.3	8	15	US-10-006-869-5251	Sequence 5251, Appl	183	3	27.3	9	12	US-09-932-165-985	Sequence 985, Appl
111	3	27.3	8	15	US-10-006-869-5253	Sequence 5253, Appl	184	3	27.3	9	12	US-09-932-165-987	Sequence 987, Appl
112	3	27.3	8	15	US-10-006-869-5299	Sequence 5299, Appl	185	3	27.3	9	12	US-09-932-165-1163	Sequence 1163, Appl
113	3	27.3	8	15	US-10-006-869-5301	Sequence 5301, Appl	186	3	27.3	9	12	US-09-932-165-1163	Sequence 1163, Appl
114	3	27.3	8	15	US-10-193-799-8	Sequence 8, Appl	187	3	27.3	9	12	US-09-932-165-1186	Sequence 1186, Appl
115	3	27.3	8	15	US-10-193-799-9	Sequence 9, Appl	188	3	27.3	9	12	US-10-294-157-16	Sequence 16, Appl
116	3	27.3	8	15	US-10-193-799-10	Sequence 10, Appl	189	3	27.3	9	12	US-09-968-744A-36	Sequence 36, Appl
117	3	27.3	8	15	US-10-224-285-26	Sequence 26, Appl	190	3	27.3	9	12	US-10-158-883B-36	Sequence 56, Appl
118	3	27.3	8	15	US-10-193-799-40	Sequence 40, Appl	191	3	27.3	9	12	US-10-190-082-253	Sequence 253, Appl
119	3	27.3	8	15	US-10-193-799-40	Sequence 40, Appl	192	3	27.3	9	12	US-10-190-082-338	Sequence 338, Appl
120	3	27.3	8	15	US-10-193-799-42	Sequence 42, Appl	193	3	27.3	9	12	US-10-190-082-470	Sequence 470, Appl
121	3	27.3	8	15	US-10-193-799-45	Sequence 45, Appl	194	3	27.3	9	12	US-10-375-992-178	Sequence 178, Appl
122	3	27.3	8	15	US-10-193-799-47	Sequence 47, Appl	195	3	27.3	9	12	US-09-794-451-423	Sequence 423, Appl
123	3	27.3	9	7	US-09-441-824-4	Sequence 84, Appl	196	3	27.3	9	12	US-09-794-451-528	Sequence 528, Appl
124	3	27.3	9	7	US-09-441-824-10	Sequence 10, Appl	197	3	27.3	9	12	US-10-271-617-10	Sequence 10, Appl
125	3	27.3	9	7	US-09-441-824-21	Sequence 21, Appl	198	3	27.3	9	12	US-10-271-617-13	Sequence 13, Appl
126	3	27.3	9	7	US-09-765-786-172	Sequence 172, Appl	199	3	27.3	9	12	US-10-271-617-22	Sequence 22, Appl
127	3	27.3	9	9	US-09-373-918-4	Sequence 4, Appl	200	3	27.3	9	12	US-10-271-617-24	Sequence 24, Appl
128	3	27.3	9	9	US-09-373-918-4	Sequence 4, Appl	201	3	27.3	9	12	US-10-271-617-27	Sequence 27, Appl
129	3	27.3	9	9	US-09-779-233-1	Sequence 10, Appl	202	3	27.3	9	12	US-09-827-271-444	Sequence 444, Appl
130	3	27.3	9	9	US-09-884-141-1	Sequence 1, Appl	203	3	27.3	9	12	US-09-935-384-225	Sequence 225, Appl
131	3	27.3	9	9	US-09-192-834-20	Sequence 20, Appl	204	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
132	3	27.3	9	9	US-09-926-297-6	Sequence 6, Appl	205	3	27.3	9	12	US-09-935-384-338	Sequence 338, Appl
133	3	27.3	9	9	US-09-948-116-4	Sequence 4, Appl	206	3	27.3	9	12	US-09-935-384-625	Sequence 625, Appl
134	3	27.3	9	9	US-09-941-495-6	Sequence 6, Appl	207	3	27.3	9	12	US-10-022-066-322	Sequence 322, Appl
135	3	27.3	9	9	US-09-954-245-11	Sequence 43, Appl	208	3	27.3	9	12	US-10-245-4158-6	Sequence 6, Appl
136	3	27.3	9	10	US-09-940-039-222	Sequence 222, Appl	209	3	27.3	9	12	US-10-286-457-111	Sequence 111, Appl
137	3	27.3	9	10	US-09-940-039-414	Sequence 444, Appl	210	3	27.3	9	12	US-10-286-457-465	Sequence 465, Appl
138	3	27.3	9	10	US-09-940-039-414	Sequence 1, Appl	211	3	27.3	9	12	US-10-144-188-26	Sequence 26, Appl
139	3	27.3	9	10	US-09-940-039-414	Sequence 1, Appl	212	3	27.3	9	12	US-10-210-148-48	Sequence 48, Appl
140	3	27.3	9	10	US-09-940-039-414	Sequence 1, Appl	213	3	27.3	9	12	US-10-210-148-58	Sequence 58, Appl
141	3	27.3	9	10	US-09-940-039-414	Sequence 1, Appl	214	3	27.3	9	12	US-10-210-148-94	Sequence 94, Appl
142	3	27.3	9	10	US-09-940-039-414	Sequence 22, Appl	215	3	27.3	9	12	US-10-293-580-33	Sequence 33, Appl
143	3	27.3	9	10	US-09-940-039-414	Sequence 6, Appl	216	3	27.3	9	12	US-10-293-580-50	Sequence 50, Appl
144	3	27.3	9	10	US-09-940-039-414	Sequence 40, Appl	217	3	27.3	9	12	US-10-293-580-52	Sequence 52, Appl
145	3	27.3	9	10	US-09-940-039-414	Sequence 12, Appl	218	3	27.3	9	12	US-10-157-175-81	Sequence 81, Appl
146	3	27.3	9	10	US-09-940-039-414	Sequence 4, Appl	219	3	27.3	9	12	US-10-219-313A-454	Sequence 454, Appl
147	3	27.3	9	10	US-09-940-039-414	Sequence 64, Appl	220	3	27.3	9	12	US-10-412-105-30	Sequence 30, Appl
148	3	27.3	9	10	US-09-940-039-414	Sequence 64, Appl	221	3	27.3	9	15	US-10-062-710-198	Sequence 198, Appl
149	3	27.3	9	10	US-09-940-039-414	Sequence 185, Appl	222	3	27.3	9	15	US-10-046-801-10	Sequence 10, Appl
150	3	27.3	9	10	US-09-940-039-414	Sequence 503, Appl	223	3	27.3	9	15	US-10-158-596A-56	Sequence 56, Appl
151	3	27.3	9	10	US-09-940-039-414	Sequence 4, Appl	224	3	27.3	9	15	US-10-157-7758-56	Sequence 503, Appl
152	3	27.3	9	10	US-09-940-039-414	Sequence 58, Appl	225	3	27.3	9	15	US-10-006-869-503	Sequence 3074, Appl
153	3	27.3	9	10	US-09-940-039-414	Sequence 58, Appl	226	3	27.3	9	15	US-10-006-869-3076	Sequence 3076, Appl
154	3	27.3	9	10	US-09-940-039-414	Sequence 71, Appl	227	3	27.3	9	15	US-10-006-869-3119	Sequence 3119, Appl
155	3	27.3	9	10	US-09-940-039-414	Sequence 113, Appl	228	3	27.3	9	15	US-10-006-869-3121	Sequence 3121, Appl
156	3	27.3	9	10	US-09-940-039-414	Sequence 134, Appl	229	3	27.3	9	15	US-10-006-869-3164	Sequence 3164, Appl
157	3	27.3	9	10	US-09-940-039-414	Sequence 172, Appl	230	3	27.3	9	15	US-10-006-869-3166	Sequence 3166, Appl
158	3	27.3	9	10	US-09-940-039-414	Sequence 6, Appl	231	3	27.3	9	15	US-10-006-869-3209	Sequence 3209, Appl
159	3	27.3	9	10	US-09-940-039-414	Sequence 6, Appl	232	3	27.3	9	15	US-10-006-869-3211	Sequence 3211, Appl
160	3	27.3	9	10	US-09-940-039-414	Sequence 72, Appl	233	3	27.3	9	15	US-10-006-869-3254	Sequence 3254, Appl
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382	3	27.3	10	11	US-09-572-434B-680	Sequence 588, App	455	3	27.3	10	12	US-09-793-451-568	Sequence 568, App
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384	3	27.3	10	11	US-09-572-434B-682	Sequence 590, App	457	3	27.3	10	12	US-09-793-451-704	Sequence 704, App
385	3	27.3	10	11	US-09-572-434B-683	Sequence 591, App	458	3	27.3	10	12	US-09-793-451-768-60	Sequence 60, App
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389	3	27.3	10	11	US-09-572-434B-687	Sequence 595, App	462	3	27.3	10	12	US-09-935-384-553	Sequence 553, App
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391	3	27.3	10	11	US-09-572-434B-689	Sequence 597, App	464	3	27.3	10	12	US-09-935-384-684	Sequence 684, App
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394	3	27.3	10	11	US-09-572-434B-692	Sequence 600, App	467	3	27.3	10	12	US-10-262-435-64	Sequence 64, App
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399	3	27.3	10	11	US-09-572-434B-697	Sequence 605, App	472	3	27.3	10	12	US-10-262-435-69	Sequence 69, App
400	3	27.3	10	11	US-09-572-434B-698	Sequence 606, App	473	3	27.3	10	12	US-10-262-435-70	Sequence 70, App
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405	3	27.3	10	11	US-09-572-434B-703	Sequence 611, App	478	3	27.3	10	12	US-10-262-435-75	Sequence 75, App
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438	3	27.3	10	11	US-09-572-434B-736	Sequence 644, App	511	3	27.3	10	12	US-10-262-435-108	Sequence 108, App
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440	3	27.3	10	11	US-09-572-434B-738	Sequence 646, App	513	3	27.3	10	12	US-10-262-435-110	Sequence 110, App
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443	3	27.3	10	11	US-09-572-434B-741	Sequence 649, App	516	3	27.3	10	12	US-10-262-435-113	Sequence 113, App
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446	3	27.3	10	11	US-09-572-434B-744	Sequence 652, App	519	3	27.3	10	12	US-10-262-435-116	Sequence 116, App
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452	3	27.3	10	11	US-09-572-434B-750	Sequence 658, App	525	3	27.3	10	12	US-10-262-435-122	Sequence 122, App
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## ALIGNMENTS

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Sequence 22, Application US/10165044

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GENERAL INFORMATION

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6 PRIOR APPLICATION NUMBER: WO 99/29411
7 PRIOR FILING DATE: 1999-06-01
8 PRIOR APPLICATION NUMBER: PCT/US 99/01440
9 PRIOR FILING DATE: 2000-12-06
10 NUMBER OF SEQ ID NOS: 57
11 SOFTWARE: FASTSEQ for Windows Version 4.0
12 SEQ ID NO: 22
13 LENGTH: 15
14 TYPE: FRT
15 ORGANISM: Homo Sapiens
16 US-09-787-443-12

```

Query Match 46.4% Score 41 DB 10 Length 15  
 Best Local Similarity 100.0% Prod. No. 09  
 Matches 5 Conservative 0 Mismatches 0 Indels 0

QY 6 MKER 10  
 LR 5 MKER 7

```

1 TITLE OF INVENTION: ANTIGEN-DEPENDENT SEQUENCE
2 TITLE OF INVENTION: OF FACTOR VIII AND PARHENS ANOZ-6
3 NUMBER OF SEQUENCES: 20
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Kuehner, Marlene, 2005 5th Ave
6 STREET: 625 Newport Center Building 1110 11th Floor
7 CITY: Newport Beach
8 STATE: CA
9 COUNTRY: U.S.A.
10 ZIP: 92660
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette
13 MEDIUM: IBM Compatible
14 OPERATING SYSTEM: DOS
15 SOFTWARE: FASTSEQ Version 1.5
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/294,111
18 FILING DATE:
19 CLASSIFICATION: 424
20 PCT APPLICATION DATA:
21 APPLICATION NUMBER: PCT/BE 99/00004
22 FILING DATE: 14-JUL-1995
23 ADDRESS/AGENCY INFORMATION:
24 NAME: Altman, Daniel E
25 REGISTRATION NUMBER: 34,115
26 REFERENCE/PATENT NUMBER: VANRA44-111,100
27 TECHNICAL INFORMATION:
28 TELEPHONE: 714 750-0424
29 TELEFAX: 714 750-9502
30 TEXT:
31 INFORMATION FOR SEQ ID NO: 15:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 9 amino acids
34 TYPE: coding acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: No. US0610147900A1
38 FRAGMENT TYPE: internal
39 US-09-787-443-12

```

```

1 RESULT 1
2 US-09-779-408-215
3 Sequence 203, Applicant: US/09/779,408
4 Patent No. US2002/015072A1
5 GENERAL INFORMATION:
6 APPLICANT: Mary Ellis
7 APPLICANT: Daniel E.H. Altar
8 APPLICANT: Elia M. Chalikias-Eld
9 APPLICANT: Rene S. Hubert
10 APPLICANT: Elana Levin
11 APPLICANT: Steve Chappell Mitchell
12 APPLICANT: Aya Jakubovics
13 TITLE OF INVENTION: 349073 A TISSUE SPECIFIC PROTEIN
14 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
15 FILE REFERENCE: 129,408U1
16 CURRENT APPLICATION NUMBER: US/09/779,408
17 PRIOR FILING DATE: 2001-02-08
18 PRIOR APPLICATION NUMBER: 60/181,620
19 PRIOR FILING DATE: 2000-02-08
20 NUMBER OF SEQ ID NOS: 718
21 SOFTWARE: FASTSEQ for Windows Version 4.0
22 SEQ ID NO: 43
23 LENGTH: 5
24 TYPE: FRT
25 ORGANISM: Homo Sapiens
26 US-09-779-408-215

```

Query Match 46.4% Score 41 DB 10 Length 9  
 Best Local Similarity 100.0% Prod. No. 50105  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 MKER 10  
 LR 5 MKER 8

```

1 RESULT 4
2 US-09-779-408-615
3 Sequence 203, Applicant: US/09/779,408
4 Patent No. US2002/015072A1
5 GENERAL INFORMATION:
6 APPLICANT: Mary Ellis
7 APPLICANT: Daniel E.H. Altar
8 APPLICANT: Elia M. Chalikias-Eld
9 APPLICANT: Rene S. Hubert
10 APPLICANT: Elana Levin
11 APPLICANT: Steve Chappell Mitchell
12 APPLICANT: Aya Jakubovics
13 TITLE OF INVENTION: 349073 A TISSUE SPECIFIC PROTEIN
14 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
15 FILE REFERENCE: 129,408U1
16 CURRENT APPLICATION NUMBER: US/09/779,408
17 PRIOR FILING DATE: 2001-02-08
18 PRIOR APPLICATION NUMBER: 60/181,620
19 PRIOR FILING DATE: 2000-02-08
20 NUMBER OF SEQ ID NOS: 718
21 SOFTWARE: FASTSEQ for Windows Version 4.0
22 SEQ ID NO: 615
23 LENGTH: 9
24 TYPE: FRT
25 ORGANISM: Homo Sapiens
26 US-09-779-408-615

```

Query Match 46.4% Score 41 DB 10 Length 9

```

Query Match: 66.4%, Score 4, DB 12, Length 9;
Best Local Similarity: 100.0%, Pred. No. 5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 MKPR 9
DB 6 MKPR 7

RESULT 7
US 17-210-148-18
Sequence 18: Application US/1021-148
Publication No. US2004012286A1
GENERAL INFORMATION:
APPLICANT: SODERSTROM, Karl Jester
TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
FILE REFERENCE: TROM0002
CURRENT APPLICATION NUMBER: US/01/210,148
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US/00/243,111
PRIOR FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patent Invention 4.2
SEQ ID NO 18
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 17-210-148-18

Query Match: 66.4%, Score 4, DB 12, Length 9;
Best Local Similarity: 100.0%, Pred. No. 5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 MKPR 8
DB 1 MKPR 4

RESULT 8
US 10-210-148-57
Sequence 57: Application US/10210-148
Publication No. US2004012280A1
GENERAL INFORMATION:
APPLICANT: SODERSTROM, Karl Jester
TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
FILE REFERENCE: TROM0002
CURRENT APPLICATION NUMBER: US/1 /210,148
CURRENT FILING DATE: 2002-7-31
PRIOR APPLICATION NUMBER: US/02/243,111
PRIOR FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patent Invention 4.2
SEQ ID NO 57
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 10-210-148-57

Query Match: 66.4%, Score 4, DB 12, Length 9;
Best Local Similarity: 100.0%, Pred. No. 5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 MKPR 9
DB 2 MKPR 5

RESULT 9
US 09-779-306-704
Sequence 704: Application US/09/779-306
Publication No. US20040155972A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Alati
APPLICANT: Pia M. Chaitin-Rind
APPLICANT: Roger S. Robert
APPLICANT: Eliseo Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jakovovits
TITLE OF INVENTION: 340D73: A CLASS OF PEPTIDES FOR T1N
TITLE OF INVENTION: HIGHLY EXPRESSED IN EPITHELIAL CANCER
FILE REFERENCE: 129-40511
CURRENT APPLICATION NUMBER: US/09/779-306
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US/01/021,121
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 718
SOFTWARE: FASTSEQ for Windows Version 1.1
SEQ ID NO 704
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 09-779-306-704

Query Match: 66.4%, Score 4, DB 12, Length 9;
Best Local Similarity: 100.0%, Pred. No. 5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 MKPR 10
DB 1 MKPR 4

RESULT 10
US 09-779-306-704
Sequence 704: Application US/09/779-306
Publication No. US20040155972A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Alati
APPLICANT: Pia M. Chaitin-Rind
APPLICANT: Roger S. Robert
APPLICANT: Eliseo Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jakovovits
TITLE OF INVENTION: 340D73: A CLASS OF PEPTIDES FOR T1N
TITLE OF INVENTION: HIGHLY EXPRESSED IN EPITHELIAL CANCER
FILE REFERENCE: 129-40511
CURRENT APPLICATION NUMBER: US/09/779-306
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US/01/021,121
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 718
SOFTWARE: FASTSEQ for Windows Version 1.1
SEQ ID NO 704
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 09-779-306-704

Query Match: 66.4%, Score 4, DB 12, Length 9;
Best Local Similarity: 100.0%, Pred. No. 5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 MKPR 10
DB 1 MKPR 4

RESULT 11
US 09-779-306-704
Sequence 704: Application US/09/779-306
Publication No. US20040155972A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Alati
APPLICANT: Pia M. Chaitin-Rind
APPLICANT: Roger S. Robert
APPLICANT: Eliseo Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jakovovits
TITLE OF INVENTION: 340D73: A CLASS OF PEPTIDES FOR T1N
TITLE OF INVENTION: HIGHLY EXPRESSED IN EPITHELIAL CANCER
FILE REFERENCE: 129-40511
CURRENT APPLICATION NUMBER: US/09/779-306
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US/01/021,121
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 718
SOFTWARE: FASTSEQ for Windows Version 1.1
SEQ ID NO 704
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 09-779-306-704

```

1 APPLICANT: Mary Paris  
 2 APPLICANT: Pia M. Challita-Eid  
 3 APPLICANT: Arthur B. Reitano  
 4 APPLICANT: Steve Chappell Mitchell  
 5 APPLICANT: Daniel E.H. Afar  
 6 APPLICANT: Aya Jakovovits  
 7 TITLE OF INVENTION: GIP-BINDING PROTEIN INSERT IN TREATMENT  
 8 TITLE OF INVENTION: AND DETECTION OF CANCER  
 9 FILE REFERENCE: 129 60SU1  
 10 CURRENT APPLICATION NUMBER: US/2008/4 765  
 11 PRIORITY FILING DATE: 2001-09-21  
 12 PRIOR APPLICATION NUMBER: 56/197,647  
 13 PRIORITY FILING DATE: 2000-04-12  
 14 NUMBER OF SEQ ID NOS: 770  
 15 SOFTWARE: PUSSEQ FOR WINDOWS VERSION: 4.0  
 16 SEQ ID NO: 576  
 17 LENGTH: 70  
 18 TYPE: PRF  
 19 ORGANISM: Homo sapiens  
 20 US-09-854 765, 576

```

Query Match          36.44; Score 47; ID 91 Length 137
Best Local Similarity 100.00; Pval No. 1.4e-021
Matches      4; Conservative 0; Mismatches 0; Indels 0

QY      8 PRS 11
      11
DQ      2 PRS 6
      11

RESID 10
US-09-814-765-691
1 Sequence 691 Application US/09824765
2 Patent No. US200505478A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Paris
5 APPLICANT: Psa M. Chalhita-Eid
6 APPLICANT: Arthur B. Raitaco
7 APPLICANT: Steve Chappell Mitchell
8 APPLICANT: Daniel E.H. Alar
9 APPLICANT: Asa Jakobovits
10 TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN PEPTAININ
11 TITLE OF INVENTION: AND DETECTION OF CANCER
12 FILE REFERENCE: 129 6US01
13 CURRENT APPLICATION NUMBER: US/09/814-765
14 CURPENT FILING DATE: 2007-09-21
15 PRIOR APPLICATION NUMBER: 60/117,647
16 PRIOR FILING DATE: 2000-04-12
17 NUMBER OF SEQ. ID NOS: 770
18 SOFTWARE: FASTSEQ for Windows Version 4.3
19 SEQ. ID NOS: 1
20 GENCHE 10
21 TYPE: PRT
22 ORGANISM: Homo sapiens
23 US-09-814-765-691

```

```

Query Match      36.4%  Score 41  Pos 9  Length 10
Best Local Similarity 100.0%  Pred. N 4  Rec 0.1
Matches 4: Conservative 0: Miscellaneous 0: Models

QY      6 FRRS 11
      11 1
LE      2 FRRS 5

PES01.1
US-59-779 408 130
: Sequence 139, Application US/59779408
: Patent No. US20029150972A1
: GENERAL INFORMATION:
: APPLICANT: Mary Fails
: APPLICANT: Dorian, E.H., Atar
: APPLICANT: Ed M. Challa, Ed

```

```

1  APPLICANT: Rene S. Hubert.
2  APPLICANT: Diana Levin
3  APPLICANT: Steve Chappell Mitchell
4  APPLICANT: Aya Jakobovits
5  TITLE OF INVENTION: 4P3d7: A TISSUE SPECIFIC PROTEIN
6  TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
7  FILE REFERENCE: 129-40SU1
8  CURRENT APPLICATION NUMBER: US/59779,308
9  PRIOR FILING DATE: 2001-02-08
10 PRIOR APPLICATION NUMBER: 60/181,920
11 PRIOR FILING DATE: 2000-02-08
12 NUMBER OF SEQ. Lf. Ns: 718
13 SOFTWARE: FASTSEQ for Windows Version: 4.0
14 SEQ. ID NO: 140
15 LENGTH: 10
16 TYPE: PRT
17 ORGANISM: Homo Sapiens
18 US-05-779-308-140

```

```

Query Match          16.4%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3; se-02;
Matches 4; Conservative 0; Mismatches 0; Indels

QY      7 KPRR 10
      IIII
LU      7 KPRR 10

RESULT 12
US-09-779-308-339
: Sequence 339; Application US/04779-308
: Patent No. US20020150972A;
: GENERAL INFORMATION:
: APPLICANT: Mary Paris
: APPLICANT: Daniel E.H. Ate;
: APPLICANT: Pia M. Chalita-Eid
: APPLICANT: Rene S. Hubert
: APPLICANT: Flana Levie
: APPLICANT: Steve Chappell Mitchell
: APPLICANT: Ava Jakabovits
: TITLE OF INVENTION: 34P307; A TISSUE SPECIFIC PROTEIN
: TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
: FILE REFERENCE: 129.40US01
: CURRENT APPLICATION NUMBER: US/09/779,308
: CURRENT FILING DATE: 2001-02-08
: PRIOR APPLICATION NUMBER: 60/181,020
: PRIOR FILING DATE: 2000-02-08
: NUMBER OF SEQ ID NOS: 718
: SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
: SEQ ID NO 339
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-779-308-339

```

```

Query Match: 46.4%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pctd. No. 3 3e-02;
Matches 4; Conservative 0; Mismatches 0; Indels
QY 7 KPRR 10
DB 3 KPRR 5
RESULT 13
US: 09-779-304-351
: Sequence 351, Application US/09779308
: Patent No. US20020150972A1
: GENERAL INFORMATION:
: APPLICANT: Mary Paris
: APPLICANT: Daniel E.H. Ator
: APPLICANT: P.M. Chaffin-Rid
: APPLICANT: Roger S. Hubert

```

```

1 APPLICANT: Elana Levin
2 APPLICANT: Steve Chappell Mitchell
3 APPLICANT: Aya Jakobovits
4 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
5 FILE REFERENCE: 129.4US01
6 CURRENT APPLICATION NUMBER: US/09/779,308
7 PRIOR FILING DATE: 2001-02-08
8 PRIOR APPLICATION NUMBER: 60/181,620
9 NUMBER OF SEQ ID NOS: 718
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 531
12 LENGTH: 10
13 TYPE: PR1
14 ORGANISM: Homo Sapiens
15 US-09-779-408-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

RESULT 14
US-09-779-408-531
1 Sequence 531: Application US/09779308
2 Patent No. US20020150972A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Fatis
5 APPLICANT: Daniel E.H. Atar
6 APPLICANT: Pia M. Chailita-Eid
7 APPLICANT: Rene S. Hubert
8 APPLICANT: Elana Levin
9 APPLICANT: Steve Chappell Mitchell
10 APPLICANT: Aya Jakobovits
11 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
12 FILE REFERENCE: 129.4US01
13 CURRENT APPLICATION NUMBER: US/09/779,308
14 CURRENT FILING DATE: 2001-02-08
15 PRIOR APPLICATION NUMBER: 60/181,620
16 PRIOR FILING DATE: 2000-02-08
17 NUMBER OF SEQ ID NOS: 718
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO: 531
20 LENGTH: 10
21 TYPE: PR1
22 ORGANISM: Homo Sapiens
23 US-09-779-408-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

```

```

1 APPLICANT: Elana Levin
2 APPLICANT: Steve Chappell Mitchell
3 APPLICANT: Aya Jakobovits
4 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
5 FILE REFERENCE: 129.4US01
6 CURRENT APPLICATION NUMBER: US/09/779,308
7 PRIOR FILING DATE: 2001-02-08
8 PRIOR APPLICATION NUMBER: 60/181,620
9 NUMBER OF SEQ ID NOS: 718
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 519
12 LENGTH: 10
13 TYPE: PR1
14 ORGANISM: Homo Sapiens
15 US-09-779-308-519

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

RESULT 15
US-09-779-308-519
1 Sequence 531: Application US/09779308
2 Patent No. US20020150972A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Fatis
5 APPLICANT: Daniel E.H. Atar
6 APPLICANT: Pia M. Chailita-Eid
7 APPLICANT: Rene S. Hubert
8 APPLICANT: Elana Levin
9 APPLICANT: Steve Chappell Mitchell
10 APPLICANT: Aya Jakobovits
11 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
12 FILE REFERENCE: 129.4US01
13 CURRENT APPLICATION NUMBER: US/09/779,308
14 CURRENT FILING DATE: 2001-02-08
15 PRIOR APPLICATION NUMBER: 60/181,620
16 PRIOR FILING DATE: 2000-02-08
17 NUMBER OF SEQ ID NOS: 718
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO: 531
20 LENGTH: 10
21 TYPE: PR1
22 ORGANISM: Homo Sapiens
23 US-09-779-308-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

```

```

1 APPLICANT: Elana Levin
2 APPLICANT: Steve Chappell Mitchell
3 APPLICANT: Aya Jakobovits
4 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
5 FILE REFERENCE: 129.4US01
6 CURRENT APPLICATION NUMBER: US/09/779,308
7 PRIOR FILING DATE: 2001-02-08
8 PRIOR APPLICATION NUMBER: 60/181,620
9 NUMBER OF SEQ ID NOS: 718
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 531
12 LENGTH: 10
13 TYPE: PR1
14 ORGANISM: Homo Sapiens
15 US-09-779-308-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

RESULT 16
US-09-779-308-531
1 Sequence 519: Application US/09779308
2 Patent No. US20020150972A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Fatis
5 APPLICANT: Daniel E.H. Atar
6 APPLICANT: Pia M. Chailita-Eid
7 APPLICANT: Rene S. Hubert
8 APPLICANT: Elana Levin

```

1 APPLICANT: AYA JAKOBOWITS  
 2 TITLE OF INVENTION: 340357: A TISSUE SPECIFIC PROTEIN  
 3 FILE REFERENCE: 129.4US01  
 4 CURRENT APPLICATION NUMBER: US/09/779,308  
 5 PRIOR FILING DATE: 2001-02-08  
 6 PRIOR APPLICATION NUMBER: 60/181,620  
 7 PRIOR FILING DATE: 2000-02-08  
 8 NUMBER OF SEQ ID NOS: 718  
 9 SOFTWARE: FASTSEQ for Windows Version 4.0  
 10 SEQ ID NO: 644  
 11 LENGTH: 10  
 12 TYPE: PRT  
 13 ORGANISM: Homo Sapiens  
 14 US-09-779,308,644

Query Match: 36.4%, Score 4: 19 10: Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 3, Re+02;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 18  
 US-09-779,308,644  
 1 Sequence 666: Application US/09/779,308  
 2 Patent No. US20020150972A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Paris  
 5 APPLICANT: Daniel E.H. Afari  
 6 APPLICANT: Pia M. Chailita-Fid  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits  
 11 TITLE OF INVENTION: 340357: A TISSUE SPECIFIC PROTEIN  
 12 FILE REFERENCE: 129.4US01  
 13 CURRENT APPLICATION NUMBER: US/09/779,308  
 14 PRIOR FILING DATE: 2001-02-08  
 15 PRIOR APPLICATION NUMBER: 60/181,620  
 16 PRIOR FILING DATE: 2000-02-08  
 17 NUMBER OF SEQ ID NOS: 718  
 18 SOFTWARE: FASTSEQ for Windows Version 4.0  
 19 SEQ ID NO: 644  
 20 LENGTH: 10  
 21 TYPE: PRT  
 22 ORGANISM: Homo Sapiens  
 23 US-09-779,308,644

Query Match: 36.4%, Score 4: 19 10: Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 3, Re+02;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 19  
 US-09-779,308,644  
 1 Sequence 644: Application US/09/779,308  
 2 Patent No. US20020150972A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Paris  
 5 APPLICANT: Daniel E.H. Afari  
 6 APPLICANT: Pia M. Chailita-Fid  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits

1 TITLE OF INVENTION: 340357: A TISSUE SPECIFIC PROTEIN  
 2 FILE REFERENCE: 129.4US01  
 3 CURRENT APPLICATION NUMBER: US/09/779,308  
 4 PRIOR FILING DATE: 2001-02-08  
 5 PRIOR APPLICATION NUMBER: 60/181,620  
 6 PRIOR FILING DATE: 2000-02-08  
 7 NUMBER OF SEQ ID NOS: 718  
 8 SOFTWARE: FASTSEQ for Windows Version 4.0  
 9 SEQ ID NO: 644  
 10 LENGTH: 10  
 11 TYPE: PRT  
 12 ORGANISM: Homo Sapiens  
 13 US-09-779,308,644

Query Match: 36.4%, Score 4: 19 10: Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 3, Re+02;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 20  
 US-09-779,308,666  
 1 Sequence 666: Application US/09/779,308  
 2 Patent No. US20020150972A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Paris  
 5 APPLICANT: Daniel E.H. Afari  
 6 APPLICANT: Pia M. Chailita-Fid  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits  
 11 TITLE OF INVENTION: 340357: A TISSUE SPECIFIC PROTEIN  
 12 FILE REFERENCE: 129.4US01  
 13 CURRENT APPLICATION NUMBER: US/09/779,308  
 14 PRIOR FILING DATE: 2001-02-08  
 15 PRIOR APPLICATION NUMBER: 60/181,620  
 16 PRIOR FILING DATE: 2000-02-08  
 17 NUMBER OF SEQ ID NOS: 718  
 18 SOFTWARE: FASTSEQ for Windows Version 4.0  
 19 SEQ ID NO: 666  
 20 LENGTH: 10  
 21 TYPE: PRT  
 22 ORGANISM: Homo Sapiens  
 23 US-09-779,308,666

Query Match: 36.4%, Score 4: 19 10: Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 3, Re+02;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 21  
 US-09-966,422B,15  
 1 Sequence 15: Application US/09/966,422B  
 2 Publication No. US20030044892A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Bristol Myers Squibb Company  
 5 TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HSPRBMV6, EXPRESSED  
 6 FILE REFERENCE: 1004387/3553 4119US3  
 7 CURRENT APPLICATION NUMBER: US/09/966,422B  
 8 PRIOR FILING DATE: 2002-05-07  
 9 PRIOR APPLICATION NUMBER: 60/245,602  
 10 PRIOR FILING DATE: 2000-09-27

```

1 PRIORITY APPLICATION NUMBER: 60/302,604
2 PRIOR FILING DATE: 2001-07-19
3 PRIOR APPLICATION NUMBER: 60/311,412
4 PRIOR FILING DATE: 2001-08-26
5 NUMBER OF SEQ ID NOS: 81
6 SOFTWARE: Patent in version 1.0
7 SEQ ID NO: 1
8 LENGTH: 1
9 TYPE: PRT
10 ORGANISM: Homo sapiens
11 US 09-787-443-12
12
13 Query Match: 36.4% Score 4: DB 11: Length 10;
14 Best Local Similarity: 100.0% Prod. No. 34002;
15 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
16
17 Q1 8 PERFS 11
18 1
19 2 PERFS 1
20
21 RESULT 24
22 US 09-572-404B-2518
23 Sequence 2518: Application US/09572404B
24 Publication No. US2003028374A1
25 GENERAL INFORMATION:
26 APPLICANT: Proteome Ltd
27 TITLE OF INVENTION: Complementary peptide ligands from the human genome
28 FILE REFERENCE: Human Patent US/09/572,404B
29 CURRENT APPLICATION NUMBER: US/09/572,404B
30 CURRENT FILING DATE: 2003-05-17
31 NUMBER OF SEQ ID NOS: 4203
32 SOFTWARE: Patent in version 1.0
33 SEQ ID NO: 2518
34 LENGTH: 1
35 TYPE: PRT
36 ORGANISM: Homo Sapiens
37 FEATURE:
38 OTHER INFORMATION: Sequence located in SPT at 224-233 and may interact with Sequ
39 US 09-572-404B-2518
40
41 Query Match: 46.4% Score 4: DB 11: Length 10;
42 Best Local Similarity: 100.0% Prod. No. 34002;
43 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
44
45 Q1 8 PERFS 11
46 1
47 4 PERFS 7
48
49 RESULT 29
50 US 09-572-404B-263
51 Sequence 263: Application US/09572406A
52 Publication No. US2003028374A1
53 GENERAL INFORMATION:
54 APPLICANT: Proteome Ltd
55 TITLE OF INVENTION: Complementary peptide ligands
56 FILE REFERENCE:
57 CURRENT APPLICATION NUMBER: US/09/572,406A
58 CURRENT FILING DATE: 2003-05-17
59 NUMBER OF SEQ ID NOS: 144
60 SOFTWARE: Patent in version 1.0
61 SEQ ID NO: 263
62 LENGTH: 1
63 TYPE: PRT
64 ORGANISM: Arabidopsis thaliana
65 OTHER INFORMATION: Sequence located in CYP8A5 or P2085 9. at 265-264 and may
66 US 09-572-404B-263
67
68 Query Match: 34.4% Score 4: DB 12: Length 10;
69 Best Local Similarity: 100.0% Prod. No. 34002;
70 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
71
72 Q1 1 PERFS 4
73 1
74 1 PERFS 3
75
76 RESULT 29
77 US 09-572-404B-266
78 Sequence 266: Application US/09572406A
79 Publication No. US2003028374A1
80 GENERAL INFORMATION:
81 APPLICANT: Proteome Ltd
82 TITLE OF INVENTION: Complementary peptide ligands from the human genome
83 FILE REFERENCE: Human Patent
84 CURRENT APPLICATION NUMBER: US/09/572,406A
85 CURRENT FILING DATE: 2003-05-17
86 NUMBER OF SEQ ID NOS: 4203
87 SOFTWARE: Patent in version 1.0
88 SEQ ID NO: 266
89 LENGTH: 1
90 TYPE: PRT
91 ORGANISM: Homo Sapiens
92 FEATURE:
93 OTHER INFORMATION: Synthesized peptide
94 US 09-787-443-12
95
96 Query Match: 36.4% Score 4: DB 11: Length 10;
97 Best Local Similarity: 100.0% Prod. No. 34002;
98 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
99
100 Q1 8 PERFS 11
101 1
102 1 PERFS 1
103
104 RESULT 27
105 US 09-572-404B-266
106 Sequence 266: Application US/09572406A
107 Publication No. US2003028374A1
108 GENERAL INFORMATION:
109 APPLICANT: Proteome Ltd
110 TITLE OF INVENTION: Complementary peptide ligands from the human genome
111 FILE REFERENCE: Human Patent
112 CURRENT APPLICATION NUMBER: US/09/572,406A
113 CURRENT FILING DATE: 2003-05-17
114 NUMBER OF SEQ ID NOS: 4203
115 SOFTWARE: Patent in version 1.0
116 SEQ ID NO: 266
117 LENGTH: 1
118 TYPE: PRT
119 ORGANISM: Homo Sapiens
120 FEATURE:
121 OTHER INFORMATION: Synthesized peptide

```



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US 09 572 270A-231
? Sequence 243, Application US/09572270A
? Publication No. US20030148368A1
? GENERAL INFORMATION:
? APPLICANT: Proteom Ltd
? TITLE OF INVENTION: Inter-complementary peptide binding
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/09572270A
? CURRENT FILING DATE: 2000-05-17
? NUMBER OF SEQ ID NOS: 1144
? SOFTWARE: ProPatent version 1.0
? SEQ ID NO 231
? LENGTH: 10
? TYPE: PR1
? ORGANISM: Arabidopsis thaliana
? OTHER INFORMATION: Sequence located in CYPRUS at 250-265 and may
US 09 572 270A-231

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGRK 4
   11
SD 3 AGRK 8

RESULT 27
US 09 572 270A-231
? Sequence 243, Application US/09572270A
? Publication No. US20030148368A1
? GENERAL INFORMATION:
? APPLICANT: Proteom Ltd
? TITLE OF INVENTION: Inter-complementary peptide binding
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/09572270A
? CURRENT FILING DATE: 2000-05-17
? NUMBER OF SEQ ID NOS: 1144
? SOFTWARE: ProPatent version 1.0
? SEQ ID NO 233
? LENGTH: 10
? TYPE: PR1
? ORGANISM: Arabidopsis thaliana
? OTHER INFORMATION: Sequence located in CYPRUS at 250-265 and may
US 09 572 270A-231

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGRK 4
   11
SD 4 AGRK 7

RESULT 28
US 10 190 082 352
? Sequence 342, Application US/10190082
? Publication No. US20030148264A1
? GENERAL INFORMATION:
? APPLICANT: Lasky, Lawrence A.
? APPLICANT: Sidhu, Sachdev S.
? APPLICANT: Held, Heiko A.
? TITLE OF INVENTION: PHAGE DISPLAYED PEZ DOMAIN AND PEPTIDES
? FILE REFERENCE: P1905R1
? CURRENT APPLICATION NUMBER: US/10190082
? CURRENT FILING DATE: 2002-07-04
? PRIOR APPLICATION NUMBER: US 60/466,604
? PRIOR FILING DATE: 2001-07-06
? NUMBER OF SEQ ID NOS: 683
? SEQ ID NO 352
? LENGTH: 10
? TYPE: PR1

```

```

? ORGANISM: Artificial sequence
? FEATURE:
? OTHER INFORMATION: Synthetic
US-10-190 082 352

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 5
   11
SD 1 KRRK 4

RESULT 29
US-10-262-272A-15
? Sequence 15, Application US/10262272A
? Publication No. US20030170671A1
? GENERAL INFORMATION:
? APPLICANT: Bristol Myers Squibb Company
? TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR. HGPBRMY6
? FILE REFERENCE: D0944 CIP
? CURRENT APPLICATION NUMBER: US/10/262,272A
? CURRENT FILING DATE: 2002-05-27
? PRIOR APPLICATION NUMBER: U.S. 09/965,422
? PRIOR FILING DATE: 2001-09-26
? NUMBER OF SEQ ID NOS: 91
? SOFTWARE: Patent version 4.2
? SEQ ID NO 15
? LENGTH: 10
? TYPE: PR1
? ORGANISM: Homo sapiens
US-10-262-272A-15

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TMKP 5
   11
SD 3 TMKP 5

RESULT 30
US-09-832-355A-B
? Sequence 8, Application US/09832355A
? Publication No. US2003022761A1
? GENERAL INFORMATION:
? APPLICANT: Kossler, Eric
? APPLICANT: Kossler, Eric
? TITLE OF INVENTION: VEGF FUSION PROTEINS
? FILE REFERENCE: 20564
? CURRENT APPLICATION NUMBER: US/09/832,355A
? CURRENT FILING DATE: 2001-04-19
? NUMBER OF SEQ ID NOS: 126
? SOFTWARE: Patent version 4.0
? SEQ ID NO 8
? LENGTH: 11
? TYPE: PR1
? ORGANISM: Homo sapiens
US 09-832-355A-B

Query Match          36.4%  Score 4; DB 11; Length 11;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRRR 10
   11
SD 8 KRRR 11

RESULT 31
US-10-190 942 33

```

```

1 Sequence 73: Application US/05/101190A
2 Publication No. US20030069181A
3 GENERAL INFORMATION:
4 APPLICANT: Wesq Almet J.
5 TITLE OF INVENTION: Artificial Sequence
6 FILE OF INVENTION: Basis for Multiplication of a Protein
7 FILE REFERENCE: 891.8
8 CURRENT APPLICATION NUMBER: US/05/101190A
9 PRIOR FILING DATE: 2002-05-24
10 PRIOR APPLICATION NUMBER: US 69/293,131
11 PRIOR FILING DATE: 2001-05-25
12 NUMBER OF SEQ ID NOS: 82
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO: 93
15 LENGTH: 12
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 NAME/KEY: MOD_RES
20 LOCATION: 1
21 OTHER INFORMATION: VEG: all sphex 31
22 US 10:54,942-94
23
24 Query Match: 36.4% Score 41 DP 25 Length 12
25 Best Local Similarity: 100.0% Pred. No. 3 bc+02
26 Matches: 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0
27
28 US 7 KERR 10
29
30 DB:
31
32 RESULT 32
33 US 10:54,942-94
34 Sequence 17: Application US/1001190A
35 Publication No. US2003010422A
36 GENERAL INFORMATION:
37 APPLICANT: Rothlis, Paul D.
38 APPLICANT: Flizzello, Raymond
39 APPLICANT: Glattuso, Joseph C.
40 APPLICANT: Gambleto, Andrea
41 TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
42 FACILITATE BREAK AND CLEAVAGE OF ANGIOGENIC AND VASCULAR
43 ENDOTHELIAL CELL GROWTH
44 FILE OF INVENTION: OF PROTEINS, DNA AND VASCLES
45 FILE REFERENCE: AP42573 AAA 07/496,9247
46 CURRENT APPLICATION NUMBER: US/10/01190A
47 PRIOR FILING DATE: 2002-02-13
48 PRIOR APPLICATION NUMBER: 09/111,906
49 PRIOR FILING DATE: 1999-08-03
50 PRIOR APPLICATION NUMBER: 07/496,924
51 PRIOR FILING DATE: 2000-09-14
52 NUMBER OF SEQ ID NOS: 90
53 SOFTWARE: FastSeq for Windows Version 4.0
54 SEQ ID NO: 17
55 LENGTH: 12
56 TYPE: PRT
57 ORGANISM: Artificial Sequence
58 FEATURE:
59 NAME/KEY: MOD_RES
60 LOCATION: 1
61 OTHER INFORMATION: random peptide library
62 US 10:075,469-17
63
64 Query Match: 36.4% Score 41 DP 25 Length 12
65 Best Local Similarity: 100.0% Pred. No. 3 bc+02
66 Matches: 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0
67
68 US 3 KKM 6
69
70 DB:
71
72 RESULT 33
73 US 10:197-994 102
74 Sequence 102: Application US/101190A
75 Publication No. US20040119021A

```

```

1 GENERAL INFORMATION:
2 APPLICANT: Kstet, Robert
3 APPLICANT: Soddiqui, Sadiq
4 APPLICANT: Little, Robert
5 TITLE OF INVENTION: Capture Capabilities, Collections Thereof
6 FILE OF INVENTION: Add Methods For Analyzing The Proteome And Complex
7 FILE REFERENCE: 2474-2355
8 CURRENT APPLICATION NUMBER: US/10/197,994
9 PRIOR FILING DATE: 2002-07-16
10 PRIOR APPLICATION NUMBER: 69/686,809
11 PRIOR FILING DATE: 2001-07-16
12 PRIOR APPLICATION NUMBER: 69/614,124
13 PRIOR FILING DATE: 2001-08-21
14 PRIOR APPLICATION NUMBER: 69/363,444
15 PRIOR FILING DATE: 2002-03-11
16 NUMBER OF SEQ ID NOS: 149
17 SOFTWARE: FastSeq for Windows Version 4.0
18 SEQ ID NO: 102
19 LENGTH: 12
20 TYPE: PRT
21 ORGANISM: Homo Sapiens
22 FEATURE:
23 NAME/KEY: MOD_RES
24 LOCATION: 1
25 OTHER INFORMATION: Xaa is pyroglutamic acid
26 US 10:197-994-102
27
28 Query Match: 36.4% Score 41 DP 15 Length 12
29 Best Local Similarity: 100.0% Pred. No. 3 bc+02
30 Matches: 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0
31
32 US 7 KERR 10
33
34 DB:
35
36 RESULT 34
37 US 09:985-672 2
38 Sequence 2: Application US/09985672
39 Patent No. US2002155064A
40 GENERAL INFORMATION:
41 APPLICANT: Reub, Jean Claude
42 TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF
43 PROTEIN IN TISSUES
44 FILE OF INVENTION: MALIGNANT HUMAN TUMORS
45 FILE REFERENCE: 1588-304
46 CURRENT APPLICATION NUMBER: US/09/985,672
47 PRIOR FILING DATE: 2001-07-15
48 PRIOR APPLICATION NUMBER: US/09/566,899
49 PRIOR FILING DATE: 1999-08-03
50 PRIOR APPLICATION NUMBER: 07/0598/31564
51 PRIOR FILING DATE: 1998-12-02
52 PRIOR APPLICATION NUMBER: EP 97200297.6
53 PRIOR FILING DATE: 1997-02-04
54 NUMBER OF SEQ ID NOS: 3
55 SOFTWARE: PatentId Ver. 2.0
56 SEQ ID NO: 2
57 LENGTH: 12
58 TYPE: PRT
59 ORGANISM: Homo sapiens
60 FEATURE:
61 NAME/KEY: SITE
62 LOCATION: (1)
63 OTHER INFORMATION: This site is pyroglutamate.
64 US 09:985-672-2
65
66 Query Match: 36.4% Score 41 DP 10 Length 13
67 Best Local Similarity: 100.0% Pred. No. 4 bc+02
68 Matches: 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0
69
70 US 7 KERR 10
71
72 DB:
73
74 US 4 KERR 7

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: TITLE OF INVENTION: SMALL INTESTINE
: FILE REFERENCE: 00049NP/3953-4119US3
: CURRENT APPLICATION NUMBER: US/09/966,422B
: CURRENT FILING DATE: 2002-05-07
: PRIOR APPLICATION NUMBER: 66/235,602
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: 60/306,604
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 66/415,412
: PRIOR FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 81
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 35
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09 966-422B:35

Query Match: 36.4%; Score 4; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 TMKP 8
   III
TB 6 TMKP 9

RESULT 3e
US-10-169-223:25
: Sequence 25, Application US/10/169223
: Publication No. US20040152946A1
: GENERAL INFORMATION:
: APPLICANT: SHIMIZU, Shigeaki
: APPLICANT: TSUTSUMOTO, Yoshinobu
: TITLE OF INVENTION: BH4-Fused Polypeptides
: FILE REFERENCE: 1422-05379
: CURRENT APPLICATION NUMBER: US/10/169,223
: CURRENT FILING DATE: 2002-11-05
: PRIOR APPLICATION NUMBER: JP 11-371449
: PRIOR FILING DATE: 1999-12-27
: PRIOR APPLICATION NUMBER: PCT/JP00/09274
: PRIOR FILING DATE: 2000-12-26
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: Patent in version 3.1
: SEQ ID NO 25
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Homo 1 lymphotropic virus
US 10-169-223:25

Query Match: 36.4%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRRS 11
   III
TB 6 PRRS 9

RESULT 39
US-10-050-200:21
: Sequence 21, Application US/10/050200
: Publication No. US20030156037A1
: GENERAL INFORMATION:
: APPLICANT: Fourie, Alno
: APPLICANT: Colles, Fawa
: APPLICANT: Karlsson, Lars
: TITLE OF INVENTION: Agglutininase-1 and -2 Peptide Substrates and Methods
: FILE REFERENCE: ORT-1417
: CURRENT APPLICATION NUMBER: US/10/050,200
: CURRENT FILING DATE: 2002-01-16
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: Patent in version 3.1

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: TITLE OF INVENTION: NOVEL ANTIMETASTASIS AGENTS
: FILE REFERENCE: 18475-025
: CURRENT APPLICATION NUMBER: US/09/966,792
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/252,469
: PRIOR FILING DATE: 2000-11-21
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patent in Ver. 2.1
: SEQ ID NO 4
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09 966-792:4

Query Match: 36.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRRP 10
   I
TB 6 KRRP 9

RESULT 46
US-09-968-792:14
: Sequence 14, Application US/09/968792
: Publication No. US20030032599A1
: GENERAL INFORMATION:
: APPLICANT: Lukowski, Andrezej W
: APPLICANT: Galt, Daniel B
: TITLE OF INVENTION: NOVEL ANTIMETASTASIS AGENTS
: FILE REFERENCE: 18475-025
: CURRENT APPLICATION NUMBER: US/09/968,792
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/252,469
: PRIOR FILING DATE: 2000-11-21
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patent in Ver. 2.1
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Homo sapiens
: NAME/KEY: VARIANT
: LOCATION: (1)
: OTHER INFORMATION: wherein Xaa is ty or try
US-09 968-792:14

Query Match: 36.4%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRRP 10
   III
TB 6 KRRP 9

RESULT 47
US-09 966-422B:35
: Sequence 35, Application US/09/966422B
: Publication No. US20030044892A1
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLIN AND F3 RECEPTOR, EXPRESSED BY

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1 300-WARE FastSeq for Windows Version 4.0
2 SEQ ID NO: 22
3 LENGTH: 15
4 TYPE: PRT
5 ORGANISM: Homo sapiens
6 FEATURES
7   OTHER INFORMATION: epitope 1-2001 (1-2001) 1-2 domain 1-2001
8   OTHER INFORMATION: VIII
9 US 09-853 97A 2
10
11 Query Match: 46.4%; Score 4; DB 9; Length 8;
12 Best Local Similarity: 100.0%; Pred. No. 4; DB 9;
13 Matches: 4; Conservative 0; Mismatches 0; Indels 0;
14
15 27 1 PER 4
16 11
17 9 PER 12
18
19 RESULT 47
20 US 09-853 97A 2
21 Sequence 24, Application US/09-853 97A
22 Patent No. US2002/004456A1
23 GENERAL INFORMATION
24 APPLICANT: AVERBACK, PAUL
25 APPLICANT: GEMMEL, JACK
26 TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
27 TITLE OF INVENTION: CONDITIONS REQ DURING THE REMOVAL OF RESTRICTION OF CHLRS
28 FILE REFERENCE: 59003.000010
29 CURRENT APPLICATION NUMBER: US/09-853 97A
30 CURRENT FILING DATE: 2002-05-15
31 PRIOR APPLICATION NUMBER: 667401.447
32 PRIOR FILING DATE: 2002-11-16
33 NUMBER OF SEQ ID NOS: 47
34 SOFTWARE: PatentIn version 4.2
35 SEQ ID NO: 22
36 LENGTH: 15
37 TYPE: PRT
38 ORGANISM: Homo sapiens
39 US 09-853 97A 2
40
41 Query Match: 46.4%; Score 4; DB 9; Length 8;
42 Best Local Similarity: 100.0%; Pred. No. 4; DB 9;
43 Matches: 4; Conservative 0; Mismatches 0; Indels 0;
44
45 27 2 PER 4
46 11
47 9 PER 12
48
49 RESULT 47
50 US 09-853 97A 2
51 Sequence 41, Application US/09-853 97A
52 Patent No. US2002/004225A1
53 GENERAL INFORMATION
54 APPLICANT: Stewart, Mary
55 APPLICANT: Kozma, Sarah
56 APPLICANT: Thomas, George
57 TITLE OF INVENTION: Drosophila melanogaster 2-3 domain
58 FILE REFERENCE: 4-2097/A
59 CURRENT APPLICATION NUMBER: US/09-853 97A
60 CURRENT FILING DATE: 2001-03-20
61 PRIOR APPLICATION NUMBER: 09/230,247
62 PRIOR FILING DATE: 1999-04-16
63 NUMBER OF SEQ ID NOS: 5
64 SOFTWARE: PatentIn Ver. 2.0
65 SEQ ID NO: 4
66 LENGTH: 4
67 TYPE: PRT
68 ORGANISM: Artificial Sequence
69 FEATURES
70 OTHER INFORMATION: Described in US 2002/004225A1
71 OTHER INFORMATION: Trademark of Sequencing
```

```
US 09-853 97A 4
1 Query Match: 47.0%; Score 4; DB 9; Length 8;
2 Best Local Similarity: 100.0%; Pred. No. 4; DB 9;
3 Matches: 4; Conservative 0; Mismatches 0; Indels 0;
4
5 27 1 PER 10
6 11
7 4 PER 5
8
9 RESULT 46
10 US 09-853 97A 4
11 Sequence 6, Application US/09-853 97A
12 Patent No. US2002/004456A1
13 GENERAL INFORMATION
14 APPLICANT: Achileva, Samuel L.
15 APPLICANT: Rajagopalan, Radhavan
16 APPLICANT: Dorshow, Richard B.
17 APPLICANT: Baga, Joseph E.
18 APPLICANT: Mallinckrodt, Inc.
19 TITLE OF INVENTION: Lumor-Targeted optical Contrast Agents
20 FILE REFERENCE: 860-65
21 CURRENT APPLICATION NUMBER: US/09-853 97A
22 CURRENT FILING DATE: 2001-05-23
23 PRIOR APPLICATION NUMBER: US 09/484,320
24 PRIOR FILING DATE: 2000-01-18
25 NUMBER OF SEQ ID NOS: 8
26 SOFTWARE: FASTSEQ for Windows Version 4.0
27 SEQ ID NO: 6
28 LENGTH: 8
29 TYPE: PRT
30 ORGANISM: Artificial Sequence
31 FEATURES
32 NAME/KEY: 400 RES
33 LOCATION: (1)-(1)
34 OTHER INFORMATION: X-ray at location 1 represents D-Lys. Artificial sequence is
35 OTHER INFORMATION: completely synthesized.
36 US 09-853 97A 4
37
38 Query Match: 47.0%; Score 4; DB 9; Length 8;
39 Best Local Similarity: 100.0%; Pred. No. 4; DB 9;
40 Matches: 4; Conservative 0; Mismatches 0; Indels 0;
41
42 27 1 PER 10
43 11
44 4 PER 4
45
46 RESULT 47
47 US 09-853 97A 4
48 Sequence 41, Application US/09-853 97A
49 Patent No. US2002/004456A1
50 GENERAL INFORMATION
51 APPLICANT: Stewart, Mary
52 APPLICANT: Kozma, Sarah
53 APPLICANT: Thomas, George
54 TITLE OF INVENTION: Assays for Protein Kinases Using
55 Fluorescent Protein Substrates
56 FILE REFERENCE: 4-2097/A
57 CURRENT APPLICATION NUMBER: 09/230,247
58 CURRENT FILING DATE: 2001-03-20
59 PRIOR APPLICATION NUMBER: 09/230,247
60 PRIOR FILING DATE: 1999-04-16
61 NUMBER OF SEQ ID NOS: 5
62 SOFTWARE: PatentIn Ver. 2.0
63 SEQ ID NO: 4
64 LENGTH: 4
65 TYPE: PRT
66 ORGANISM: Artificial Sequence
67 FEATURES
68 OTHER INFORMATION: Described in US 2002/004456A1
69 OTHER INFORMATION: Trademark of Sequencing
```

1 FILING DATE: 19 Jun 2003  
 2 CLASSIFICATION: UNKNOWN  
 3 PUBLICATION DATA  
 4 APPLICATION NUMBER: us/09/044312  
 5 FILING DATE: unknown  
 6 ADDRESS/AGENT INFORMATION  
 7 NAME: STORELLO, JOHN S.  
 8 REGISTRATION NUMBER: 52061546A  
 9 REFERENCE/DOCKET NUMBER: 2003-09-044312  
 10 TELEPHONE: (415) 576-0200  
 11 TELEFAX: (415) 576-0200  
 12 INFORMATION FOR SEQ ID NO. 41:  
 13 SEQUENCE CHARACTERISTICS  
 14 LENGTH: 8 amino acids  
 15 TYPE: amino acid  
 16 STRANDEDNESS: unknown  
 17 TOPOLOGY: linear  
 18 MOLECULE TYPE: peptide  
 19 SEQUENCE DESCRIPTION: SEQ ID NO. 41:  
 20 US-09-044312-41  
 21  
 22 Quality Match: 27.0%, Score 41, DB 9, Length 8;  
 23 Best Local Similarity: 100.0%, Pos: 50-05;  
 24 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 25  
 26 Q7 9 RES 11  
 27 11  
 28 4 RES 3  
 29  
 30 US-09-044312-42  
 31  
 32 Sequence 20: Application US/09/044312  
 33 Patent No. US2003/01142A1  
 34 GENERAL INFORMATION  
 35 APPLICANT: Storello, John S.  
 36 TITLE OF INVENTION: MEMBRANE-BINDING CYTOKINE COMPOSITIONS  
 37 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 38 RESPONSE USING SAME  
 39  
 40 NUMBER OF SEQUENCES: 50  
 41 CORRESPONDENCE ADDRESS  
 42 ADDRESSEE: CAMPBELL & FIDRES, LLP  
 43 STREET: 4370 La Colina Village Drive, Suite 700  
 44 CITY: San Diego  
 45 STATE: California  
 46 COUNTRY: United States  
 47 ZIP: 92121  
 48 COMPUTER READABLE FORM  
 49 MEDIUM TYPE: floppy disk  
 50 COMPUTER: IBM PC compatible  
 51 OPERATING SYSTEM: PC DOS/MS-DOS  
 52 SOFTWARE: Export to Release #1.0, Version #1.25  
 53 CURRENT APPLICATION DATA  
 54 APPLICATION NUMBER: US/09/044312  
 55 FILING DATE: 19 May 2003  
 56 CLASSIFICATION: unknown  
 57 PUBLICATION DATA  
 58 APPLICATION NUMBER: 09/201,943  
 59 FILING DATE: unknown  
 60 ADDRESS/AGENT INFORMATION  
 61 NAME: Campbell, John A.  
 62 REGISTRATION NUMBER: 52,061,546  
 63 REFERENCE/DOCKET NUMBER: US-09-044312-42  
 64 TELECOMMUNICATION INFORMATION  
 65 TELEPHONE: (619) 576-0200  
 66 TELEFAX: (619) 576-0200  
 67 INFORMATION FOR SEQ ID NO. 20:  
 68 SEQUENCE CHARACTERISTICS  
 69 LENGTH: 8 amino acids  
 70 TYPE: amino acid  
 71 TOPOLOGY: linear  
 72 MOLECULE TYPE: peptide  
 73 SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
 74 US-09-044312-20  
 75  
 76 Quality Match: 27.0%, Score 41, DB 9, Length 8;  
 77 Best Local Similarity: 100.0%, Pos: 50-05;  
 78 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 79  
 80 Q7 8 RES 10  
 81 11  
 82 5 RES 7  
 83  
 84 US-09-044312-21  
 85  
 86 Sequence 10: Application US/09/044312  
 87 Patent No. US2003/01142A1  
 88 GENERAL INFORMATION  
 89 APPLICANT: Storello, John S.  
 90 TITLE OF INVENTION: MEMBRANE-BINDING CYTOKINE COMPOSITIONS  
 91 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 92 RESPONSE USING SAME  
 93  
 94 NUMBER OF SEQUENCES: 48  
 95 CORRESPONDENCE ADDRESS  
 96 ADDRESSEE: CAMPBELL & FIDRES, LLP  
 97 STREET: 4370 La Colina Village Drive, Suite 700  
 98 CITY: San Diego  
 99 STATE: California  
 100 COUNTRY: USA  
 101 ZIP: 92121  
 102 COMPUTER READABLE FORM  
 103 MEDIUM TYPE: floppy disk  
 104 COMPUTER: IBM PC compatible  
 105 OPERATING SYSTEM: PC DOS/MS-DOS  
 106 SOFTWARE: Export to Release #1.0, Version #1.25  
 107 CURRENT APPLICATION DATA  
 108 APPLICATION NUMBER: US/09/044312  
 109 FILING DATE: 19 Jun 2003  
 110 CLASSIFICATION: unknown  
 111 PUBLICATION DATA  
 112 APPLICATION NUMBER: 09/097,000  
 113 FILING DATE: unknown  
 114 ADDRESS/AGENT INFORMATION  
 115 NAME: STORELLO, JOHN S.  
 116 REGISTRATION NUMBER: 52,061,546  
 117 REFERENCE/DOCKET NUMBER: US-09-044312-21  
 118 TELECOMMUNICATION INFORMATION  
 119 TELEPHONE: (415) 576-0200  
 120 TELEFAX: (415) 576-0200  
 121 INFORMATION FOR SEQ ID NO. 42:  
 122 SEQUENCE CHARACTERISTICS  
 123 LENGTH: 8 amino acids  
 124 TYPE: amino acid  
 125 STRANDEDNESS: unknown  
 126 TOPOLOGY: linear

1 MOLECULE TYPE: peptide  
 2 SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
 3 US-09-044312-42  
 4  
 5 Quality Match: 27.0%, Score 41, DB 9, Length 8;  
 6 Best Local Similarity: 100.0%, Pos: 50-05;  
 7 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 8  
 9 Q7 9 RES 11  
 10 11  
 11 4 RES 3  
 12  
 13 US-09-044312-43  
 14  
 15 Sequence 20: Application US/09/044312  
 16 Patent No. US2003/01142A1  
 17 GENERAL INFORMATION  
 18 APPLICANT: Storello, John S.  
 19 TITLE OF INVENTION: MEMBRANE-BINDING CYTOKINE COMPOSITIONS  
 20 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 21 RESPONSE USING SAME  
 22  
 23 NUMBER OF SEQUENCES: 50  
 24 CORRESPONDENCE ADDRESS  
 25 ADDRESSEE: CAMPBELL & FIDRES, LLP  
 26 STREET: 4370 La Colina Village Drive, Suite 700  
 27 CITY: San Diego  
 28 STATE: California  
 29 COUNTRY: United States  
 30 ZIP: 92121  
 31 COMPUTER READABLE FORM  
 32 MEDIUM TYPE: floppy disk  
 33 COMPUTER: IBM PC compatible  
 34 OPERATING SYSTEM: PC DOS/MS-DOS  
 35 SOFTWARE: Export to Release #1.0, Version #1.25  
 36 CURRENT APPLICATION DATA  
 37 APPLICATION NUMBER: US/09/044312  
 38 FILING DATE: 19 May 2003  
 39 CLASSIFICATION: unknown  
 40 PUBLICATION DATA  
 41 APPLICATION NUMBER: 09/201,943  
 42 FILING DATE: unknown  
 43 ADDRESS/AGENT INFORMATION  
 44 NAME: Campbell, John A.  
 45 REGISTRATION NUMBER: 52,061,546  
 46 REFERENCE/DOCKET NUMBER: US-09-044312-42  
 47 TELECOMMUNICATION INFORMATION  
 48 TELEPHONE: (619) 576-0200  
 49 TELEFAX: (619) 576-0200  
 50 INFORMATION FOR SEQ ID NO. 20:  
 51 SEQUENCE CHARACTERISTICS  
 52 LENGTH: 8 amino acids  
 53 TYPE: amino acid  
 54 TOPOLOGY: linear  
 55 MOLECULE TYPE: peptide  
 56 SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
 57 US-09-044312-20  
 58  
 59 Quality Match: 27.0%, Score 41, DB 9, Length 8;  
 60 Best Local Similarity: 100.0%, Pos: 50-05;  
 61 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 62  
 63 Q7 8 RES 10  
 64 11  
 65 5 RES 7  
 66  
 67 US-09-044312-21  
 68  
 69 Sequence 10: Application US/09/044312  
 70 Patent No. US2003/01142A1  
 71 GENERAL INFORMATION  
 72 APPLICANT: Storello, John S.  
 73 TITLE OF INVENTION: MEMBRANE-BINDING CYTOKINE COMPOSITIONS  
 74 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 75 RESPONSE USING SAME  
 76  
 77 NUMBER OF SEQUENCES: 48  
 78 CORRESPONDENCE ADDRESS  
 79 ADDRESSEE: CAMPBELL & FIDRES, LLP  
 80 STREET: 4370 La Colina Village Drive, Suite 700  
 81 CITY: San Diego  
 82 STATE: California  
 83 COUNTRY: USA  
 84 ZIP: 92121  
 85 COMPUTER READABLE FORM  
 86 MEDIUM TYPE: floppy disk  
 87 COMPUTER: IBM PC compatible  
 88 OPERATING SYSTEM: PC DOS/MS-DOS  
 89 SOFTWARE: Export to Release #1.0, Version #1.25  
 90 CURRENT APPLICATION DATA  
 91 APPLICATION NUMBER: US/09/044312  
 92 FILING DATE: 19 Jun 2003  
 93 CLASSIFICATION: unknown  
 94 PUBLICATION DATA  
 95 APPLICATION NUMBER: 09/097,000  
 96 FILING DATE: unknown  
 97 ADDRESS/AGENT INFORMATION  
 98 NAME: STORELLO, JOHN S.  
 99 REGISTRATION NUMBER: 52,061,546  
 100 REFERENCE/DOCKET NUMBER: US-09-044312-21  
 101 TELECOMMUNICATION INFORMATION  
 102 TELEPHONE: (415) 576-0200  
 103 TELEFAX: (415) 576-0200  
 104 INFORMATION FOR SEQ ID NO. 42:  
 105 SEQUENCE CHARACTERISTICS  
 106 LENGTH: 8 amino acids  
 107 TYPE: amino acid  
 108 STRANDEDNESS: unknown  
 109 TOPOLOGY: linear

1 APPLICANT: De Smet, Charles  
2 TITLE OF INVENTION: TOMER ASSOCIATED NUCLEOTIDES AND USES THEREOF  
3 FILING REFERENCE: 10461/7054  
4 CURRENT APPLICATION NUMBER: US/09/225,884  
5 CURRENT FILING DATE: 2001-09-07  
6 PRIOR APPLICATION NUMBER: 09/185,730  
7 PRIOR FILING DATE: 2001-10-03  
8 NUMBER OF SEQ ID NOS: 43  
9 SEQ ID NO 10  
10 LENGTH: 8  
11 TYPE: PRT  
12 ORGANISM: Homo sapiens  
13 US 09/225,884, 10  
14  
15 Query Match: 27 Amino Acids Score: 105.100, Length: 84  
16 Best Local Similarity: 100.000, Pos: Non-Specific  
17 Matches: 81 Conservative 0; Mismatch 0; Indel 0; Gaps 0;  
18  
19 QY 8 PER 10  
20 III  
21 DL 5 PER 7

Search Completed: September 30, 2003, 11:06:50  
Job Time: 24.5 sec

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	100.0	11	21	AAY68540	NCAM Ig1 binding p
2	11	100.0	11	23	ABG69340	Human neural cell
3	6	45.5	14	22	AAY68541	Human peptide #215
4	5	45.5	15	21	AAY68261	Human STRAP-1 pep
5	5	45.5	15	22	AAY68264	Human STRAP-1 pep
6	4	36.4	8	5	AAP40573	Immunogenic peptide
7	4	36.4	8	8	AAP40573	Sequence of cyclic
8	4	36.4	8	15	AAK71743	Cyclic antigenic peptide
9	4	36.4	8	15	AAK71743	Neurotensin receptor
9	4	36.4	8	15	AAK71743	Neurotensin receptor



83	4	36.4	12	15	AAR71765	Neurotensin receptor	256	3	27.3	8	4	AAP10497	Sequence of tatf1
84	4	36.4	12	16	AAR70711	CMC interictal EEG	257	3	27.3	8	4	AAP50069	Arginine vasopress
85	4	36.4	12	19	AAR74694	Amino acid sequence	258	3	27.3	8	5	AAP50071	Arginine vasopress
86	4	36.4	12	19	AAW55956	Human vascular pe	259	3	27.3	8	13	AAR24414	GPase B like enzym
87	4	36.4	12	19	AAW54449	Vascular endothelial	260	3	27.3	8	14	AAR40979	HCV core protein N
88	4	36.4	12	19	AAW45569	Amino acid sequen	261	3	27.3	8	14	AAR40980	HCV core protein N
89	4	36.4	12	20	AAW41444	Protein derived fr	262	3	27.3	8	14	AAR40981	HCV core protein N
90	4	36.4	12	20	AAW55540	Immunoglobulin IgG	263	3	27.3	8	14	AAR40989	HCV core protein N
91	4	36.4	12	20	AAW48411	Peptide tested for	264	3	27.3	8	14	AAR40990	HCV core protein N
92	4	36.4	12	21	AAW34528	Peptide #52 inhibi	265	3	27.3	8	14	AAR40991	HCV core protein N
93	4	36.4	12	21	AAW86399	Texas Red Binding	266	3	27.3	8	14	AAR40992	HCV core protein N
94	4	36.4	12	21	AAW81146	Texas Red Binding	267	3	27.3	8	14	AAR40993	HCV core protein N
95	4	36.4	12	21	AAW81149	Texas Red Binding	268	3	27.3	8	14	AAR40997	HCV core protein N
96	4	36.4	12	21	AAW55679	Human vascular end	269	3	27.3	8	14	AAR46860	Insulin-like growth
97	4	36.4	12	21	AAW59621	Vascular endothelial	270	3	27.3	8	14	AAR46860	Insulin-like growth
98	4	36.4	12	22	AAR61022	Internalizing pep	271	3	27.3	8	14	AAR35958	Hepatitis C virus
99	4	36.4	12	22	AAR97900	Human VEGF/VRF pep	272	3	27.3	8	14	AAR35959	Hepatitis C virus
100	4	36.4	12	22	AAW34574	VEGF VRF actinatio	273	3	27.3	8	14	AAR35960	Hepatitis C virus
101	4	36.4	12	22	AAW345615	Neurotensin peptid	274	3	27.3	8	14	AAR35777	Hepatitis C virus
102	4	36.4	12	22	AAW345668	Neurotensin peptid	275	3	27.3	8	14	AAR35778	Hepatitis C virus
103	4	36.4	12	22	AAW345672	Neurotensin peptid	276	3	27.3	8	14	AAR35779	Hepatitis C virus
104	4	36.4	12	22	AAW345622	Neurotensin peptid	277	3	27.3	8	14	AAR35780	Hepatitis C virus
105	4	36.4	12	22	AAW345623	Neurotensin peptid	278	3	27.3	8	14	AAR43499	La/SSB epitope 89
106	4	36.4	12	22	AAW345671	Neurotensin peptid	279	3	27.3	8	15	AAR47846	Hepatitis C virus
107	4	36.4	12	22	AAW24537	Neurotensin peptid	280	3	27.3	8	15	AAR61570	Dynorphin-like pol
108	4	36.4	12	23	AAW24537	Neurotensin peptid	281	3	27.3	8	15	AAR61570	Dynorphin-like pol
109	4	36.4	13	14	AAR47605	Neurotensin (Leu21	282	3	27.3	8	15	AAR62145	HIV-1 gp120/41 pro
110	4	36.4	13	14	AAR47642	Neurotensin (Leu21	283	3	27.3	8	15	AAR62145	HIV-1 gp120/41 pro
111	4	36.4	13	14	AAR47642	Neurotensin (Leu21	284	3	27.3	8	15	AAR62145	HIV-1 gp120/41 pro
112	4	36.4	13	15	AAR61582	Protease inhibitor	285	3	27.3	8	15	AAR62145	HIV-1 gp120/41 pro
113	4	36.4	13	15	AAR71764	Neurotensin recept	286	3	27.3	8	16	AAR21555	Neurotensin recept
114	4	36.4	13	15	AAR71773	Neurotensin recept	287	3	27.3	8	16	AAR21555	Neurotensin recept
115	4	36.4	13	15	AAW21724	Neurotensin (Leu21	288	3	27.3	8	16	AAR21556	Neurotensin recept
116	4	36.4	13	15	AAW21724	Neurotensin (Leu21	289	3	27.3	8	16	AAR21556	Neurotensin recept
117	4	36.4	13	15	AAW21724	Neurotensin (Leu21	290	3	27.3	8	16	AAR21556	Neurotensin recept
118	4	36.4	13	15	AAW21724	Neurotensin (Leu21	291	3	27.3	8	16	AAR21556	Neurotensin recept
119	4	36.4	13	21	AAW16544	Immunotact peptide	292	3	27.3	8	16	AAR66346	HIV-1 protease inh
120	4	36.4	13	21	AAW16544	Immunotact peptide	293	3	27.3	8	16	AAR66346	HIV-1 protease inh
121	4	36.4	13	21	AAW16544	Immunotact peptide	294	3	27.3	8	16	AAR66346	HIV-1 protease inh
122	4	36.4	13	21	AAW16544	Immunotact peptide	295	3	27.3	8	16	AAR66346	HIV-1 protease inh
123	4	36.4	13	22	AAW24537	Neurotensin (Leu21	296	3	27.3	8	16	AAR66346	HIV-1 protease inh
124	4	36.4	13	22	AAW24537	Neurotensin (Leu21	297	3	27.3	8	16	AAR66346	HIV-1 protease inh
125	4	36.4	13	22	AAW24537	Neurotensin (Leu21	298	3	27.3	8	16	AAR66346	HIV-1 protease inh
126	4	36.4	13	22	AAW24537	Neurotensin (Leu21	299	3	27.3	8	16	AAR66346	HIV-1 protease inh
127	4	36.4	13	22	AAW24537	Neurotensin (Leu21	300	3	27.3	8	16	AAR66346	HIV-1 protease inh
128	4	36.4	13	22	AAW24537	Neurotensin (Leu21	301	3	27.3	8	16	AAR66346	HIV-1 protease inh
129	4	36.4	13	22	AAW24537	Neurotensin (Leu21	302	3	27.3	8	16	AAR66346	HIV-1 protease inh
130	4	36.4	13	22	AAW24537	Neurotensin (Leu21	303	3	27.3	8	16	AAR66346	HIV-1 protease inh
131	4	36.4	13	22	AAW24537	Neurotensin (Leu21	304	3	27.3	8	16	AAR66346	HIV-1 protease inh
132	4	36.4	13	22	AAW24537	Neurotensin (Leu21	305	3	27.3	8	16	AAR66346	HIV-1 protease inh
133	4	36.4	13	22	AAW24537	Neurotensin (Leu21	306	3	27.3	8	16	AAR66346	HIV-1 protease inh
134	4	36.4	13	22	AAW24537	Neurotensin (Leu21	307	3	27.3	8	16	AAR66346	HIV-1 protease inh
135	4	36.4	13	22	AAW24537	Neurotensin (Leu21	308	3	27.3	8	16	AAR66346	HIV-1 protease inh
136	4	36.4	13	22	AAW24537	Neurotensin (Leu21	309	3	27.3	8	16	AAR66346	HIV-1 protease inh
137	4	36.4	13	22	AAW24537	Neurotensin (Leu21	310	3	27.3	8	16	AAR66346	HIV-1 protease inh
138	4	36.4	13	22	AAW24537	Neurotensin (Leu21	311	3	27.3	8	16	AAR66346	HIV-1 protease inh
139	4	36.4	13	22	AAW24537	Neurotensin (Leu21	312	3	27.3	8	16	AAR66346	HIV-1 protease inh
140	4	36.4	13	22	AAW24537	Neurotensin (Leu21	313	3	27.3	8	16	AAR66346	HIV-1 protease inh
141	4	36.4	13	22	AAW24537	Neurotensin (Leu21	314	3	27.3	8	16	AAR66346	HIV-1 protease inh
142	4	36.4	13	22	AAW24537	Neurotensin (Leu21	315	3	27.3	8	16	AAR66346	HIV-1 protease inh
143	4	36.4	13	22	AAW24537	Neurotensin (Leu21	316	3	27.3	8	16	AAR66346	HIV-1 protease inh
144	4	36.4	13	22	AAW24537	Neurotensin (Leu21	317	3	27.3	8	16	AAR66346	HIV-1 protease inh
145	4	36.4	13	22	AAW24537	Neurotensin (Leu21	318	3	27.3	8	16	AAR66346	HIV-1 protease inh
146	4	36.4	13	22	AAW24537	Neurotensin (Leu21	319	3	27.3	8	16	AAR66346	HIV-1 protease inh
147	4	36.4	13	22	AAW24537	Neurotensin (Leu21	320	3	27.3	8	16	AAR66346	HIV-1 protease inh
148	4	36.4	13	22	AAW24537	Neurotensin (Leu21	321	3	27.3	8	16	AAR66346	HIV-1 protease inh
149	4	36.4	13	22	AAW24537	Neurotensin (Leu21	322	3	27.3	8	16	AAR66346	HIV-1 protease inh
150	4	36.4	13	22	AAW24537	Neurotensin (Leu21	323	3	27.3	8	16	AAR66346	HIV-1 protease inh
151	4	36.4	13	22	AAW24537	Neurotensin (Leu21	324	3	27.3	8	16	AAR66346	HIV-1 protease inh
152	4	36.4	13	22	AAW24537	Neurotensin (Leu21	325	3	27.3	8	16	AAR66346	HIV-1 protease inh
153	4	36.4	13	22	AAW24537	Neurotensin (Leu21	326	3	27.3	8	16	AAR66346	HIV-1 protease inh
154	4	36.4	13	22	AAW24537	Neurotensin (Leu21	327	3	27.3	8	16	AAR66346	HIV-1 protease inh
155	4	36.4	13	22	AAW24537	Neurotensin (Leu21	328	3	27.3	8	16	AAR66346	HIV-1 protease inh



375	3	27.3	8	22	AA302490	Hepatitis C virus	448	3	27.3	8	24	AA374475	Human PRAME epitop
376	3	27.3	8	22	AA302491	Hepatitis C virus	449	3	27.3	8	24	AA374497	Human tuftsin. HO
377	3	27.3	8	22	AA302492	Hepatitis C virus	450	3	27.3	9	7	AA374497	Sequence encoded b
378	3	27.3	8	22	AA374493	Hepatitis C virus	451	3	27.3	9	7	AA374497	Sequence of peptid
379	3	27.3	8	22	AA374494	Hepatitis C virus	452	3	27.3	9	11	AA374497	Example of arginin
380	3	27.3	8	22	AA374495	Hepatitis C virus	453	3	27.3	9	13	AA374497	Transactivation-de
381	3	27.3	8	22	AA374496	Hepatitis C virus	454	3	27.3	9	14	AA374497	Anti-hepatic pept
382	3	27.3	8	22	AA374497	Hepatitis C virus	455	3	27.3	9	14	AA374497	Protected hANF(99-
383	3	27.3	8	22	AA374498	Hepatitis C virus	456	3	27.3	9	14	AA374497	Hepatitis B virus-
384	3	27.3	8	22	AA374499	Hepatitis C virus	457	3	27.3	9	15	AA374497	Hepatitis B virus-
385	3	27.3	8	22	AA374500	Hepatitis C virus	458	3	27.3	9	15	AA374497	Hepatitis C virus-
386	3	27.3	8	22	AA374501	Hepatitis C virus	459	3	27.3	9	15	AA374497	HIV derived HLA-bi
387	3	27.3	8	22	AA374502	Hepatitis C virus	460	3	27.3	9	15	AA374497	Fibronectin-derive
388	3	27.3	8	22	AA374503	Hepatitis C virus	461	3	27.3	9	15	AA374497	Fibronectin fragme
389	3	27.3	8	22	AA374504	Hepatitis C virus	462	3	27.3	9	15	AA374497	Light chain CDR3 f
390	3	27.3	8	22	AA374505	Hepatitis C virus	463	3	27.3	9	15	AA374497	Fasciola hepatica
391	3	27.3	8	22	AA374506	Hepatitis C virus	464	3	27.3	9	15	AA374497	Fasciola hepatica
392	3	27.3	8	22	AA374507	Hepatitis C virus	465	3	27.3	9	15	AA374497	Peptide fragment (
393	3	27.3	8	22	AA374508	Hepatitis C virus	466	3	27.3	9	15	AA374497	Neurotensin recept
394	3	27.3	8	22	AA374509	Hepatitis C virus	467	3	27.3	9	15	AA374497	Neurotensin recept
395	3	27.3	8	22	AA374510	Hepatitis C virus	468	3	27.3	9	15	AA374497	HLA-A2.1 algorithm
396	3	27.3	8	22	AA374511	Hepatitis C virus	469	3	27.3	9	15	AA374497	HLA-A2.1 algorithm
397	3	27.3	8	22	AA374512	Hepatitis C virus	470	3	27.3	9	15	AA374497	Antigen fragment 1
398	3	27.3	8	22	AA374513	Hepatitis C virus	471	3	27.3	9	15	AA374497	33 kD fibronectin
399	3	27.3	8	22	AA374514	Hepatitis C virus	472	3	27.3	9	15	AA374497	HIV peptide fragme
400	3	27.3	8	22	AA374515	Hepatitis C virus	473	3	27.3	9	15	AA374497	HIV-B31-11(H-11)
401	3	27.3	8	22	AA374516	Hepatitis C virus	474	3	27.3	9	15	AA374497	HIV(B35)ARV2-28, h
402	3	27.3	8	22	AA374517	Hepatitis C virus	475	3	27.3	9	15	AA374497	Anti-cytomegalovir
403	3	27.3	8	22	AA374518	Hepatitis C virus	476	3	27.3	9	15	AA374497	Immunogenic peptid
404	3	27.3	8	22	AA374519	Hepatitis C virus	477	3	27.3	9	15	AA374497	HPE3 peptide deriv
405	3	27.3	8	22	AA374520	Hepatitis C virus	478	3	27.3	9	15	AA374497	Protein kinase A p
406	3	27.3	8	22	AA374521	Hepatitis C virus	479	3	27.3	9	15	AA374497	Protein kinase A p
407	3	27.3	8	22	AA374522	Hepatitis C virus	480	3	27.3	9	15	AA374497	Human leucocyte an
408	3	27.3	8	22	AA374523	Hepatitis C virus	481	3	27.3	9	15	AA374497	Human leucocyte an
409	3	27.3	8	22	AA374524	Hepatitis C virus	482	3	27.3	9	15	AA374497	Human leucocyte an
410	3	27.3	8	22	AA374525	Hepatitis C virus	483	3	27.3	9	15	AA374497	Human leucocyte an
411	3	27.3	8	22	AA374526	Hepatitis C virus	484	3	27.3	9	15	AA374497	Human leucocyte an
412	3	27.3	8	22	AA374527	Hepatitis C virus	485	3	27.3	9	15	AA374497	Milk derived anti-
413	3	27.3	8	22	AA374528	Hepatitis C virus	486	3	27.3	9	15	AA374497	Tumour rejection a
414	3	27.3	8	22	AA374529	Hepatitis C virus	487	3	27.3	9	15	AA374497	Tumour rejection a
415	3	27.3	8	22	AA374530	Hepatitis C virus	488	3	27.3	9	15	AA374497	Tumour rejection a
416	3	27.3	8	22	AA374531	Hepatitis C virus	489	3	27.3	9	15	AA374497	Tumour rejection a
417	3	27.3	8	22	AA374532	Hepatitis C virus	490	3	27.3	9	15	AA374497	Light chain CDR3 o
418	3	27.3	8	22	AA374533	Hepatitis C virus	491	3	27.3	9	15	AA374497	VEGF exon V. Homo
419	3	27.3	8	22	AA374534	Hepatitis C virus	492	3	27.3	9	15	AA374497	IL-10 agonist pept
420	3	27.3	8	22	AA374535	Hepatitis C virus	493	3	27.3	9	15	AA374497	IL-10 agonist pept
421	3	27.3	8	22	AA374536	Hepatitis C virus	494	3	27.3	9	15	AA374497	IL-10 agonist pept
422	3	27.3	8	22	AA374537	Hepatitis C virus	495	3	27.3	9	15	AA374497	IL-10 agonist pept
423	3	27.3	8	22	AA374538	Hepatitis C virus	496	3	27.3	9	15	AA374497	IL-10 agonist pept
424	3	27.3	8	22	AA374539	Hepatitis C virus	497	3	27.3	9	15	AA374497	IL-10 agonist pept
425	3	27.3	8	22	AA374540	Hepatitis C virus	498	3	27.3	9	15	AA374497	IL-10 agonist pept
426	3	27.3	8	22	AA374541	Hepatitis C virus	499	3	27.3	9	15	AA374497	IL-10 agonist pept
427	3	27.3	8	22	AA374542	Hepatitis C virus	500	3	27.3	9	24	AA374542	protein transducti
428	3	27.3	8	22	AA374543	Hepatitis C virus	501	3	27.3	9	24	AA374542	
429	3	27.3	8	22	AA374544	Hepatitis C virus	502	3	27.3	9	24	AA374542	
430	3	27.3	8	22	AA374545	Hepatitis C virus	503	3	27.3	9	24	AA374542	
431	3	27.3	8	22	AA374546	Hepatitis C virus	504	3	27.3	9	24	AA374542	
432	3	27.3	8	22	AA374547	Hepatitis C virus	505	3	27.3	9	24	AA374542	
433	3	27.3	8	22	AA374548	Hepatitis C virus	506	3	27.3	9	24	AA374542	
434	3	27.3	8	22	AA374549	Hepatitis C virus	507	3	27.3	9	24	AA374542	
435	3	27.3	8	22	AA374550	Hepatitis C virus	508	3	27.3	9	24	AA374542	
436	3	27.3	8	22	AA374551	Hepatitis C virus	509	3	27.3	9	24	AA374542	
437	3	27.3	8	22	AA374552	Hepatitis C virus	510	3	27.3	9	24	AA374542	
438	3	27.3	8	22	AA374553	Hepatitis C virus	511	3	27.3	9	24	AA374542	
439	3	27.3	8	22	AA374554	Hepatitis C virus	512	3	27.3	9	24	AA374542	
440	3	27.3	8	22	AA374555	Hepatitis C virus	513	3	27.3	9	24	AA374542	
441	3	27.3	8	22	AA374556	Hepatitis C virus	514	3	27.3	9	24	AA374542	
442	3	27.3	8	22	AA374557	Hepatitis C virus	515	3	27.3	9	24	AA374542	
443	3	27.3	8	22	AA374558	Hepatitis C virus	516	3	27.3	9	24	AA374542	
444	3	27.3	8	22	AA374559	Hepatitis C virus	517	3	27.3	9	24	AA374542	
445	3	27.3	8	22	AA374560	Hepatitis C virus	518	3	27.3	9	24	AA374542	
446	3	27.3	8	22	AA374561	Hepatitis C virus	519	3	27.3	9	24	AA374542	
447	3	27.3	8	22	AA374562	Hepatitis C virus	520	3	27.3	9	24	AA374542	
448	3	27.3	8	22	AA374563	Hepatitis C virus	521	3	27.3	9	24	AA374542	
449	3	27.3	8	22	AA374564	Hepatitis C virus	522	3	27.3	9	24	AA374542	
450	3	27.3	8	22	AA374565	Hepatitis C virus	523	3	27.3	9	24	AA374542	
451	3	27.3	8	22	AA374566	Hepatitis C virus	524	3	27.3	9	24	AA374542	
452	3	27.3	8	22	AA374567	Hepatitis C virus	525	3	27.3	9	24	AA374542	
453	3	27.3	8	22	AA374568	Hepatitis C virus	526	3	27.3	9	24	AA374542	
454	3	27.3	8	22	AA374569	Hepatitis C virus	527	3	27.3	9	24	AA374542	
455	3	27.3	8	22	AA374570	Hepatitis C virus	528	3	27.3	9	24	AA374542	
456	3	27.3	8	22	AA374571	Hepatitis C virus	529	3	27.3	9	24	AA374542	
457	3	27.3	8	22	AA374572	Hepatitis C virus	530	3	27.3	9	24	AA374542	
458	3	27.3	8	22	AA374573	Hepatitis C virus	531	3	27.3	9	24	AA374542	
459	3	27.3	8	22	AA374574	Hepatitis C virus	532	3	27.3	9	24	AA374542	
460	3	27.3	8	22	AA374575	Hepatitis C virus	533	3	27.3	9	24	AA374542	
461	3	27.3	8	22	AA374576	Hepatitis C virus	534	3	27.3	9	24	AA374542	
462	3	27.3	8	22	AA374577	Hepatitis C virus	535	3	27.3	9	24	AA374542	
463	3	27.3	8	22	AA374578	Hepatitis C virus	536	3	27.3	9	24	AA374542	
464	3	27.3	8	22	AA374579	Hepatitis C virus	537	3	27.3	9	24	AA374542	
465	3	27.3	8	22	AA374580	Hepatitis C virus	538	3	27.3	9	24	AA374542	
466	3	27.3	8	22	AA374581	Hepatitis C virus	539	3	27.3	9	24	AA374542	
467	3	27.3	8	22	AA374582	Hepatitis C virus	540	3	27.3	9	24	AA374542	
468	3	27.3	8	22	AA374583	Hepatitis C virus	541	3	27.3	9	24	AA374542	
469	3	27.3	8	22	AA374584	Hepatitis C virus	542	3	27.3	9	24	AA374542	
470	3	27.3	8	22	AA374585	Hepatitis C virus	543	3	27.3	9	24	AA374542	
471	3	27.3	8	22	AA374586	Hepatitis C virus	544	3	27.3	9	24	AA374542	
472	3	27.3	8	22	AA374587	Hepatitis C virus	545	3	27.3	9	24	AA374542	
473	3	27.3	8	22	AA374588	Hepatitis C virus	546	3	27.3	9	24	AA374542	
474	3	27.3	8	22	AA374589	Hepatitis C virus	547	3	27.3	9	24	AA374542	
475	3	27.3	8	22	AA374590	Hepatitis C virus	548	3	27.3	9	24	AA374542	
476	3	27.3	8	22	AA374591	Hepatitis C virus	549	3	27.3	9	24	AA374542	
477	3	27.3	8	22	AA374592	Hepatitis C virus	550	3	27.3	9	24	AA374542	
478	3	27.3											

XX OS Synthetic.

XX PN WO200018801-A2.

XX FT 06-APR-2000.

XX 24-SEP-1999; 94WO-DK05500.

XX 29-SEP-1998; 98DK-0001232.

XX 29-APR-1999; 99DK-0000592.

XX (KCNK/) KONN L C B.

XX (HCKK/) BOCK E.

XX (HOLK/) HOLM A.

XX (OLSE/) OLSEN M.

XX (OSTE/) OSTERGAARD S.

XX (JENS/) JENSEN P H.

XX (POLJ/) POLSEN F M.

XX (SOKO/) SOROKA V.

XX (RALE/) RALETS I.

XX (BERE/) BEREZIN V.

XX Romm LCB, Bock E, Holm A, Olsson M, OSTERGAARD S, Jensen PH, Polsen FM, Soroka V, Ralets I, Berezin V.

XX WPI: 2000 293111/25.

XX Compositions that bind neural cell adhesion molecules useful for treating disorders of the nervous system and muscles e.g. Alzheimer's and Parkinson's diseases.

XX Example 4: Page 25; 119pp; English.

XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule. NCAM is found in three forms, two of which are transmembrane forms, while the third is attached via a lipid anchor to the cell membrane. All three NCAM forms have an extracellular structure consisting of five immunoglobulin domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-terminal. The present sequence represents a peptide which binds to the NCAM 1/1 domain. The peptide can be used in a compound which binds to NCAM 1/1/2 domains, and is capable of stimulating or promoting neurite outgrowth from NCAM presenting cells, and is also capable of promoting the proliferation of NCAM presenting cells, and is also capable of promoting the treatment of normal, degenerated or damaged NCAM presenting cells. The compound may in particular be used to treat diseases of the central and peripheral nervous systems such as post-operative nerve damage, traumatic nerve damage, impaired myelination of nerve fibres, conditions resulting from a stroke, Parkinson's disease, Alzheimer's disease, dementia, sclerosis, nerve degeneration associated with diabetes, mellitus, disorders affecting the circulation, stroke or neuro-muscular transmission and schizophrenia. Conditions affecting the muscles may also be treated with the compound, such as conditions associated with impaired function of neuromuscular connections (e.g. genetic or traumatic shock or traumatic atrophic muscle disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also be treated using the compound. The compound is used in a prosthetic nerve guide, and also to stimulate the ability to learn, and to stimulate the memory of a subject.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQKTKPKRRS 11

DB 1 ARQKTKPKRRS 11

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RES021 4

AB069340

ID AB069340 standard; Peptide: 11 AA.

XX AC AB069340;

XX DT 21-OCT-2002 (first entry)

XX DE Human neural cell adhesion molecule (NCAM) peptide #12.

XX KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival; acute myocardial infarction; central nervous system disorder; stroke; peripheral nervous system disorder; postoperative nerve damage; traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia; postischaemic damage; multifarct dementia; multiple sclerosis; nerve degeneration; diabetes mellitus; neuro-muscular degeneration; Alzheimer's disease; Parkinson's disease; Huntington's disease; atrophic muscle disorder; gonad degeneration; nephrosis.

XX OS Homo sapiens.

XX PN WO200247719-A2.

XX PD 20-JUN-2002.

XX 12-DEC-2001; 2002WO-DK00822.

XX 12-DEC-2000; 2000DK-0001864.

XX (ENKA ) ENKAM PHARM AS.

XX Bock E, Berezin V, Kohler LH;

XX WPI: 2002-583473/62.

XX Use of a compound comprising a peptide of neural cell adhesion molecule, in the preparation of medicament for preventing death of cells presenting NCAM or NCAM ligand and treating central nervous system diseases.

XX Disclosure: Page 16; 57pp; English.

XX The invention relates to use of a compound (I) comprising a peptide which comprises at least 5 contiguous amino acid residues of a sequence of the neural cell adhesion molecule (NCAM), its fragment, variant or its mimic, for the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand. (I) is useful in the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand. The medicament is for the stimulation of the survival of heart muscle cells, such as survival after acute myocardial infarction. The medicament is for the treatment of diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, e.g. resulting from spinal cord injury, impaired myelination of nerve fibres, postischaemic damage, e.g. resulting from a stroke, multifarct dementia, multiple sclerosis, nerve degeneration associated with diabetes mellitus, neuro-muscular degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and Huntington's disease. The medicament is for the treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as genetic or traumatic atrophic muscle disorders, and for the treatment of diseases of conditions of various organs, such as degenerative conditions of the gonads, pancreas (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).

XX AB069329-AB069352 represent human NCAM peptides of the invention.

Sequence 11 AA;

Query Match 100.0%; Score 11; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQKTKPKRRS 11

DB 1 ARQKTKPKRRS 11

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CC inhibitors or to target therapeutic agents to their site of action. STRAP  
CC nucleic acids may be used for recombinant protein production, as  
CC diagnostic and prognostic reagents, for identifying STRAP-expressing  
CC cells for screening inhibitors of STRAP expression and for therapeutic  
CC modulation/inhibition of STRAP expression. Since high levels of STRAP  
CC proteins are exposed on the cell surface, they are easily targeted by  
CC systemically administered agents, and because they are expressed mainly  
CC on prostate epithelial cells, agents targeted to them should have  
CC minimal side effects on other tissues.

XX Query Match 45.5%, Score 5, DB 22, Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 43;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA:

QY 6 MKPKR 10  
DB 3 MKPKR 7

RESULT 5  
AAP40573  
10 AAP40573 standard; Peptide: 8 AA.  
XX AAP40573:

XX 16-AUG 2002 (updated)  
XX 16-FEB 1992 (first entry)

XX Sequence of cyclic analogue of neurotensin.  
XX Neurotransmitter, neuromodulator, neurotensin.  
XX Synthetic.

XX Key Location/Qualifiers

XX Modified site 1 Label: D Lys

XX US44 03559. A.

XX 27-MAR 1984.

XX 02-JUL-1982; E2US 0494750.

XX 02-JUL-1982; E2US 0394750.

XX (MERK) MERCK & CO INC.

XX Holly FW, Christy ME, Sheppard KL, Strachan RG, Varma SL;  
XX Weber LF;

XX WPI: 1984-094629/15.

XX Cyclic octapeptide analogues of neurotensin - having  
XX neurotensin-like activity

XX Claim 3: column 6; App: English.

XX The peptides of the invention have neurotensin like activity.  
XX neurotensin is eqd. CNS active as a neurotransmitter or  
XX neuromodulator.

XX (Updated on 16-AUG-2002 to add missing GS field.)

XX Query Match 36.4%, Score 4, DB 5, Length 8;  
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRK 10  
DB 1 KPRK 4

RESULT 7  
AAP21985

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10 AAK71749 standard; peptide: 8 AA.  
 11 AAK71749.  
 12 25-MAR-2003 (updated)  
 13 01-JAN-1995 (first entry)  
 14 Cyclic octapeptide with hypotensive activity.  
 15 Cyclic octapeptide with hypotensive activity.  
 16 Cyclic octapeptide; hypotensive; SS.  
 17 Synthesized.  
 18 S01134-20 A  
 19 15 JUL 1986.  
 20 13 JUL 1983; R350-3620434.  
 21 13 JUL 1983; R350-3620434.  
 22 (AAR) AS LATE ORGANIC SYNTHESIS (NSI).  
 23 Chapuis JJ. Grinshtein IV. Vequer RE;  
 24 WEI 1187 035268/05.  
 25 Novel cyclic octapeptide with hypotensive activity has low  
 26 toxicity and is stable to carboxy peptidase.  
 27 (abstracted page 1; 7pp; Russian).  
 28 The novel biologically active cyclic octapeptide which possesses  
 29 hypotensive activity is stable to carboxypeptidase activity. The  
 30 synthesis of the peptide involves acylation of the peptide chain,  
 31 using dicyclohexyl carbodiimide as the condensing agent and tert  
 32 butylhydroxy carbonyl for protecting the alpha amino groups. Final  
 33 purification is secured by paper electrophoresis. The peptide shows  
 34 a weak hypotensive activity that increases by a factor of 2. The  
 35 ED50 is 9 mg/kg, eq the cellular dose is more than 10,000 fold  
 36 greater than the depressive effect dose.  
 37 (Updated on 25-MAR-2003 to correct AA field.)  
 38 Sequence: 8 AA.

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 35-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAK71749  
 10 AAK71749 standard; peptide: 8 AA.  
 11 AAK71749.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Cyclic octapeptide with hypotensive activity.  
 15 Cyclic octapeptide with hypotensive activity.  
 16 Cyclic octapeptide; hypotensive; SS.  
 17 Synthesized.  
 18 S01134-20 A  
 19 15 JUL 1986.  
 20 13 JUL 1983; R350-3620434.  
 21 13 JUL 1983; R350-3620434.  
 22 (AAR) AS LATE ORGANIC SYNTHESIS (NSI).  
 23 Chapuis JJ. Grinshtein IV. Vequer RE;  
 24 WEI 1187 035268/05.  
 25 Novel cyclic octapeptide with hypotensive activity has low  
 26 toxicity and is stable to carboxy peptidase.  
 27 (abstracted page 1; 7pp; Russian).  
 28 The novel biologically active cyclic octapeptide which possesses  
 29 hypotensive activity is stable to carboxypeptidase activity. The  
 30 synthesis of the peptide involves acylation of the peptide chain,  
 31 using dicyclohexyl carbodiimide as the condensing agent and tert  
 32 butylhydroxy carbonyl for protecting the alpha amino groups. Final  
 33 purification is secured by paper electrophoresis. The peptide shows  
 34 a weak hypotensive activity that increases by a factor of 2. The  
 35 ED50 is 9 mg/kg, eq the cellular dose is more than 10,000 fold  
 36 greater than the depressive effect dose.  
 37 (Updated on 25-MAR-2003 to correct AA field.)  
 38 Sequence: 8 AA.

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 35-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAK71749  
 10 AAK71749 standard; peptide: 8 AA.  
 11 AAK71749.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Cyclic octapeptide with hypotensive activity.  
 15 Cyclic octapeptide with hypotensive activity.  
 16 Cyclic octapeptide; hypotensive; SS.  
 17 Synthesized.  
 18 S01134-20 A  
 19 15 JUL 1986.  
 20 13 JUL 1983; R350-3620434.  
 21 13 JUL 1983; R350-3620434.  
 22 (AAR) AS LATE ORGANIC SYNTHESIS (NSI).  
 23 Chapuis JJ. Grinshtein IV. Vequer RE;  
 24 WEI 1187 035268/05.  
 25 Novel cyclic octapeptide with hypotensive activity has low  
 26 toxicity and is stable to carboxy peptidase.  
 27 (abstracted page 1; 7pp; Russian).  
 28 The novel biologically active cyclic octapeptide which possesses  
 29 hypotensive activity is stable to carboxypeptidase activity. The  
 30 synthesis of the peptide involves acylation of the peptide chain,  
 31 using dicyclohexyl carbodiimide as the condensing agent and tert  
 32 butylhydroxy carbonyl for protecting the alpha amino groups. Final  
 33 purification is secured by paper electrophoresis. The peptide shows  
 34 a weak hypotensive activity that increases by a factor of 2. The  
 35 ED50 is 9 mg/kg, eq the cellular dose is more than 10,000 fold  
 36 greater than the depressive effect dose.  
 37 (Updated on 25-MAR-2003 to correct AA field.)  
 38 Sequence: 8 AA.

FT substituted by Lys or Orn.  
 XX  
 10 EP66804-A2.  
 11 20-JUL-1994.  
 12 27-DEC-1993; 94EL 004-0185.  
 13 00-DEC-1992; 94CA 2050450.  
 14 (JYMC) UNIV 960110.  
 15 Haddad A. Faute M. Gaudreau P;  
 16 WP: 1994-226757/28.  
 17 New fluorescent markers for neurotensin receptors - useful for in  
 18 vitro labelling of neurotensin receptors on cell surface and to  
 19 isolate neurotensin-receptor-expressing cells  
 20 Claim 2: Page 5; 19pp; English.  
 21 The invention concerns highly sensitive fluorescent probes which  
 22 allow for rapid and precise characterisation of neurotensin  
 23 receptor binding properties on whole cells. The probes are of  
 24 formula R1-C(=X) R in which R1 is a fluorophore chosen from  
 25 fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 26 or sulphur; and R is a neurotensin-type polypeptide sequence  
 27 containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 28 Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745  
 29 AAK71772. The R1-CX-acyl group is linked to the peptide via the  
 30 N-terminus in position 1. The N-terminal amino acid may also be  
 31 substituted by Lys or Orn.  
 32 The present sequence represents one of the claimed peptide  
 33 sequences for R.  
 34 (Updated on 25-MAR-2003 to correct PN field.)  
 35 Sequence: 8 AA.

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 35-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAK71750  
 10 AAK71750 standard; peptide: 8 AA.  
 11 AAK71750.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Neurotensin receptor fluorescent probe.  
 15 Neurotensin; N1; receptor; probe; fluorescent.  
 16 Synthesized.  
 17 Key: Location/Qualifiers  
 18 Modified-site: 1  
 19 /note: "N-acylated with fluorescent label. See (r  
 20 below. Also this amino acid can be  
 21 substituted by Lys or Orn."  
 22 EP66804-A2.  
 23 20-JUL-1994.  
 24 27-DEC-1993; 94EL 004-0185.  
 25 00-DEC-1992; 94CA 2050450.  
 26 (JYMC) UNIV 960110.  
 27 Haddad A. Faute M. Gaudreau P;  
 28 WP: 1994-226757/28.  
 29 New fluorescent markers for neurotensin receptors - useful for in  
 30 vitro labelling of neurotensin receptors on cell surface and to  
 31 isolate neurotensin-receptor-expressing cells  
 32 Claim 2: Page 5; 19pp; English.  
 33 The invention concerns highly sensitive fluorescent probes which  
 34 allow for rapid and precise characterisation of neurotensin  
 35 receptor binding properties on whole cells. The probes are of  
 36 formula R1-C(=X) R in which R1 is a fluorophore chosen from  
 37 fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 38 or sulphur; and R is a neurotensin-type polypeptide sequence  
 39 containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 40 Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745  
 41 AAK71772. The R1-CX-acyl group is linked to the peptide via the  
 42 N-terminus in position 1. The N-terminal amino acid may also be  
 43 substituted by Lys or Orn.  
 44 The present sequence represents one of the claimed peptide  
 45 sequences for R.  
 46 (Updated on 25-MAR-2003 to correct PN field.)  
 47 Sequence: 8 AA.

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 35-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAK71750  
 10 AAK71750 standard; peptide: 8 AA.  
 11 AAK71750.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Neurotensin receptor fluorescent probe.  
 15 Neurotensin; N1; receptor; probe; fluorescent.  
 16 Synthesized.  
 17 Key: Location/Qualifiers  
 18 Modified-site: 1  
 19 /note: "N-acylated with fluorescent label. See (r  
 20 below. Also this amino acid can be  
 21 substituted by Lys or Orn."  
 22 EP66804-A2.  
 23 20-JUL-1994.  
 24 27-DEC-1993; 94EL 004-0185.  
 25 00-DEC-1992; 94CA 2050450.  
 26 (JYMC) UNIV 960110.  
 27 Haddad A. Faute M. Gaudreau P;  
 28 WP: 1994-226757/28.  
 29 New fluorescent markers for neurotensin receptors - useful for in  
 30 vitro labelling of neurotensin receptors on cell surface and to  
 31 isolate neurotensin-receptor-expressing cells  
 32 Claim 2: Page 5; 19pp; English.  
 33 The invention concerns highly sensitive fluorescent probes which  
 34 allow for rapid and precise characterisation of neurotensin  
 35 receptor binding properties on whole cells. The probes are of  
 36 formula R1-C(=X) R in which R1 is a fluorophore chosen from  
 37 fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 38 or sulphur; and R is a neurotensin-type polypeptide sequence  
 39 containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 40 Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745  
 41 AAK71772. The R1-CX-acyl group is linked to the peptide via the  
 42 N-terminus in position 1. The N-terminal amino acid may also be  
 43 substituted by Lys or Orn.  
 44 The present sequence represents one of the claimed peptide  
 45 sequences for R.  
 46 (Updated on 25-MAR-2003 to correct PN field.)  
 47 Sequence: 8 AA.







CC ordered hydrophobic interactions and have multiple attachment sites near  
 CC to the dye chromophore for ease of forming linearized structures. The  
 CC presence of rigid and extended chromophore backbones confers rigid  
 CC fluorescence quantum yield and extends their maximum absorption beyond  
 CC 400 nm. Conjugation of biomolecules is readily achievable. The present  
 CC sequence represents the amino acid sequence of neurotensin analogue, used  
 CC in the method of the invention.

XX  
 XX  
 XX Sequence 8 AA:  
 Query Match 46.4% Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0% Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10  
 DB 1 KPRR 4

RESULT 14  
 AAB73426  
 ID AAB73426 standard: peptide; 8 AA.  
 AC AAB73426  
 XX  
 XX 25-JUN-2001 (first entry)  
 XX  
 XX Neurotensin analogue peptide; SEQ ID NO:7.  
 XX  
 XX Neurotensin analogue; bioconjugate; bis-indocyanine dye;  
 KW hydrophilic; optical diagnostic imaging; tumour detection; cancer;  
 KW endoscopy; coronary angiography; atherosclerotic plaque; blood clot.  
 XX  
 XX Synthetic.

XX  
 XX Key Location/Qualifiers  
 FI Misc difference 1 /note= "D form residue"  
 FT  
 XX US6190641-B1.  
 XX DE-FEB-2001  
 XX EP-JAN-2000 2000US 0484322  
 XX JP-JAN-2000 2000US 0484322  
 XX (M/W) MALLINCKRODT INC.  
 XX Achilleto S. Rajagopalan R. Borshaw RB. Baga JE;  
 XX WPI: 2001-26428/29.  
 XX Composition containing bis-indocyanine dye and carrier, useful for  
 XX diagnosis and therapy, e.g. of tumours, with the dye residue at the  
 XX attachment.

XX  
 XX Example 9, Column 13; 15pp; English.

XX The invention relates to compositions comprising a hydrophilic  
 XX bis-indocyanine dye with a heterocyclic group in the polymethylene chain,  
 XX and a pharmaceutically acceptable carrier or excipient. The invention  
 XX also relates to diagnostic and therapeutic methods that involve  
 XX administering the bis-indocyanine dye compositions to a human; and  
 XX a method for making compositions of the invention by conjugating dyes  
 XX to peptides or biomolecules by solid phase synthesis. The bis-indocyanine  
 XX dye compositions are useful for optical tomographic imaging of organs;  
 XX monitoring organ function; coronary angiography; fluorescent endoscopy;  
 XX detection, imaging and therapy (pharmacodynamic or localised) of tumours;  
 XX laser-guided surgery (particularly for detecting microvascularities during  
 XX laparoscopy); and photocoagulation and sclerotherapy methods. A  
 XX particular application is diagnosis of atherosclerotic plaques and blood  
 XX clots. Also, measuring the pattern of blood circulation at a vessel block.

CC of the invention can be used for diagnosis of tumours and other diseases.  
 CC The bis-indocyanine dyes are designed not to aggregate in solution  
 CC (by preventing intra- and inter-molecular hydrophobic interactions);  
 CC to have many attachment sites near to the chromophore for formation of  
 CC a dendrimer; to allow easy conjugation to biomolecules; and to have a  
 CC rigid and extended chromophore backbone that enhances the fluorescent  
 CC quantum yield and extends the absorbance maximum to beyond 600 nm.  
 CC Sequences AAB73421-AAB73426 represent synthetic peptides used in an  
 CC exemplification to illustrate the use of bis-indocyanine dyes of the  
 CC invention to prepare bioconjugates. The present sequence represents a  
 CC neurotensin analogue peptide.

XX Sequence 8 AA:

Query Match 46.4% Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0% Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10

DB 1 KPRR 4

RESULT 15

AAB73442

ID AAB73442 standard: peptide; 8 AA.

AC AAB73442

XX 25-JUN-2001 (first entry)

XX Neurotensin analogue peptide; SEQ ID NO:7.

XX Neurotensin analogue; bioconjugate; bis-indocyanine dye;

KW hydrophilic; optical diagnostic imaging; tumour detection; cancer;

KW endoscopy; coronary angiography; atherosclerotic plaque; blood clot.

XX Synthetic.

XX Key Location/Qualifiers

FI Misc difference 1 /note= "D form residue"

FT

XX US6190641-B1.

XX DE-FEB-2001

XX EP-JAN-2000 2000US 0484322

XX JP-JAN-2000 2000US 0484322

XX (M/W) MALLINCKRODT INC.

XX Achilleto S. Rajagopalan R. Borshaw RB. Baga JE;

XX WPI: 2001-26428/29.

XX Novel indocyanine dyes that absorb and emit light in near infrared  
 XX region of electromagnetic spectrum, useful for imaging, diagnosis and  
 XX therapy of various diseased states -

XX Example 9; Column 14; 15pp; English.

XX The invention relates to compositions comprising a hydrophilic

XX bis-indocyanine dye with a heterocyclic group in the polymethylene chain,

XX and a pharmaceutically acceptable carrier or excipient. The invention

XX also relates to diagnostic and therapeutic methods that involve

XX administering the bis-indocyanine dye compositions to a human; and

XX a method for making compositions of the invention by conjugating dyes

XX to peptides or biomolecules by solid phase synthesis. The bis-indocyanine

XX dye compositions are useful for optical tomographic imaging of organs;

XX monitoring organ function; coronary angiography; fluorescent endoscopy;

XX detection, imaging and therapy (pharmacodynamic or localised) of tumours;

laser assisted surgery (particularly for detecting micrometastases during laparascopy); and photoacoustic and sonotactile methods. A particular application is diagnosis of atherosclerotic plaques and blood clots. Also, measuring the pattern of blood circulation of a composition of the invention can be used for diagnosis of tumours and other diseases. The fluorescent dyes are designed not to interfere in solution, (by preventing intra- and inter-molecular hydrophobic interactions) to have many attachment sites (due to the design of the structure) and a dendrimer, to allow easy conjugation to a biomolecule and to have a rigid and extended chromophore backbone that enhances the fluorescence quantum yield and extends the absorption maximum to the near infrared. Sequences AA97427-AA97442 represent synthetic peptides used in an experiment to illustrate the use of the fluorescent dyes of the invention to prepare bioconjugates. The present sequence represents a neurotensin analogue peptide.

Sequence: 8 AA;

Query Match: 46.4% Score 4; DB: 22; Length 8;  
Best Local Similarity: 100.0%; Prod. No. 9.3e+05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 7 KPRR 10  
II  
DL 1 KPRR 4

RESIDUE 12  
AA97427 standard: peptide; 8 AA;  
XX  
AC AA97427;  
XX  
Z1 25 APR 2003 (first entry)  
XX  
DE Neurotensin analogue peptide SEQ ID NO:7;  
XX  
KW Optical Modality: cyanine dye; imaging; diagnosis; detection; tumour;  
KW optical diagnostic imaging; therapy; cytostatic; blood clot;  
KW atherosclerotic plaque; photodynamic therapy; LAGS; micrometastasis;  
KW laser assisted guided surgery;  
XX  
CS Synthesis;  
XX  
FH Key: location/qualifiers  
FI Mismatch Difference: 1  
FT /index /form residue"

US6180095-B1

10 JAN 2003

18 JAN 2003; 2003US0484418

18 JAN 2003; 2003US0484418

(PLCN) MALLIN+KROGT INC.

Achileto S. Rajadopalai R. Borskow RB. Bugaj JE;

WPI: 2001 20.699/20.

Composition useful for imaging, diagnosis and therapy of various diseased states comprises cyanine dyes that absorb and emit light in near infrared region of electromagnetic spectrum

Example 9: Column 14; 15pp; English.

The present invention describes a composition which comprises cyanine dyes (1). (1) has cytostatic activity. (1) is useful for performing a diagnostic or therapeutic procedure, e.g. for diagnosing atherosclerotic plaques and blood clots, and for localised therapy, photodynamic therapy and laser assisted guided surgery (LAGS) for the detection of micrometastases. (1) are also useful for imaging, diagnosis and therapy of various diseased states, for optical diagnostic imaging and therapy, in endoscopic applications for the detection of tumours and other abnormalities, for photoacoustic tumour imaging, detection and therapy and for sonotactile tumour imaging, detection and therapy. (1) prevent dye adsorption in solution, predisposed to form dendrimers, capable of absorbing or emitting beyond 800 nm, have good photophysical properties, and have tissue-specific targeting capability. The present sequence represents a peptide which is used in an example from the present invention.

Sequence: 8 AA;

Query Match: 46.4% Score 4; DB: 22; Length 8;  
Best Local Similarity: 100.0%; Prod. No. 9.3e+05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 7 KPRR 10  
II  
DL 1 KPRR 4

RESIDUE 12  
AA97427 standard: peptide; 8 AA;  
XX  
AC AA97427;  
XX  
Z1 25 APR 2003 (first entry)  
XX  
DE Neurotensin analogue peptide SEQ ID NO:7;  
XX  
KW Optical Modality: cyanine dye; imaging; diagnosis; detection; tumour;  
KW optical diagnostic imaging; therapy; cytostatic; blood clot;  
KW atherosclerotic plaque; photodynamic therapy; LAGS; micrometastasis;  
KW laser assisted guided surgery;  
XX  
CS Synthesis;  
XX  
FH Key: location/qualifiers  
FI Mismatch Difference: 1  
FT /index /form residue"

US6180095-B1

10 JAN 2003

18 JAN 2003; 2003US0484418

18 JAN 2003; 2003US0484418

(PLCN) MALLIN+KROGT INC.

Achileto S. Rajadopalai R. Borskow RB. Bugaj JE;

WPI: 2001 20.699/20.

Composition useful for imaging, diagnosis and therapy of various diseased states

Example 9: Column 14; 15pp; English.

The present invention relates to a composition with fluorescent dyes

the invention is useful for performing a diagnostic or therapeutic

procedure, e.g. for diagnosing atherosclerotic plaques and blood clots,

and for localised therapy, photodynamic therapy and laser assisted

guided surgery (LAGS) for the detection of micrometastases

Sequence: 8 AA;

Query Match: 46.4% Score 4; DB: 22; Length 8;

Best Local Similarity: 100.0%; Prod. No. 9.3e+05;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;





PF 09 Ark 1999 99DE-101771A  
 XX  
 PF 09 Ark 1999 99DE-101771A  
 XX  
 DA (GIAJ-) INST DIAGNOSTIKFORSCHUNG GMBH  
 XX  
 PF Lilla K. Becker A., Sommer W., Wiedenmann B., Hessehaus B.  
 PF Wilkner-Engert R., Schneider-Mergener J.  
 XX  
 PF WPI: 2301 003424/01.  
 XX  
 PF New conjugates of vasoactive intestinal peptide, somatostatin or  
 PF neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 PF fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 PF Claim 17, Page 17; 32pp; German.  
 XX  
 CC This invention describes novel conjugates (1) of vasoactive intestinal  
 CC peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 CC The products of the invention can also be used for a diagnostic method  
 CC comprising administering (1) to a patient, either intravenously or to the  
 CC bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 CC bladder by spraying and then washing out excess (1), and then performing  
 CC an endoscopic investigation by local excitation of fluorescence at an  
 CC excitation wavelength of 350-1200 nm and site-specific detection of the  
 CC fluorescence emitted by the dye. (1) are useful for in-vivo diagnosis of  
 CC tumors, other diseased tissues or adenomas by means of optical detection  
 CC procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 CC inflammatory tissues by means of endoscopic procedures in the  
 CC gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 CC for in-vivo fluorescence and/or absorption diagnosis of breast tumors by  
 CC means of optical mammography (transillumination or optical tomography of  
 CC the breast). The peptide component provides receptor-specific binding to  
 CC target tissues and the polymethine dye provides a fluorescence signal  
 CC that is detectable with high sensitivity.  
 XX  
 SQ Sequence: 8 AA:  
 Query Match: 56.4%; Score 4; DP 22; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9; 3e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KRR 10  
 LQ 1  
 LQ 1 KRR 4  
 PFSGT 24  
 AAG5269  
 CC AAG5269 Standard; Peptide: 8 AA.  
 XX  
 AC AAG5269  
 GT GKNV-2001 (first entry)  
 XX  
 BE Neurotensin analogue peptide sequence.  
 XX  
 KW Fluorescent bioconjugates: indocyanine; dye; therapy; endoscopic;  
 KW optical diagnosis; imaging; tumor; photoacoustic tumor imaging;  
 KW somifluorescence; gastroscopy; neurotensin.  
 XX  
 QS Synthetic.  
 XX  
 XX Key: Position/Qualifiers  
 PF Miss difference: /note "G-term res.due"  
 PF  
 XX LSG254 (9-B).  
 PF 24 (9), 2001.  
 XX  
 PF 10 AAG 2000 200005 000120  
 XX  
 PF 10 AAG 2000 200005 000120  
 XX  
 PF 09 Ark 1999 99DE-101771A  
 XX  
 PF 09 Ark 1999 99DE-101771A  
 XX  
 DA (GIAJ-) INST DIAGNOSTIKFORSCHUNG GMBH

XX  
 PF Lilla K. Becker A., Sommer W., Wiedenmann B., Hessehaus B.  
 PF Wilkner-Engert R., Schneider-Mergener J.  
 XX  
 PF WPI: 2001 003424/01.  
 XX  
 PF New conjugates of vasoactive intestinal peptide, somatostatin or  
 PF neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 PF fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 PF Claim 17, Page 17; 32pp; German.  
 XX  
 CC This invention describes novel conjugates (1) of vasoactive intestinal  
 CC peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 CC The products of the invention can also be used for a diagnostic method  
 CC comprising administering (1) to a patient, either intravenously or to the  
 CC bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 CC bladder by spraying and then washing out excess (1), and then performing  
 CC an endoscopic investigation by local excitation of fluorescence at an  
 CC excitation wavelength of 350-1200 nm and site-specific detection of the  
 CC fluorescence emitted by the dye. (1) are useful for in-vivo diagnosis of  
 CC tumors, other diseased tissues or adenomas by means of optical detection  
 CC procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 CC inflammatory tissues by means of endoscopic procedures in the  
 CC gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 CC for in-vivo fluorescence and/or absorption diagnosis of breast tumors by  
 CC means of optical mammography (transillumination or optical tomography of  
 CC the breast). The peptide component provides receptor-specific binding to  
 CC target tissues and the polymethine dye provides a fluorescence signal  
 CC that is detectable with high sensitivity.  
 XX  
 SQ Sequence: 8 AA:  
 Query Match: 56.4%; Score 4; DP 22; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9; 3e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KRR 10  
 LQ 1  
 LQ 1 KRR 4  
 PFSGT 24  
 AAG5269  
 CC AAG5269 Standard; Peptide: 8 AA.  
 XX  
 AC AAG5269  
 GT GKNV-2001 (first entry)  
 XX  
 BE Neurotensin analogue peptide sequence.  
 XX  
 KW Fluorescent bioconjugates: indocyanine; dye; therapy; endoscopic;  
 KW optical diagnosis; imaging; tumor; photoacoustic tumor imaging;  
 KW somifluorescence; gastroscopy; neurotensin.  
 XX  
 QS Synthetic.  
 XX  
 XX Key: Position/Qualifiers  
 PF Miss difference: /note "G-term res.due"  
 PF  
 XX LSG254 (9-B).  
 PF 24 (9), 2001.  
 XX  
 PF 10 AAG 2000 200005 000120  
 XX  
 PF 10 AAG 2000 200005 000120  
 XX  
 PF 09 Ark 1999 99DE-101771A  
 XX  
 PF 09 Ark 1999 99DE-101771A  
 XX  
 DA (GIAJ-) INST DIAGNOSTIKFORSCHUNG GMBH



XX Fluorescence efficiency of the dye molecules, located associate in  
 CC solution, form starburst dendrimers, are rapid as of absorption of emitting  
 CC light in the near infrared region and can be recovered tissue specific.  
 CC The present amino acid sequence represents a synthetic neurotensin and the  
 CC peptide that was used in the methods of the invention for synthesis of  
 CC peptide-dye conjugates.

SC Sequence 8 AA:

Query Match: 36.4%, Score 4; DB 15; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRP 10

DB 111

2 KPRP 5

RESULT 27

AAR71754

ID AAR71754 standard; peptide: 9 AA;

XX AC AAR71754;

XX 25-MAR-2003 (updated)

DI 15-MAY-1995 (first entry)

XX NEUROTENSIN RECEPTOR FLUORESCENT PROBE.

XX NEUROTENSIN; N1: RECEPTOR; PROBE: FLUORESCENT.

XX SYNTHETIC.

XX KEY

XX MODIFIED SITE

XX LOCATION/QUALIFIERS

XX /NOTE: "N-acylated with fluorescent label. See CC

XX below. Also this amino acid can be

XX substituted by Lys or Orn."

XX EP066504 A2.

XX 20-JUL-1994.

XX 27-DEC-1993.

XX 30-DEC-1992.

XX (CYPN) UNIV MICHIGAN.

XX BEAULIEU A. FAURE M. GADREAU P.

XX WPL 1994-224757/28.

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SC Sequence 9 AA:

Query Match: 36.4%, Score 4; DB 15; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRP 10

DB 111

2 KPRP 5

RESULT 28

AAR71754

ID AAR71754 standard; peptide: 9 AA;

XX AC AAR71754;

XX 25-MAR-2003 (updated)

DI 15-MAY-1995 (first entry)

XX NEUROTENSIN RECEPTOR FLUORESCENT PROBE.

XX NEUROTENSIN; N1: RECEPTOR; PROBE: FLUORESCENT.

XX SYNTHETIC.

XX KEY

XX MODIFIED SITE

XX LOCATION/QUALIFIERS

XX /NOTE: "N-acylated with fluorescent label. See CC

XX below. Also this amino acid can be

XX substituted by Lys or Orn."

XX EP066504 A2.

XX 20-JUL-1994.

XX 27-DEC-1993.

XX 30-DEC-1992.

XX (CYPN) UNIV MICHIGAN.

XX BEAULIEU A. FAURE M. GADREAU P.

XX WPL 1994-224757/28.

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XX

Query Match: 36.4%, Score 4; DB 15; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SC Sequence 9 AA:

Query Match: 36.4%, Score 4; DB 15; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

The invention concerns highly sensitive fluorescent probes which allow for rapid and precise characterisation of neurotensin receptor binding properties on whole cells. The probes are of formula R1-C(-X)-R in which R1 is a fluorophore chosen from fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin-type polypeptide sequence containing the core sequence Arg-Pro-Tyr-Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via the N-terminus in position 1. The N-terminal amino acid may also be substituted by Lys or Orn.

The present sequence represents one of the claimed peptide sequences for R.

(Updated on 25-MAR-2003 to correct PN field.)

Claim 2; Page 5; 19pp; English.

New fluorescent markers for neurotensin receptors - useful for in vitro labelling of neurotensin receptors on cell surface and to isolate neurotensin-receptor expressing cells





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XX 05 Delivered:
XX
XX DE1997713-A1
XX
XX 19 OCT 2000
XX
XX 09 APR 1999; 99DE-1017713
XX
XX 09 APR 1999; 99DE-1017713
XX
XX (DIAG-) INST DIAGNOSTIKFORSCHUNG GMBH
XX
XX Licha K, Becker A, Sommer W, Wiedenmann B, Hossenius G;
XX Volkmur-Engert K, Schneider-Mergener J;
XX WPL 2001-003423/01
XX
XX New conjugates of vasoactive intestinal peptide, somatostatin or
XX neurotensin peptides and polymethylene dyes are used for e.g. in-vivo
XX fluorescence diagnosis of tumors and other diseased tissues -
XX
XX Claim 17: Page 17: 32pp; German
XX
XX This invention describes novel conjugates (I) of vasoactive intestinal
XX peptide (VIP), somatostatin or neurotensin peptides and polymethylene dyes.
XX The products of the invention can also be used for a diagnostic method
XX comprising administering (I) to a patient, either intravenously or to the
XX bronchi by inhalation or to the gastrointestinal tract, esophagus or
XX bladder by spraying and then washing out excess (I), and then performing
XX an endoscopic investigation by local excitation of fluorescence at an
XX excitation wavelength of 350-1200 nm and site-specific detection of the
XX fluorescence emitted by the dye. (I) are useful for in-vivo diagnosis of
XX tumors, other diseased tissues or adenomas by means of optical detection
XX procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or
XX gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or
XX inflammatory tissues by means of endoscopic procedures in the
XX gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or
XX for in-vivo fluorescence and/or absorption diagnosis of breast tumors by
XX means of optical mammography (transillumination or optical tomography of
XX the breast). The peptide component provides receptor-specific binding to
XX target tissues and the polymethylene dye provides a fluorescence signal
XX that is detectable with high sensitivity.
XX
XX Sequence 9 AA:
XX
XX Query Match 36.4%, Score 10, DB 22, Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 KPRK 10
XX IIII
XX 2 KPRK 5
XX
XX RESULT 42
XX AAB45640
XX ID AAB45630 Standard: Peptide; 9 AA.
XX
XX AC AAB45685;
XX
XX UT 09 MAR 2001 (first entry)
XX
XX DE Neurotensin peptide analog #14.
XX
XX KW Vasoactive intestinal peptide; somatostatin; neurotensin; diagnosis;
XX polymethylene dye; fluorescence; detection; tumor; adenoma; esophagus;
XX gastrointestinal tract; bronchial tract; bladder; cervix; breast;
XX optical mammography; optical tomography.
XX
XX OS Unidentified.
XX
XX PN DE1997713-A1.
XX
XX PD 19-OCT-2000.
XX
XX PF 09-APR-1999; 99DE-1017713.
XX
XX PR 09-APR-1999; 99DE-1017713.

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XX 19-OCT-2000.
XX
XX 09-APR-1999; 99DE-1017713.
XX
XX 09-APR-1999; 99DE-1017713.
XX
XX (DIAG-) INST DIAGNOSTIKFORSCHUNG GMBH.
XX
XX Licha K, Becker A, Sommer W, Wiedenmann B, Hossenius G;
XX Volkmur-Engert K, Schneider-Mergener J;
XX WPL 2001-003423/01.
XX
XX New conjugates of vasoactive intestinal peptide, somatostatin or
XX neurotensin peptides and polymethylene dyes are used for e.g. in-vivo
XX fluorescence diagnosis of tumors and other diseased tissues -
XX
XX Claim 17: Page 17: 32pp; German.
XX
XX This invention describes novel conjugates (I) of vasoactive intestinal
XX peptide (VIP), somatostatin or neurotensin peptides and polymethylene dyes.
XX The products of the invention can also be used for a diagnostic method
XX comprising administering (I) to a patient, either intravenously or to the
XX bronchi by inhalation or to the gastrointestinal tract, esophagus or
XX bladder by spraying and then washing out excess (I), and then performing
XX an endoscopic investigation by local excitation of fluorescence at an
XX excitation wavelength of 350-1200 nm and site-specific detection of the
XX fluorescence emitted by the dye. (I) are useful for in-vivo diagnosis of
XX tumors, other diseased tissues or adenomas by means of optical detection
XX procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or
XX gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or
XX inflammatory tissues by means of endoscopic procedures in the
XX gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or
XX for in-vivo fluorescence and/or absorption diagnosis of breast tumors by
XX means of optical mammography (transillumination or optical tomography of
XX the breast). The peptide component provides receptor-specific binding to
XX target tissues and the polymethylene dye provides a fluorescence signal
XX that is detectable with high sensitivity.
XX
XX Sequence 9 AA:
XX
XX Query Match 36.4%, Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 KPRK 10
XX IIII
XX 2 KPRK 5
XX
XX RESULT 43
XX AAB45681
XX ID AAB45681 Standard: Peptide; 9 AA.
XX
XX AC AAB45681;
XX
XX UT 09 MAR 2001 (first entry)
XX
XX DE Neurotensin peptide analog #14.
XX
XX KW Vasoactive intestinal peptide, somatostatin; neurotensin; diagnosis;
XX polymethylene dye; fluorescence; detection; tumor; adenoma; esophagus;
XX gastrointestinal tract; bronchial tract; bladder; cervix; breast;
XX optical mammography; optical tomography.
XX
XX OS Unidentified.
XX
XX PN DE1997713-A1.
XX
XX PD 19-OCT-2000.
XX
XX PF 09-APR-1999; 99DE-1017713.
XX
XX PR 09-APR-1999; 99DE-1017713.

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The invention relates to a polypeptide, designated 34P47, encoding a 34P47-related protein, comprising a sequence of amino acid residues fully defined in the specification. The presence of elevated 34P47 mRNA or protein expression indicates the presence of cancer occurring in prostate, bladder, kidney, brain, bone, stomach, ovary, testis, colon, breast, pancreatic, stomach, colon, rectal leukocytes, liver, and lung tissues, and in melanocytes. An anti-34P47 antibody, the 34P47-related protein, an antisense polynucleotide, a composition, the 34P47 polynucleotide, or a ribozyme capable of targeting the 34P47 polynucleotide, is useful for inhibiting the development of a cancer expressing 34P47 in a patient. The present sequence is a portion of human 34P47. Kindred of a large number of 34P47 peptides to various human MHC classes I and Class II molecules was identified.

$S_2$	Sequence	9 AA;	36.4%; Score 4; The 2nd column
	Query Match		
	Best local Similarity	100.0%	Pred. from query
	Matches	4	Conservative 0; Miscellaneous

Q7 7 APR 10  
I I  
ID 1 REF 4

KSLD 1 68  
ABBY 1972  
ID 8851972 standard: population AA.  
XX  
AC AGO 1972:  
XX  
ID Feb 20 1972 (first entry)  
XX  
XX Human 42317 BLA B7 9 Ref 61100 201.

KW	Hansen, 541-1073, cytochrome c, varietal, deer, 1000000, 1000000
KW	Indian, 1000000, 1000000, 1000000, 1000000, 1000000, 1000000
KW	HLA A1, HLA A11, HLA A2, HLA A21, HLA A22, HLA A23
XX	Hansen, 541-1073, 1000000, 1000000, 1000000, 1000000

01 N  
 02 XX  
 03 XX  
 04 XX  
 05 XX  
 06 XX  
 07 XX  
 08 XX  
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 98 XX  
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 00 XX

US  
XX

Abstract: Page 89: 112pp; English

The invention relates to a polypeptide isolated, isolated 34p07, encoding a 34p07-related protein, comprising at least part of a 30% nucleotide identity derived in the specification, the presence of a conserved 34p07-34p07 or protein expression indicates the presence of a protein occurring in prostate, bladder, kidney, brain, bone, ovary, testis, uterine, ovary, breast, pancreas, stomach, colon, rectal, leukocytes, liver, and lung 11833, and in melanocytes. An antibody against the 34p07-related protein, an antisense polynucleotide to complementarity to 34p07, polynucleotide, or a ribozyme capable of cleaving the 34p07 polynucleotide, 34p07-34p07, but that of the above, and 11833-34p07 expressed 34p07 in a patient, the presence of a protein, a polypeptide,

human 34P3D7. Binding of a large number of 34P3D7 peptides to various human MHC class I and class II molecules was predicted.

Sequence: y AA:

Query Material: 36,48; Score: 4; DB: 23; Length: 9;  
Best Local Similarity: 100,08; Pred. No.: 9,3e+05;

QY	7 KPS	10
1	1	1
4	1	4

$$\frac{1}{f} = \frac{1}{f_1} + \frac{1}{f_2}$$

ABRZ3893  
ID ABRZ5H63 standard - Port Jive - AA

XX  
A. ABBY & SONS

14-MAY-2003 (TUE) 0000 UTC

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XY

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XX

[illegible]

176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994,

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XX  
1042[illegible]

10 APR-2001: 2001US 283112P

1. ☐ 2. ☐ 3. ☐ 4. ☐ 5. ☐ 6. ☐ 7. ☐ 8. ☐ 9. ☐ 10. ☐ 11. ☐ 12. ☐ 13. ☐ 14. ☐ 15. ☐ 16. ☐ 17. ☐ 18. ☐ 19. ☐ 20. ☐ 21. ☐ 22. ☐ 23. ☐ 24. ☐ 25. ☐ 26. ☐ 27. ☐ 28. ☐ 29. ☐ 30. ☐ 31. ☐ 32. ☐ 33. ☐ 34. ☐ 35. ☐ 36. ☐ 37. ☐ 38. ☐ 39. ☐ 40. ☐ 41. ☐ 42. ☐ 43. ☐ 44. ☐ 45. ☐ 46. ☐ 47. ☐ 48. ☐ 49. ☐ 50. ☐ 51. ☐ 52. ☐ 53. ☐ 54. ☐ 55. ☐ 56. ☐ 57. ☐ 58. ☐ 59. ☐ 60. ☐ 61. ☐ 62. ☐ 63. ☐ 64. ☐ 65. ☐ 66. ☐ 67. ☐ 68. ☐ 69. ☐ 70. ☐ 71. ☐ 72. ☐ 73. ☐ 74. ☐ 75. ☐ 76. ☐ 77. ☐ 78. ☐ 79. ☐ 80. ☐ 81. ☐ 82. ☐ 83. ☐ 84. ☐ 85. ☐ 86. ☐ 87. ☐ 88. ☐ 89. ☐ 90. ☐ 91. ☐ 92. ☐ 93. ☐ 94. ☐ 95. ☐ 96. ☐ 97. ☐ 98. ☐ 99. ☐ 100. ☐

XX  
XX

P. Morrison R., Morrison RK, Kaitano AM;

2017年12月27日

New composition comprising a substance that modulates the structure of proteins and polypeptides, useful for therapeutic, prognostic and diagnostic reasons for eliciting cellular or humoral immune response in cancer patients.

Page 30 of 30

The present invention relates to novel human cancer-related genes and proteins (A2782, A2782A168 and A2782A186). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

[illegible]

Query Match: 0.93      Score: 4      Lik 24      Length 9.

```

pos, low, start, end, file, no, size)
Matches: 4, Serialized: 0, Mismatches: 0, Indexes: 0,
pos: 100, start: 100, end: 100, file: NO, no: 1, size: 0

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108



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XX 24 OCT-2002
XX 10 APR-2001: 2002W0-0511654
XX 10 APR-2001: 2001US-282749F
XX 10 APR-2001: 2001US-283112F
XX 25 APR-2001: 2001US-285640F
XX (ADEN-) AGENSYS INC.
XX Jakobovits A., Challinor-Eid PM, Paris M, Ge W, Hubert RS,
XX Morrison K., Morrison RK., Nathan AB.
XX WPI: 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and/or
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX Claim 1: Page 397; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABZ78169-ABZ78195). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulation or
XX inhibiting the expression of the protein, as tools for modulation or
XX as therapeutic agents; the proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX Sequence 9 AA:
XX
XX Query Match 46.4% Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.36+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 ROKT 5
XX 1 1
XX 1 ROKT 4
XX
XX RESULT 44
XX AAR71757
XX ID AAR71757 standard: peptide; 10 AA.
XX AC AAR71757;
XX DT 25-MAR-2003 (updated)
XX ET 15-MAY-1995 (first entry)
XX
XX LE Neofoliesin receptor: immunosens probe.
XX KW Neofoliesin; NP1 receptor; probe; fluorescent.
XX OS Syntactic.
XX
XX FH Key location/Qualifiers
XX FT Modified-site ;
XX FT Note "N-acylated with fluorescent label. See CC
XX FT below. Also this amino acid can be
XX FT substituted by lys or Orn."
XX
XX PN EP066804-A2
XX
XX PD 20-JUL-1994.
XX
XX PF 27-DEC-1993; 93EP 0403185.
XX
XX PR 30-DEC-1992; 92CA 2086453.
XX
XX PA (UYMC-) UNIV MGNILL.
XX
XX PL Beaudet A., Faure M., Gaudreau P.
XX
XX WPI: 1994-223757/28.
XX
XX New 11 different markets for neofoliesin receptors - useful for in

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XX Jakobovits A., Challinor-Eid PM, Paris M, Ge W, Hubert RS,
XX Morrison K., Morrison RK., Nathan AB.
XX WPI: 2003-075555/07
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and/or
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX Claim 1: Page 399; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABZ78169-ABZ78195). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulation or
XX inhibiting the expression of the protein, as tools for modulation or
XX as therapeutic agents; the proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX Sequence 9 AA:
XX
XX Query Match 46.4% Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.36+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 ROKT 5
XX 1 1
XX 1 ROKT 4
XX
XX RESULT 44
XX AAR71757
XX ID AAR71757 standard: peptide; 10 AA.
XX AC AAR71757;
XX DT 25-MAR-2003 (updated)
XX ET 15-MAY-1995 (first entry)
XX
XX LE Neofoliesin receptor: immunosens probe.
XX KW Neofoliesin; NP1 receptor; probe; fluorescent.
XX OS Syntactic.
XX
XX FH Key location/Qualifiers
XX FT Modified-site ;
XX FT Note "N-acylated with fluorescent label. See CC
XX FT below. Also this amino acid can be
XX FT substituted by lys or Orn."
XX
XX PN EP066804-A2
XX
XX PD 20-JUL-1994.
XX
XX PF 27-DEC-1993; 93EP 0403185.
XX
XX PR 30-DEC-1992; 92CA 2086453.
XX
XX PA (UYMC-) UNIV MGNILL.
XX
XX PL Beaudet A., Faure M., Gaudreau P.
XX
XX WPI: 1994-223757/28.
XX
XX New 11 different markets for neofoliesin receptors - useful for in

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PT vitro labelling of neurotensin receptors on cell surface and to  
 XX isolate neurotensin receptor expressing cells  
 PS Claim 2: Page 5; 19pp; English.  
 XX The invention concerns highly sensitive fluorescent probes which  
 CC allow for rapid and precise characterisation of neurotensin  
 CC receptor binding properties on whole cells. The probes are of  
 CC formula R1-C(-X)-R in which R1 is a fluorophore chosen from  
 CC fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 CC or sulphur; and R is a neurotensin-type polypeptide sequence  
 CC containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 CC Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745  
 CC AAK71772. The R1-CX-acyl group is linked to the peptide via the  
 CC N-terminus in position 1. The N-terminal amino acid may also be  
 CC substituted by lys or orn.  
 CC The present sequence represents one of the claimed peptide  
 CC sequences for R.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence: 10 AA;  
 SQ  
 Query Match: 36.4%; Score 4; DB 15; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 4e-02;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 07 7 KPER 10  
 08 III  
 09 3 KPER 5  
 RESULT 46  
 AAK71758  
 XX AAK71758 standard; peptide: 10 AA;  
 XX AAK71758;  
 XX 25-MAR-2003 (updated)  
 XX 13-MAY-2003 (first entry)  
 XX Neurotensin receptor fluorescent probe  
 XX Neurotensin, NT1 receptor; for use in assays  
 XX Synthesis  
 XX Key: location/updates  
 XX Modified site /date "N-acylated with 6-oxo-2,3-dihydro-4H-pyridine-5-carboxylic acid, MS: theoretical 444.1666 Da, synthesized 13-MAY-2003"  
 XX PROBABLY A2  
 XX 20-JUL-1994  
 XX 27-DEC-1993 5SEP-2003195;  
 XX 09-SEP-1992 92CA-2086453;  
 XX (JPM73) GNV McGill;  
 XX awarded A. Faure M. Gaudreau P.  
 XX W11: 1994-226757/28;  
 XX New fluorescent markers for neurotensin receptors: useful for in  
 XX vitro labelling of neurotensin receptors on cell surface and to  
 XX isolate neurotensin-receptor expressing cells  
 XX Claim 2: Page 5; 19pp; English.  
 XX The invention concerns highly sensitive fluorescent probes which

CC allow for rapid and precise characterisation of neurotensin  
 CC receptor binding properties on whole cells. The probes are of  
 CC formula R1-C(-X)-R in which R1 is a fluorophore chosen from  
 CC fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 CC or sulphur; and R is a neurotensin-type polypeptide sequence  
 CC containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 CC Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745  
 CC AAK71772. The R1-CX-acyl group is linked to the peptide via the  
 CC N-terminus in position 1. The N-terminal amino acid may also be  
 CC substituted by lys or orn.  
 CC The present sequence represents one of the claimed peptide  
 CC sequences for R.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence: 10 AA;  
 SQ  
 Query Match: 36.4%; Score 4; DB 15; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 4e-02;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 07 7 KPER 10  
 08 III  
 09 3 KPER 5  
 RESULT 46  
 AAK71758  
 XX AAK71758 standard; peptide: 10 AA;  
 XX AAK71758;  
 XX 13-SEP-2001 (first entry)  
 XX Human complementary peptide, SEQ ID NO: 286;  
 XX Human: complementary peptide; ligand; drug discovery; drug design.  
 XX Homo-sapiens.  
 XX W0200142277-A2;  
 XX 24-JUN-2001;  
 XX 13-SEP-2001 25-OW-026,4775;  
 XX 13-SEP-1993 59-DE-0029464;  
 XX (PROT.) PRODEM LTD.  
 XX Robert's GW, Heul JF;  
 XX WPI: 2001 408415/43;  
 XX A set of peptide ligands consisting of specific complementary peptides  
 XX to proteins encoded by genes of the human genome, useful in an assay  
 XX for screening and identifying of one or more novel peptides which are  
 XX drug candidates or pro-drugs.  
 XX Example 4: Page 81; 84pp; English.  
 XX The invention relates to a set of complementary peptide ligands  
 XX generated from the human genome. The complementary peptides  
 XX interact with their relevant target proteins encoded in the human  
 XX genome. They can be used as reagents in drug discovery and as lead  
 XX ligands to facilitate drug design and development. The present  
 XX sequence is a complementary peptide provided in the specification.  
 XX Sequence: 10 AA;  
 SQ  
 Query Match: 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 4e-02;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





the specific complementary peptides to proteins encoded by genes of plant or animal origin. The present sequence is the 5' end peptide for Arabidopsis thaliana. The peptides of the present invention are used in an assay to identify a peptide, especially a peptide polypeptide or homologue. The peptides are also useful for tools for genetic and research and development.

Supply 10 A;

Query Match = 36.4%. Score for the 22, 16, and 10 best used similarity 100%, but 40, 60, and 80%.

65	I APOX 4
	III
66	J APOX 8

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 2007-2008  
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## References

PLATE 1

## 2. Materials and Methods

SECRET

107-Nir-20

06:43:20

iii.  $\{1, 2, 3, \dots, n\}$

2013

$$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$
[illegible]

# III A.5.1.1

1. Controlled

### Example 2

— 1998 —

### Summary

1.  $\mathcal{L}(\mathbf{y}) = \mathcal{L}(\mathbf{y}^*) + \mathcal{L}(\mathbf{y} - \mathbf{y}^*)$

C. J. Devlin

2011.12.29

1927. July 21. July 22. July 23. July 24. July 25. July 26. July 27. July 28. July 29. July 30. August 1. August 2. August 3. August 4. August 5. August 6. August 7. August 8. August 9. August 10. August 11. August 12. August 13. August 14. August 15. August 16. August 17. August 18. August 19. August 20. August 21. August 22. August 23. August 24. August 25. August 26. August 27. August 28. August 29. August 30. September 1. September 2. September 3. September 4. September 5. September 6. September 7. September 8. September 9. September 10. September 11. September 12. September 13. September 14. September 15. September 16. September 17. September 18. September 19. September 20. September 21. September 22. September 23. September 24. September 25. September 26. September 27. September 28. September 29. September 30. October 1. October 2. October 3. October 4. October 5. October 6. October 7. October 8. October 9. October 10. October 11. October 12. October 13. October 14. October 15. October 16. October 17. October 18. October 19. October 20. October 21. October 22. October 23. October 24. October 25. October 26. October 27. October 28. October 29. October 30. November 1. November 2. November 3. November 4. November 5. November 6. November 7. November 8. November 9. November 10. November 11. November 12. November 13. November 14. November 15. November 16. November 17. November 18. November 19. November 20. November 21. November 22. November 23. November 24. November 25. November 26. November 27. November 28. November 29. November 30. December 1. December 2. December 3. December 4. December 5. December 6. December 7. December 8. December 9. December 10. December 11. December 12. December 13. December 14. December 15. December 16. December 17. December 18. December 19. December 20. December 21. December 22. December 23. December 24. December 25. December 26. December 27. December 28. December 29. December 30.

## Method

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[illegible]

11-2011

[illegible]
$$\begin{array}{r} \text{C}_2 \\ \vdots \end{array} \quad \begin{array}{c} \text{ARUK } 4 \\ - \\ \text{ARUK } 7 \end{array}$$

Manuscript accepted: September 19, 2004; final version accepted: November 4, 2004

**2. protein-protein search, using a model**

Received September 30, 2003; accepted November 11, 2003.

File: US 09-787-443-14

Perfect Score: 11

Sequence. . . . . 111 REFERENCES. . . . . 111

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Scoring table: 0.100
          60.0 - 60.0: 1.00
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Searched: 1946; sep. 19872673; reindex.

0 2 2 1 3

Total number of hits satisfied criterion: 27/30/27

Maximum length: 8

Maximum Likelihood Logit = 15

Post-processing: Last: first 500 samples

Database : A\_Geneseq\_19Jun03 : \*

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2:	/SIUS1/qcqdta/q-qnesoq/q-neseq/emb1/AA1 945 1AT *
3:	/SIUS1/qcqdta/q-qnesoq/q-neseq/emb1/AA1 945 1AT *
4:	/SIUS1/qcqdta/q-qnesoq/q-neseq/emb1/AA1 945 1AT *
5:	/SIUS1/qcqdta/q-qnesoq/q-neseq/emb1/AA1 945 1AT *
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the resulting binding product, and is derived by analysis of the total score distribution.

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Result No.	Query		Length	DB	IP	Description
	Score	Match				
1	11	100.0	11	21	AA958542	NCAM tql binding P
2	11	100.0	11	23	ABG59342	Human neural cell
3	5	45.5	8	20	AA939614	"CLA-4 VLD C891 re
4	5	45.5	9	23	AA943825	Human D43 associat
5	5	45.5	9	23	AB974712	Transcription fact
6	5	45.5	10	22	AA934020	Human Complementar
7	5	45.5	10	22	AA934022	Human Complementar
8	5	45.5	10	23	AA939322	Human neural protei
9	4	36.4	8	10	AA972248	Human neural protei

87	4	36.4	10	23	ABR93432	CTL epitope HLA pe	156	4	36.4	15	5	AAE60754	Sequence of a port
88	4	36.4	10	24	ABR94246	CTL epitope HLA pe	157	4	36.4	15	21	AAE63143	Human secreted pro
89	4	36.4	10	23	ABR94543	CTL epitope HLA pe	158	4	36.4	15	21	AAE65529	Oestrogen receptor
90	4	36.4	10	24	ABR94967	CTL epitope HLA pe	159	4	36.4	15	22	AAH99027	Human calcium ion
91	4	36.4	10	23	ABR95064	CTL epitope HLA pe	160	4	36.4	15	22	AAE64081	Alkylation-DNA-pro
92	4	36.4	10	24	ABR95113	CTL epitope HLA pe	161	4	36.4	15	23	AAH94391	Human phosphatidas
93	4	36.4	10	24	ABR95227	Human secreted fact	162	4	36.4	15	23	AAH95036	Human cell protein
94	4	36.4	10	24	ABR95395	Human cancer relat	163	4	36.4	15	23	AAH95276	Human cell signal
95	4	36.4	10	24	ABR95395	Human cancer relat	164	4	36.4	15	23	AAH95276	Oestrogen receptor
96	4	36.4	10	24	ABR95395	Human cancer relat	165	4	36.4	15	24	AAH95276	Human cancer-relat
97	4	36.4	10	24	ABR95395	Human cancer relat	166	4	36.4	15	24	AAH95276	Human cancer-relat
98	4	36.4	10	24	ABR95395	Human cancer relat	167	4	36.4	15	24	AAH95276	Human cancer-relat
99	4	36.4	10	24	ABR95395	Human cancer relat	168	4	36.4	15	24	AAH95276	Human cancer-relat
100	4	36.4	10	24	ABR95395	Human cancer relat	169	4	36.4	15	24	AAH95276	Human cancer-relat
101	4	36.4	10	24	ABR95395	Human cancer relat	170	4	36.4	15	24	AAH95276	Synthetic substrat
102	4	36.4	10	24	ABR95395	Human cancer relat	171	4	36.4	15	24	AAH95276	Linkage peptide fo
103	4	36.4	10	24	ABR95395	Human cancer relat	172	4	36.4	15	24	AAH95276	Hypotensive peptid
104	4	36.4	10	24	ABR95395	Human cancer relat	173	4	36.4	15	24	AAH95276	GMP-140 MAB CDR2L
105	4	36.4	10	24	ABR95395	Human cancer relat	174	4	36.4	15	24	AAH95276	La/SSB epitope 330
106	4	36.4	10	24	ABR95395	Human cancer relat	175	4	36.4	15	24	AAH95276	Ro/SSA epitope 263
107	4	36.4	10	24	ABR95395	Human cancer relat	176	4	36.4	15	24	AAH95276	Hepatitis C Virus
108	4	36.4	10	24	ABR95395	Human cancer relat	177	4	36.4	15	24	AAH95276	Hepatitis C Virus
109	4	36.4	10	24	ABR95395	Human cancer relat	178	4	36.4	15	24	AAH95276	Hepatitis C Virus
110	4	36.4	10	24	ABR95395	Human cancer relat	179	4	36.4	15	24	AAH95276	Hepatitis C Virus
111	4	36.4	10	24	ABR95395	Human cancer relat	180	4	36.4	15	24	AAH95276	Hepatitis C Virus
112	4	36.4	10	24	ABR95395	Human cancer relat	181	4	36.4	15	24	AAH95276	Hepatitis C Virus
113	4	36.4	10	24	ABR95395	Human cancer relat	182	4	36.4	15	24	AAH95276	Hepatitis C Virus
114	4	36.4	10	24	ABR95395	Human cancer relat	183	4	36.4	15	24	AAH95276	Protein P6(SFC) m
115	4	36.4	10	24	ABR95395	Human cancer relat	184	4	36.4	15	24	AAH95276	Dynorphin-like pol
116	4	36.4	10	24	ABR95395	Human cancer relat	185	4	36.4	15	24	AAH95276	Human TSH receptor
117	4	36.4	10	24	ABR95395	Human cancer relat	186	4	36.4	15	24	AAH95276	Human TSH receptor
118	4	36.4	10	24	ABR95395	Human cancer relat	187	4	36.4	15	24	AAH95276	Human TSH receptor
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120	4	36.4	10	24	ABR95395	Human cancer relat	189	4	36.4	15	24	AAH95276	Human TSH receptor
121	4	36.4	10	24	ABR95395	Human cancer relat	190	4	36.4	15	24	AAH95276	Human TSH receptor
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123	4	36.4	10	24	ABR95395	Human cancer relat	192	4	36.4	15	24	AAH95276	Human TSH receptor
124	4	36.4	10	24	ABR95395	Human cancer relat	193	4	36.4	15	24	AAH95276	Human TSH receptor
125	4	36.4	10	24	ABR95395	Human cancer relat	194	4	36.4	15	24	AAH95276	Human TSH receptor
126	4	36.4	10	24	ABR95395	Human cancer relat	195	4	36.4	15	24	AAH95276	Human TSH receptor
127	4	36.4	10	24	ABR95395	Human cancer relat	196	4	36.4	15	24	AAH95276	Human TSH receptor
128	4	36.4	10	24	ABR95395	Human cancer relat	197	4	36.4	15	24	AAH95276	Human TSH receptor
129	4	36.4	10	24	ABR95395	Human cancer relat	198	4	36.4	15	24	AAH95276	Human TSH receptor
130	4	36.4	10	24	ABR95395	Human cancer relat	199	4	36.4	15	24	AAH95276	Human TSH receptor
131	4	36.4	10	24	ABR95395	Human cancer relat	200	4	36.4	15	24	AAH95276	Human TSH receptor
132	4	36.4	10	24	ABR95395	Human cancer relat	201	4	36.4	15	24	AAH95276	Human TSH receptor
133	4	36.4	10	24	ABR95395	Human cancer relat	202	4	36.4	15	24	AAH95276	Human TSH receptor
134	4	36.4	10	24	ABR95395	Human cancer relat	203	4	36.4	15	24	AAH95276	Human TSH receptor
135	4	36.4	10	24	ABR95395	Human cancer relat	204	4	36.4	15	24	AAH95276	Human TSH receptor
136	4	36.4	10	24	ABR95395	Human cancer relat	205	4	36.4	15	24	AAH95276	Human TSH receptor
137	4	36.4	10	24	ABR95395	Human cancer relat	206	4	36.4	15	24	AAH95276	Human TSH receptor
138	4	36.4	10	24	ABR95395	Human cancer relat	207	4	36.4	15	24	AAH95276	Human TSH receptor
139	4	36.4	10	24	ABR95395	Human cancer relat	208	4	36.4	15	24	AAH95276	Human TSH receptor
140	4	36.4	10	24	ABR95395	Human cancer relat	209	4	36.4	15	24	AAH95276	Human TSH receptor
141	4	36.4	10	24	ABR95395	Human cancer relat	210	4	36.4	15	24	AAH95276	Human TSH receptor
142	4	36.4	10	24	ABR95395	Human cancer relat	211	4	36.4	15	24	AAH95276	Human TSH receptor
143	4	36.4	10	24	ABR95395	Human cancer relat	212	4	36.4	15	24	AAH95276	Human TSH receptor
144	4	36.4	10	24	ABR95395	Human cancer relat	213	4	36.4	15	24	AAH95276	Human TSH receptor
145	4	36.4	10	24	ABR95395	Human cancer relat	214	4	36.4	15	24	AAH95276	Human TSH receptor
146	4	36.4	10	24	ABR95395	Human cancer relat	215	4	36.4	15	24	AAH95276	Human TSH receptor
147	4	36.4	10	24	ABR95395	Human cancer relat	216	4	36.4	15	24	AAH95276	Human TSH receptor
148	4	36.4	10	24	ABR95395	Human cancer relat	217	4	36.4	15	24	AAH95276	Human TSH receptor
149	4	36.4	10	24	ABR95395	Human cancer relat	218	4	36.4	15	24	AAH95276	Human TSH receptor
150	4	36.4	10	24	ABR95395	Human cancer relat	219	4	36.4	15	24	AAH95276	Human TSH receptor
151	4	36.4	10	24	ABR95395	Human cancer relat	220	4	36.4	15	24	AAH95276	Human TSH receptor
152	4	36.4	10	24	ABR95395	Human cancer relat	221	4	36.4	15	24	AAH95276	Human TSH receptor
153	4	36.4	10	24	ABR95395	Human cancer relat	222	4	36.4	15	24	AAH95276	Human TSH receptor
154	4	36.4	10	24	ABR95395	Human cancer relat	223	4	36.4	15	24	AAH95276	Human TSH receptor
155	4	36.4	10	24	ABR95395	Human cancer relat	224	4	36.4	15	24	AAH95276	Human TSH receptor

240	27.3	8	21	AA57861	Human TAF mutant #	322	8	22	AA57861	UNAM-1 C terminal
241	27.3	8	21	AA57862	3' untranslated region	323	8	22	AA57862	CD106 C-terminal c
242	27.3	8	21	AA57863	Core polypeptide	324	8	22	AA57863	VCAM1 C-terminal c
243	27.3	8	21	AA57864	Core polypeptide	325	8	23	AA57864	HIV cytoxic lymph
244	27.3	8	21	AA57865	Enhancer polypeptide	326	8	23	AA57865	Yeast cytochrome c
245	27.3	8	21	AA57866	Scp11 HLA-B binding	327	8	23	AA57866	Yeast cytochrome c
246	27.3	8	21	AA57867	Scp11 HLA-B binding	328	8	23	AA57867	Myristoylation org
247	27.3	8	21	AA57868	Scp11 HLA-B binding	329	8	23	AA57868	Recombinase domain
248	27.3	8	21	AA57869	HIV A22 super motif	330	8	23	AA57869	MHC class I molecu
249	27.3	8	21	AA57870	HIV A22 super motif	331	8	23	AA57870	T-cell surface rec
250	27.3	8	21	AA57871	HIV A22 super motif	332	8	23	AA57871	T-cell surface rec
251	27.3	8	21	AA57872	HIV A22 super motif	333	8	23	AA57872	Endothelial cell s
252	27.3	8	21	AA57873	HIV A22 super motif	334	8	23	AA57873	Endothelial cell s
253	27.3	8	21	AA57874	HIV A22 super motif	335	8	23	AA57874	Polypeptide identi
254	27.3	8	21	AA57875	HIV A22 super motif	336	8	23	AA57875	Polypeptide identi
255	27.3	8	21	AA57876	HIV A22 super motif	337	8	23	AA57876	Rabbit platelet mi
256	27.3	8	21	AA57877	HIV A22 super motif	338	8	23	AA57877	Histone acetyltran
257	27.3	8	21	AA57878	HIV A22 super motif	339	8	23	AA57878	Myobacterium tube
258	27.3	8	21	AA57879	HIV A22 super motif	340	8	23	AA57879	Myobacterium tube
259	27.3	8	21	AA57880	HIV A22 super motif	341	8	23	AA57880	Myobacterium tube
260	27.3	8	21	AA57881	HIV A22 super motif	342	8	23	AA57881	Myobacterium tube
261	27.3	8	21	AA57882	HIV A22 super motif	343	8	23	AA57882	Myobacterium tube
262	27.3	8	21	AA57883	HIV A22 super motif	344	8	23	AA57883	Myobacterium tube
263	27.3	8	21	AA57884	HIV A22 super motif	345	8	23	AA57884	Myobacterium tube
264	27.3	8	21	AA57885	HIV A22 super motif	346	8	23	AA57885	Myobacterium tube
265	27.3	8	21	AA57886	HIV A22 super motif	347	8	23	AA57886	Myobacterium tube
266	27.3	8	21	AA57887	HIV A22 super motif	348	8	23	AA57887	Myobacterium tube
267	27.3	8	21	AA57888	HIV A22 super motif	349	8	23	AA57888	Myobacterium tube
268	27.3	8	21	AA57889	HIV A22 super motif	350	8	23	AA57889	Myobacterium tube
269	27.3	8	21	AA57890	HIV A22 super motif	351	8	23	AA57890	Myobacterium tube
270	27.3	8	21	AA57891	HIV A22 super motif	352	8	23	AA57891	Myobacterium tube
271	27.3	8	21	AA57892	HIV A22 super motif	353	8	23	AA57892	Myobacterium tube
272	27.3	8	21	AA57893	HIV A22 super motif	354	8	23	AA57893	Myobacterium tube
273	27.3	8	21	AA57894	HIV A22 super motif	355	8	23	AA57894	Myobacterium tube
274	27.3	8	21	AA57895	HIV A22 super motif	356	8	23	AA57895	Myobacterium tube
275	27.3	8	21	AA57896	HIV A22 super motif	357	8	23	AA57896	Myobacterium tube
276	27.3	8	21	AA57897	HIV A22 super motif	358	8	23	AA57897	Myobacterium tube
277	27.3	8	21	AA57898	HIV A22 super motif	359	8	23	AA57898	Myobacterium tube
278	27.3	8	21	AA57899	HIV A22 super motif	360	8	23	AA57899	Myobacterium tube
279	27.3	8	21	AA57900	HIV A22 super motif	361	8	23	AA57900	Myobacterium tube
280	27.3	8	21	AA57901	HIV A22 super motif	362	8	23	AA57901	Myobacterium tube
281	27.3	8	21	AA57902	HIV A22 super motif	363	8	23	AA57902	Myobacterium tube
282	27.3	8	21	AA57903	HIV A22 super motif	364	8	23	AA57903	Myobacterium tube
283	27.3	8	21	AA57904	HIV A22 super motif	365	8	23	AA57904	Myobacterium tube
284	27.3	8	21	AA57905	HIV A22 super motif	366	8	23	AA57905	Myobacterium tube
285	27.3	8	21	AA57906	HIV A22 super motif	367	8	23	AA57906	Myobacterium tube
286	27.3	8	21	AA57907	HIV A22 super motif	368	8	23	AA57907	Myobacterium tube
287	27.3	8	21	AA57908	HIV A22 super motif	369	8	23	AA57908	Myobacterium tube
288	27.3	8	21	AA57909	HIV A22 super motif	370	8	23	AA57909	Myobacterium tube
289	27.3	8	21	AA57910	HIV A22 super motif	371	8	23	AA57910	Myobacterium tube
290	27.3	8	21	AA57911	HIV A22 super motif	372	8	23	AA57911	Myobacterium tube
291	27.3	8	21	AA57912	HIV A22 super motif	373	8	23	AA57912	Myobacterium tube
292	27.3	8	21	AA57913	HIV A22 super motif	374	8	23	AA57913	Myobacterium tube
293	27.3	8	21	AA57914	HIV A22 super motif	375	8	23	AA57914	Myobacterium tube
294	27.3	8	21	AA57915	HIV A22 super motif	376	8	23	AA57915	Myobacterium tube
295	27.3	8	21	AA57916	HIV A22 super motif	377	8	23	AA57916	Myobacterium tube
296	27.3	8	21	AA57917	HIV A22 super motif	378	8	23	AA57917	Myobacterium tube
297	27.3	8	21	AA57918	HIV A22 super motif	379	8	23	AA57918	Myobacterium tube
298	27.3	8	21	AA57919	HIV A22 super motif	380	8	23	AA57919	Myobacterium tube
299	27.3	8	21	AA57920	HIV A22 super motif	381	8	23	AA57920	Myobacterium tube
300	27.3	8	21	AA57921	HIV A22 super motif	382	8	23	AA57921	Myobacterium tube
301	27.3	8	21	AA57922	HIV A22 super motif	383	8	23	AA57922	Myobacterium tube

376	3	27.3	9	17	AAW43418	Human leucocyte an	446	3	27.3	9	42	ABP16002	HIV A24 super moti
377	3	27.3	9	17	AAW43527	Human leucocyte an	449	3	27.3	9	42	ABP16400	HIV A24 super moti
378	3	27.3	9	17	AAW43509	Human leucocyte an	450	3	27.3	9	22	ABP17496	HIV B27 super moti
379	3	27.3	9	17	AAW43479	Human leucocyte an	451	3	27.3	9	22	ABP18774	HIV B58 super moti
380	3	27.3	9	17	AAW43432	Human leucocyte an	452	3	27.3	9	22	ABP20498	HIV A03 motif; gag
381	3	27.3	9	17	AAW43243	Human leucocyte an	453	3	27.3	9	22	ABP20861	HIV A03 motif; gag
382	3	27.3	9	17	AAW42509	SH2-1, SH2-2, SH2-3	454	3	27.3	9	22	ABP21503	HIV A03 motif; pol
383	3	27.3	9	17	AAW43062	Human leucocyte an	455	3	27.3	9	22	ABP21889	HIV A03 motif; rev
384	3	27.3	9	17	AAW43492	Human leucocyte an	456	3	27.3	9	22	ABP22189	HIV A03 motif; rev
385	3	27.3	9	17	AAW43493	Human leucocyte an	457	3	27.3	9	22	ABP22259	HIV A03 motif; vpu
386	3	27.3	9	17	AAW43434	Human leucocyte an	458	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
387	3	27.3	9	17	AAW43435	Human leucocyte an	459	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
388	3	27.3	9	17	AAW43436	Human leucocyte an	460	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
389	3	27.3	9	17	AAW43437	Human leucocyte an	461	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
390	3	27.3	9	17	AAW43438	Human leucocyte an	462	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
391	3	27.3	9	17	AAW43439	Human leucocyte an	463	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
392	3	27.3	9	17	AAW43440	Human leucocyte an	464	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
393	3	27.3	9	17	AAW43441	Human leucocyte an	465	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
394	3	27.3	9	17	AAW43442	Human leucocyte an	466	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
395	3	27.3	9	17	AAW43443	Human leucocyte an	467	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
396	3	27.3	9	17	AAW43444	Human leucocyte an	468	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
397	3	27.3	9	17	AAW43445	Human leucocyte an	469	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
398	3	27.3	9	17	AAW43446	Human leucocyte an	470	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
399	3	27.3	9	17	AAW43447	Human leucocyte an	471	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
400	3	27.3	9	17	AAW43448	Human leucocyte an	472	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
401	3	27.3	9	17	AAW43449	Human leucocyte an	473	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
402	3	27.3	9	17	AAW43450	Human leucocyte an	474	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
403	3	27.3	9	17	AAW43451	Human leucocyte an	475	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
404	3	27.3	9	17	AAW43452	Human leucocyte an	476	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
405	3	27.3	9	17	AAW43453	Human leucocyte an	477	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
406	3	27.3	9	17	AAW43454	Human leucocyte an	478	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
407	3	27.3	9	17	AAW43455	Human leucocyte an	479	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
408	3	27.3	9	17	AAW43456	Human leucocyte an	480	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
409	3	27.3	9	17	AAW43457	Human leucocyte an	481	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
410	3	27.3	9	17	AAW43458	Human leucocyte an	482	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
411	3	27.3	9	17	AAW43459	Human leucocyte an	483	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
412	3	27.3	9	17	AAW43460	Human leucocyte an	484	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
413	3	27.3	9	17	AAW43461	Human leucocyte an	485	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
414	3	27.3	9	17	AAW43462	Human leucocyte an	486	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
415	3	27.3	9	17	AAW43463	Human leucocyte an	487	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
416	3	27.3	9	17	AAW43464	Human leucocyte an	488	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
417	3	27.3	9	17	AAW43465	Human leucocyte an	489	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
418	3	27.3	9	17	AAW43466	Human leucocyte an	490	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
419	3	27.3	9	17	AAW43467	Human leucocyte an	491	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
420	3	27.3	9	17	AAW43468	Human leucocyte an	492	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
421	3	27.3	9	17	AAW43469	Human leucocyte an	493	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
422	3	27.3	9	17	AAW43470	Human leucocyte an	494	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
423	3	27.3	9	17	AAW43471	Human leucocyte an	495	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
424	3	27.3	9	17	AAW43472	Human leucocyte an	496	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
425	3	27.3	9	17	AAW43473	Human leucocyte an	497	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
426	3	27.3	9	17	AAW43474	Human leucocyte an	498	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
427	3	27.3	9	17	AAW43475	Human leucocyte an	499	3	27.3	9	22	ABP22268	HIV A03 motif; vpu
428	3	27.3	9	17	AAW43476	Human leucocyte an	500	3	27.3	9	24	ABP11139	House dust mite de

## ALIGNMENTS

## RESULT 1

AAW88542  
ID AAW88542 standard; peptide: 11 AA.

XX  
XX AAW88542

XX  
XX 37-A03-2009 (first entry)

XX  
XX NCAM lql binding peptide #14.

XX  
XX NCAM: neural cell adhesion molecule; lql: immunoglobulin domain 1;  
XX  
XX neurite outgrowth; proliferation; nerve damage; sclerosis;  
XX  
XX impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
XX  
XX Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
XX  
XX treatment: prosthetic nerve guide; treatment; nervous system.



```

RESULT 4
ID AAY496.4 Standard: peptide: b AA
XX
AC AAY496.4
XX
BT 21-NOV-1999 (first entry)
XX
DE C1A 4 VLB CDR1 region insert.
XX
KW C1A-4, cytotoxic T lymphocyte associated antigen, 35 kDa, binding agent; VLB;
KW variable-like domain; human; diagnosis; cancer; T-cell clone.
XX
CS Synthetic.
XX Homo sapiens.
XX
PN W02045115 A1.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-A000136.
XX
PR 06-MAR-1998; 98AJ-0022230.
XX
CA (C1A 4) HLA-B*27.01.
XX
PI Anna G. Garands M, Hudson E.J., Trivedi R.A., Natarajan S.
XX WPL, 1999 55:042/46.
XX
PT New binding agent comprising monomeric V like domain in which, at least
PT one complementarity determining region loop is modified, useful for
PT diagnosis of cancer.
XX
IS Example 4; Page 27; 117pp; English
XX
CC This sequence is an insert in the C-terminus of the variable-like domain (VLB)
CC of the human cytotoxic T lymphocyte associated antigen 4 (C1A-4), used
CC in the binding agent of the invention. The binding agent (1) comprises at
CC least one monomeric VLB that is derived from a C1A-4 antibody isolated and
CC has at least one CDR (complementarity determining region) loop sequence,
CC at part of it, modified or replaced so that, compared to unmodified VLB,
CC its solubility is increased and/or the structure is altered and/or it
CC is a dimeric form is created with the C1A-4 domain, for use in the
CC diagnosis of cancer, and in the treatment of cancer.
XX
CC Broad claims are also in vitro, chemically modified VLBs and solid supports for
XX diagnosis and therapeutically modified VLBs and solid supports for
XX diagnosis, steroids, pesticides, and other compounds that act as tumor
XX markers, cell or viral proteins, modified VLBs, and VLBs that cross reactivity
XX and alters binding specificity. Shows VLBs isolated from human
XX proteins, the need for a humanized sequence and VLBs also capable
XX responses) is avoided, and modified and a solid support expression in
XX Escherichia coli.
XX
SC Sequence: 8 AA;
Query Match 45.5%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Prod. No. 9.3e105;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TREKK 8
DB 1 IIII
5 TREKK 9
RESULT 5
ABR74702
ID ABR74702 Standard: Peptide: 9 AA.
XX
AC ABR74702;
XX
BT 18-APR-2002 (first entry)
XX
DE Transcription factor nuclear localisation signal peptide SEQ ID NO:466.
XX
KW Pustogent; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide lipid-polyelectrolyte complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
CS Homo sapiens.
XX Mus sp.
XX
PN W020019446 A2.

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XX
DE Human D40 associated peptide SEQ ID NO 16.
XX
KW D40; antigen; cancer testis antigen; human; cancer; cytostatic; HLA;
KW human leucocyte antigen class I; cytotoxic T cell; immunotherapy;
KW cervical cancer; epithelioid cancer; promyelogenic leukaemia;
KW oesophageal cancer; pancreatic cancer; malignant melanoma; lung cancer;
KW oral carcinoma; breast cancer; metircarcinoma; ovarian cancer;
KW gliocytoma; colon cancer.
XX
CS Homo sapiens
XX
PN W020022560 A1.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-0107784.
XX
PR 08-SEP-2000; 2000JP 02/4218.
XX
CA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Takimoto M, Kuzumaki N, Sato N, Sahara H;
XX WPL; 2002-292253/33.
XX
PI Human cancer testis antigen D40 and encoded gene, useful in diagnosis
PI and immunotherapy for cancer.
XX
CS Claim 11; Page 75; 151pp; Japanese.
XX
CC This invention describes a novel gene encoding the human protein antigen,
CC D40 which is expressed in testis and various cancers over a broad range
CC and which has cytostatic activity. Peptides derived from this protein
CC can bind with human leucocyte antigen (HLA) class I and can be used for
CC detecting cytotoxic T cells or their precursor cells. The antigen is
CC useful in diagnosis and immunotherapy for cancer including cervical
CC cancer, epithelioid cancer, promyelogenic leukaemia, oesophageal cancer,
CC pancreatic cancer, malignant melanoma, lung cancer, oral carcinoma,
CC breast cancer, metircarcinoma, ovarian cancer, gliocytoma and colon
CC cancer. AAM9813 AAM96030 represent peptides associated with the human
CC D40 antigen described in the disclosure of the invention.
XX
SC Sequence: 9 AA;
Query Match 45.5%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Prod. No. 9.3e105;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TREKK 8
DB 1 IIII
5 TREKK 9
RESULT 5
ABR74702
ID ABR74702 Standard: Peptide: 9 AA.
XX
AC ABR74702;
XX
BT 18-APR-2002 (first entry)
XX
DE Transcription factor nuclear localisation signal peptide SEQ ID NO:466.
XX
KW Pustogent; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide lipid-polyelectrolyte complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
CS Homo sapiens.
XX Mus sp.
XX
PN W020019446 A2.

```









XX (LICK ) DUCKY CO LTD  
PA (REG ) UNIV CALIFORNIA  
XX  
XX Chao JM, Kim S  
XX WFI: 1996-057806/06  
XX  
PT New stable chain analogues of monellin, sweetener for  
PT foods/beverages, pharmaceuticals, and start of a long range  
PT and acidic pH  
XX  
PS Claim 1: Column 13: (left: English  
XX  
XX Single chain analogues of the Sweet proteins, monellin, comprise a  
XX peptide homologous to residues 1-46 of the B chain of monellin  
XX (AA888043) linked through the C-terminus to a modified linker which is in  
XX turn linked to the N-terminus of a peptide homologous to residues 6-45  
XX of the native A chain (AA888035) of monellin. Monellin is isolated from  
XX "Strawberry berries" of the West African plant *Cosmosiphon*  
XX communis. The protein can be used as a substitute for sugar in  
XX sweetened foods and beverages. The single chain forms of monellin  
XX are capable of maintaining their taste when subjected to other conditions which  
XX would ordinarily denature the native protein and retain their Sweet  
XX taste. AA888037-48 represent several examples used in the analogues.  
XX (Updated on 25 MAR-2003 to correct typos.)  
XX  
SQ Sequence 8 AA:  
Query Match 36.4% Score 4 DB 17 Length 8  
Best Local Similarity 100.0% Prod.No. 9.3e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
QY 3 KIRK 5  
LE 111  
2 KIRK 5  
RESULT 13  
AAW2246  
XX AAW2246 standard: Peptide: 8 AA:  
XX  
XX AAW2246:  
XX 20-APR-1996 (first entry)  
XX  
XX Linker peptide 5 of a single chain monellin analogue.  
XX  
XX Monellin analogue: thermostable; sweetener; food; beverage;  
XX Linker:  
XX Synthesized.  
XX  
XX US5072472-A.  
XX  
XX 4: SEP 1997  
XX  
XX 06-JUN 1995; 930S-046954  
XX  
XX 01-MAR 1997; 930S-0502257  
XX 19-JUN-1997; 930S-0564341  
XX 19-JUN 1997; 930S-0564341  
XX 04-NOV 1997; 930S-0112124  
XX 18-JAN 1998; 930S-0465985  
XX 02-NOV 1993; 930S-0146326  
XX 06-JUN 1995; 930S-0469854  
XX  
XX (LICK ) DUCKY BROS CO LTD  
XX (REG ) UNIV CALIFORNIA  
XX  
XX Chao JM, Kim S  
XX  
XX WFI: 1997-488801/45  
XX  
XX Sweetening food compositions - with thermostable single chain  
XX monellin analogues  
XX  
XX Claim 7: Column 14: (left: English  
XX  
XX This is a linker peptide used in the construction of a single chain  
XX monellin analogue. This can be used as a method for sweetening a  
XX food composition. The method comprises including in the composition  
XX the single chain sweet proteinaceous analogue of monellin. This  
XX analogue contains peptide residues 1-46 of the B chain and residues 6-45  
XX of the A chain of native monellin modified only by conservative

XX DNA encoding single chain form of monellin - useful as sweetener for  
XX foods, beverages etc., also related vectors and transformed cells.  
XX  
XX Claim 1: Column 13: (left: English  
XX  
XX Linker peptides (AA893044) are used to link a peptide having at  
XX least 90% homology to amino acids 1-46 of the monellin B chain (see  
XX also AA893042) to a peptide having at least 90% homology to amino acids  
XX 1-45 of the A chain. (See also AA893041). These single chain monellin  
XX analogs (see also AA893040) can be obtd. e.g. by expression of a  
XX synthetic gene (AA11578) in transformed host cells, e.g. Escherichia  
XX coli. The analogs have up to 1,000 times the sweetness of sucrose  
XX and have improved thermostability in comparison with natural monellin.  
XX (Updated on 25-MAR-2003 to correct typos.)  
XX  
SQ Sequence 8 AA:  
Query Match 36.4% Score 4 DB 17 Length 8  
Best Local Similarity 100.0% Prod.No. 9.3e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
QY 3 KIRK 5  
LE 111  
2 KIRK 5  
RESULT 13  
AAW2246  
XX AAW2246 standard: Peptide: 8 AA:  
XX  
XX AAW2246:  
XX 20-APR-1996 (first entry)  
XX  
XX Linker peptide 5 of a single chain monellin analogue.  
XX  
XX Monellin analogue: thermostable; sweetener; food; beverage;  
XX Linker:  
XX Synthesized.  
XX  
XX US5072472-A.  
XX  
XX 4: SEP 1997  
XX  
XX 06-JUN 1995; 930S-046954  
XX  
XX 01-MAR 1997; 930S-0502257  
XX 19-JUN-1997; 930S-0564341  
XX 19-JUN 1997; 930S-0564341  
XX 04-NOV 1997; 930S-0112124  
XX 18-JAN 1998; 930S-0465985  
XX 02-NOV 1993; 930S-0146326  
XX 06-JUN 1995; 930S-0469854  
XX  
XX (LICK ) DUCKY BROS CO LTD  
XX (REG ) UNIV CALIFORNIA  
XX  
XX Chao JM, Kim S  
XX  
XX WFI: 1997-488801/45  
XX  
XX Sweetening food compositions - with thermostable single chain  
XX monellin analogues  
XX  
XX Claim 7: Column 14: (left: English  
XX  
XX This is a linker peptide used in the construction of a single chain  
XX monellin analogue. This can be used as a method for sweetening a  
XX food composition. The method comprises including in the composition  
XX the single chain sweet proteinaceous analogue of monellin. This  
XX analogue contains peptide residues 1-46 of the B chain and residues 6-45  
XX of the A chain of native monellin modified only by conservative

CC substitution. The B chain and the A chain are linked by a covalent bond  
 CC or a hydrophobic, physiologically acceptable covalent linker capable of  
 CC providing a spacing length equivalent to a peptide of 1-10 amino acids.  
 CC This linker peptide is selected so as to reside on the external portion  
 CC of the molecule and not to disturb the native conformation. This protein  
 CC can be used for sweetening foods and beverages, the monellin analogues  
 CC are thermostable and retain high intensity sweetening power even after  
 CC heating to 100 degree. C at acidic pH.

XX Sequence 8 AA;

Query Match 36.4% Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIRE 5

DB 2 KIRE 5

RESULT 16

AAW64273

DB AAW64273 standard; Peptide: 8 AA.

XX AAW64273;

XX 18 FEB 1996 (first entry)

XX Linker sequence 4 of single-chain protein sweetener monellin.

XX single chain protein; sweetener; monellin; heat stability; adjuvant;  
 KW beverage; pharmaceutical; toothbrush; dental hygiene; antibody;  
 KW purification; sucrose.

XX Synthetic.

XX GS5670339 A.

XX 24 SEP 1997.

XX 06 JUN 1995; 95US-0650945.

XX 06 MAR 1995; 95US-0652257.

XX 19 JUN 1997; 97US-0664347.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

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XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

XX 19 JUN 1997; 97US-0664343.

CC are stable under conditions where the native protein is denatured. This  
 CC protein sweetener is many times sweeter than sucrose, and can be used as  
 CC a substitute for sugar in foods and beverages (juices, hot drinks or  
 CC carbonated beverages), chewing gum, toothpastes, mouthwashes, dental  
 CC hygiene products and pharmaceuticals. They can also be used to generate  
 CC specific antibodies for their purification.

XX Sequence 8 AA;

Query Match 46.4% Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIRE 5

DB 2 KIRE 5

RESULT 16

AAW64273

DB AAW64273 standard; Peptide: 8 AA.

XX AAW64273;

XX 24 NOV 1996 (first entry)

XX MMP-7 peptide substrate.

XX MCP-7; mouse mast cell protease 7; trypsinase-7; blood clot;  
 KW anticoagulant; myocardial infarction; reocclusion; thromboembolism;  
 KW cerebral embolism; thrombosis; therapy.

XX Synthetic.

XX W05824886-A1.

XX 11 JUN 1998.

XX 25 NOV 1997; 97WO US21620.

XX 04 DEC 1996; 96US-0032354.

XX (ESIM) BRIGHAM & WOMEN'S HOSPITAL.

XX Stevens KL.

XX WPI: 1998 433504/29.

XX New compositions containing trypsinase-7, e.g. mouse mast cell  
 PT trypsinase-7 are used to treat clot formation in e.g. myocardial  
 PT infarction; reocclusion following angioplasty or pulmonary  
 PT thromboembolism

XX Example: Page 45; 92pp; English.

XX This is a substrate peptide of mouse mast cell protease 7 (MMP-7,  
 CC sec AAW64273). It is one of 21 peptides (see AAW64270-90) obtained by  
 CC incubating a phage display peptide library 2 times with a  
 CC recombinant FLAG-tagged MMP-7 polypeptide, isolating clones, and  
 CC deducing the amino acid sequence of the protease susceptible  
 CC domains in the phage fusion proteins. Only one peptide (see AAW64270)  
 CC was obtained after 4 rounds of screening. MMP-7 has been  
 CC characterised as having fibrinogen as its physiological substrate.  
 CC It can be used to prevent or treat fibrin clot formation in vitro  
 CC and in vivo. Trypsinase-7 proteases of the invention, including  
 CC MMP-7 and its homologues, can be used to treat disorders that are  
 CC mediated by reocclusion following angioplasty, such as myocardial  
 CC infarct and reocclusion following angioplasty, and are also useful  
 CC for surgical procedures that require that blood does not clot.

XX Sequence 8 AA;

Query Match 46.4% Score 4; DB 19; Length 8;

CC This linker sequence is used to prepare a recombinant single-chain form  
 CC of the protein sweetener monellin. The recombinant protein has the  
 CC formula B-A where B and A represent peptide portions of the B chain and  
 CC A chain respectively of the native monellin and A is a linker between the  
 CC B and A chains. The linker sequence A can be a covalent bond or can  
 CC consist of a peptide of 1-10 amino acids, with sufficient  
 CC hydrophobicity and length to reside on the outside of the molecule  
 CC without distortion of the native conformation. The peptide sequence glycol  
 CC oligomers can also be used as linkers. The single-chain protein sweetener  
 CC retains the sweetness properties of the double-chain native monellin, but

```

Best Local Similarity 100.0%; Prec No. 9 matches
Matches 4: Conservative 0; Mismatches 0; Gaps 0

QY 7 RKSK 10
DL 111
DE 5 RKSK 8

RESULT 17
AAW54664
ID AAW54664 standard; peptide: # AA
XX
XX
XX AAW54664
XX
XX 25 SEP 1998 (first entry)
XX
XX Peptide from P. talpaeipatum CSP 68 470 1
XX
XX Mannose; antigen; antigen-presenting cell; immunosynthetic peptide; 4 codons
XX varicella treatment.
XX
XX Synthetic
XX
XX W05813478 AA
XX
XX 10 APR 1998
XX
XX 25 SEP 1997 92W0-SL00543
XX
XX 25 SEP 1998 96EP-0202701
XX
XX (JOYE ) ELKSONIV LERGEN
XX
XX Brillion JW, Koning F;
XX
XX W01 1998 Z40641/20
XX
XX
XX Increasing uptake and presentation of antigens by adding mannose
XX residues to antigen for increased local response, useful in
XX v.a. vaccines against viral infections)
XX
XX Enclosure Page 29: 47pp; English
XX
XX
XX The peptides AAW54559 W54664 are examples of peptides to which at least
XX 1 (preferably 2) mannose can be attached to increase their uptake as
XX antigens by antigen-presenting cells. Uptake of antigenic mannose-armed
XX peptides will increase the local response, whereas uptake of antigenic
XX peptides blocks the T cell response. Peptides containing mannose
XX antigens can be used in treatment of type 1 diabetes, rheumatoid
XX arthritis, graft rejection, etc. Also, to induce self non-
XX responsiveness. Vaccines containing the peptide antigen are used to
XX prevent or treat infections by v.a. related viruses, fungi, bacteria
XX and parasites.
XX
XX Sequence # AA:
XX
XX Query Match 36.4%; Score 10; ID No. 1049478
Best Local Similarity 100.0%; Prec No. 9 matches
Matches 4: Conservative 0; Mismatches 0; Gaps 0

QY 8 RKSK 11
DL 111
DE 1 RKSK 4

RESULT 18
AAW56994
ID AAW56994 standard; peptide: # AA
XX
XX
XX AAW56994
XX
XX 25 JUL 1998 (first entry)
XX
XX
XX
XX
XX

```

Enzyme inhibitor: peptide SEQ ID NO:195.

Enzyme inhibitor: t-PA; a PA, chymotrypsin; serine protease; active, latent; substrate subtraction phage display peptide library; identification; kinase; phosphatase; serpin.

BACD SUPPONS.

W09747314-A1.

18 DEC 1997.

10 JUN 1997. 5760-02509/63.

10 JUN 1996. 9905 0019495.

(SCRI) SCRIPTES RES INS.

Ke S. Madison EL.

WPI: 1998-062346/6.

Substrate subtraction phage display peptide libraries - used to distinguish between active and latent forms of enzyme, e.g. serine protease

claim 25, Page 106; 106pp; English.

The present sequence represents an enzyme inhibitor peptide used in the method of the invention to distinguish between t-PA and u-PA. The present invention describes a substrate subtraction library for the identification of peptide substrates selective between a first enzyme (E1) and a second enzyme (E2), comprising a collection of different peptides, substantially lacking peptides that are effective substrates for E1. Also described are: (1) a method (M1) for identifying peptide substrates selective between a first enzyme (E1) and a second enzyme (E2); (2) a compound comprising the amino acid sequence of a peptide identified by M1; (3) a polypeptide for use as an enzyme inhibitor comprising one of 237 amino acid sequences (see AAM56801 to AAM56947, and AAM56949 to AAM57038); (4) a recombinant DNA vector comprising DNA (1) encoding a protease inhibitor including the sequence identified by the M1; (5) a prokaryotic or eukaryotic cell containing the vector of the M1; (6) an antibody (Ab) immunoreactive with at least one of the peptides identified by M1; and (7) a diagnostic assay for distinguishing between active and latent forms of protease inhibitors, that uses (Ab). The library and method are used for distinguishing between active and latent forms of enzyme inhibitors, e.g. proteases, kinases and phosphatases. (Ab) are used for affinity purification of recombinant peptides and for the identification of naturally occurring protease inhibitors. Enzyme-inhibiting peptides identified can be used to treat a serpin deficiency or a disorder of serine proteases.

Seq-ence 8 AA:

Query Match 36.4% Score 4. DB 19: Length 8:

Best Local Similarity 100.00; Prod. No. 9.3e-05;

Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 RKSK 10

1111

DB 3 RKSK 6

RESULT 19

AAB24556

ID AAB24556 standard; Peptide; 8 AA.

XX AC AAB24556;

XX AC AAB24556;

XX 05-JAN-2001 (first entry)

XX Cytotoxic T Lymphocyte (CTL) epitope SEQ ID NO:8.

XX

KW A1Pasec Hsp70; heat shock protein; cytot. xpr. 1; lymphocyte; CIL  
 KW immune response; infectious disease; malignant; cytotoxic; CIL  
 KW cytostatic; immunostimulant; cellular immune response; cancer  
 XX proteoglycan; leukaemia; cancer  
 XX B-cell; suppress.  
 XX W020049041 A1.  
 XX 24-MAY-2003.  
 XX 18-FEB-2003; 2006W020049041.  
 XX 19-FEB-1999; 99EP-0643535.  
 XX (SAME) SEQUENC ELECTRIC INST. etc.  
 XX Shinkura N, Udono H, Yui K;  
 XX WPI: 2000-543748/49.  
 XX Fused protein capable of inducing cellular immune response, used as  
 XX active ingredient for drug compositions in prevention and/or treatment  
 XX of infectious diseases such as malignant cancer.  
 XX Claim 5; Page 52; 72pp; Japanese.  
 XX The present invention describes a fused protein (1) prepared from a  
 XX peptide containing a CIL (cytotoxic) (peptide) epitope recognized by  
 XX cytotoxic T cells and a protein containing the Adhesin domain of a heat  
 XX shock protein. Also described are: (2) a drug composition containing (1)  
 XX as active ingredient; (3) a DNA encoding (1); (4) an expression vector  
 XX containing the DNA of (2); and (5) a transmembrane protein which can retain the  
 XX expression vector of (3). (1) has cytostatic, immunostimulant and  
 XX proteoglycan activities, and can be used as a cellular immune response  
 XX inducer. The protein is used, as an active ingredient for drug  
 XX compositions in preventing and/or treating infectious diseases such as  
 XX malaria or cancer, e.g., to provide systemic immunity against leukemias.  
 XX The present sequence represents a specifically claimed CIL epitope  
 XX for use in a fused protein of the present invention.  
 XX Sequence: 8 AA;  
 Query Match: 96.4%; Score 4; DH 21; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 KSKD 11  
 DL III  
 3 PERK 6  
 RESULT 2:  
 AAY79697  
 ID AAY79697 Standard; Peptide: 8 AA.  
 AC AAY79697;  
 DI 10-MAY-2000 (first entry)  
 XX SSX 4 derived peptide #21.  
 XX Cancer: SSX family: SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;  
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CIL;  
 KW cytostatic; melanoma; synovial sarcoma.  
 CS Homo sapiens.  
 XX W0200000824 A1.  
 XX 05-JAN-2000.  
 XX 25-JUN-1999; 99W-0534493.  
 XX 26-JUN-1998; 98US-105619.  
 XX (LEW) LEW03; INST CAN-EP RES.  
 XX 26-JUN-1998; 98US-0105659.  
 XX (LEW) LUDWIG INST CANCER RES.  
 XX Tatesi O, Schin B, Pfreundschuh M, Rammensee G, Stevanovic S;  
 XX Chen Y, Gure A, Gold L;  
 XX WPI: 2000-170334/35.  
 XX Determining the possible presence of breast, endometrial, colorectal,  
 XX lung, bladder or head-neck cancer.  
 XX Example 13, Page 21; 40pp; English.  
 XX A method has been developed for determining the possible presence of a  
 XX cancer, which is not melanoma or synovial sarcoma. The method comprises  
 XX assaying a sample taken from the subject to determine the expression of  
 XX an SSX gene, and determining the expression as a determination of the  
 XX possible presence of cancer; expression of SSX1 gene indicates possible  
 XX presence of breast, endometrial, colorectal, lung, bladder or head-neck  
 XX cancer. These cancers are also detected by SSX2 and SSX4 gene  
 XX expression. SSX2 gene expression additionally indicates possible presence  
 XX of lymphoma, renal cell cancer, glioma and prostate cancer. Expression  
 XX of SSX4 gene also indicates possible presence of ovarian or stomach  
 XX cancer. SSX5 gene expression indicates the same cancers as SSX1, except  
 XX breast cancer. Determining expression of SSX gene can be used to monitor  
 XX progress of melanoma or synovial sarcoma, which is not cancer. The  
 XX SSX-derived peptide complex stimulates proliferation of cytolytic T  
 XX cells. This is useful for treating cancer, especially melanoma. AAY78464  
 XX to AAY78469 represent specifically claimed HLA binding peptides for use  
 XX in the method of the invention. AA288452 to AA288465 represent PCR  
 XX primers used in the isolation of SSX genes in the exemplification of the  
 XX present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762  
 XX represent peptides derived from SSX proteins or NY-ESO-1, which are used  
 XX in the exemplification of the present invention.  
 XX Sequence: 8 AA;  
 Query Match: 96.4%; Score 4; DH 21; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 KSKD 11  
 DL III  
 3 KSKD 4  
 RESULT 20:  
 AAY78469  
 ID AAY78469 Standard; Peptide: 8 AA.  
 AC AAY78469;  
 DI 10-MAY-2000 (first entry)  
 XX SSX 5 derived peptide #14.  
 XX Cancer: SSX family: SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;  
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CIL;  
 KW cytostatic; melanoma; synovial sarcoma.  
 CS Homo sapiens.  
 XX W0200000824 A1.  
 XX 05-JAN-2000.  
 XX 26-JUN-1999; 99W-0514493.  
 XX 26-JUN-1998; 98W-0514493.  
 XX (LEW) LEW03; INST CAN-EP RES.





Example 14: Page 26: 40pp: English.

A method has been developed for determining the possible presence of a cancer, which is not melanoma or syngial sarcoma. The method comprises assaying a sample taken from the subject to determine the expression of an SSX gene, and determining the expression as a determination of the possible presence of cancer. Expression of SSX1 gene indicates possible presence of breast, endometrial, sarcoma, lung, bladder or head neck cancer. These cancers are also detected by SSX2 and SSX4 gene expression. SSX2 gene expression additionally indicates possible presence of lymphatic renal cell cancer, thymic and pancreatic cancer. Expression of SSX5 gene also indicates possible presence of cancer. SSX3 gene expression indicates the same cancers as SSX1, except breast cancer. Determining expression of SSX gene can be used to monitor progress of melanoma or syngial sarcoma, which is not cancer. The SSX-derived peptide complex stimulates proliferation of cytolytic T cells. This is useful for treating cancer, especially melanoma. AAY78474 to AAY78486 represent specifically chosen HLA binding peptides for use in the method of the invention. AAY8462 to AAY8465 represent PCR primers used in the isolation of SSX genes in the exemplification of the present invention. AAY8469 to AAY8480, and AAY8964 to AAY8966 represent peptides derived from SSX proteins of NY-ESO-1, which are used in the exemplification of the present invention.

Sequence # AA:

Query Match 46.4%, Score 4, DB 21, Length 8,  
Best Local Similarity 100.0%, Prod. No. 9, 3e-05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PERK R  
LII  
DL 5 PERK R

RESLI 25  
AAY78744  
ID AAY78744 standard; peptide: B AA.  
XX  
AC AAY78744;  
XX  
XX  
DT 13-APR 2002 (first entry)  
XX  
DE SSX-1 HLA binding motif: #2;  
XX  
KW SSX-2: SSX1 gene; breast cancer; melanoma; NY ESO-1; SYP 1; MAGE-3;  
KW diagnosis; detection; tumour rejection antigen precursor; PCR primers;  
KW HLA binding motif;  
XX  
CS Homo sapiens;  
XX  
FN W220600642-A1;  
XX  
ED 06-JAN-2000;  
XX  
FF 03-JUN-1999; 99W0-051223;  
XX  
FE 26-JUN-1998; 98US-0105907;  
XX  
FA (CLOW) LUTWIG INST CANCER RES;  
XX  
FI Sahlin O, Tureci O, Chen Y, Old LJ, Pfreundschuh M;  
XX  
DE WPL 2000-137070/12;  
XX  
DT Detecting breast cancer and melanoma used for diagnosis and in  
DT development of targeted therapy  
XX  
ES Example 2: Page 14: 24pp: English.

This sequence represents a HLA binding motif from the SSX-1 protein. The invention relates to a method for determining breast cancer or melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and SSX-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGE-3 for melanoma, the expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

Sequence # AA:

XX melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and  
XX SCP-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGE-3 for melanoma, the  
XX expression of at least one is an indicator of possible breast cancer, and  
XX the expression of at least two is an indicator of possible melanoma. The  
XX method is used to diagnose breast cancer and melanoma, and to develop  
XX therapies, e.g., a mixture of peptides, derived from longer antigens and  
XX known to associate with major histocompatibility complex to promote  
XX cytolytic T cell proliferation, can be prepared based on the determined  
XX pattern of antigen expression in a particular sample. Detecting two or  
XX more of the specified tumour rejection antigen precursors improves the  
XX accuracy of the assay.

Sequence # AA:

Query Match 46.4%, Score 4, DB 21, Length 8,  
Best Local Similarity 100.0%, Prod. No. 9, 3e-05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PERK R  
LII  
DL 5 PERK R

RESLI 25  
AAY78744  
ID AAY78744 standard; peptide: B AA.  
XX  
AC AAY78744;  
XX  
XX  
DT 13-APR 2002 (first entry)  
XX  
DE SSX-1 HLA binding motif: #2;  
XX  
KW SSX-2: SSX1 gene; breast cancer; melanoma; NY ESO-1; SYP 1; MAGE-3;  
KW diagnosis; detection; tumour rejection antigen precursor; PCR primers;  
KW HLA binding motif;  
XX  
CS Homo sapiens;  
XX  
FN W220600642-A1;  
XX  
ED 06-JAN-2000;  
XX  
FF 03-JUN-1999; 99W0-051223;  
XX  
FE 26-JUN-1998; 98US-0105907;  
XX  
FA (CLOW) LUTWIG INST CANCER RES;  
XX  
FI Sahlin O, Tureci O, Chen Y, Old LJ, Pfreundschuh M;  
XX  
DE WPL 2000-137070/12;  
XX  
DT Detecting breast cancer and melanoma used for diagnosis and in  
DT development of targeted therapy  
XX  
ES Example 2: Page 14: 24pp: English.

This sequence represents a HLA binding motif from the SSX-1 protein. The invention relates to a method for determining breast cancer or melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and SSX-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGE-3 for melanoma, the expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

Sequence # AA:





AC AAW4158e;  
 XX  
 DT 22-JUN-1998 (first entry)  
 XX  
 DE Melanoma antigen HOM-MEL-40: amount of HLA-A2.1 bound associated peptide  
 XX  
 EE Melanoma markers: antigen; HLA-A2.1; solid phase; first entry; HLA-A2.1  
 XX  
 KW HOM-MEL-40; amount; HLA-A2.1  
 XX  
 OS Synthesis;  
 OS Homo sapiens;  
 XX  
 XX W0244721 A1;  
 XX  
 DE 24 SEP 1997 97W0-US10926;  
 XX  
 EE 23-JUN-1997 97W0-US10926;  
 XX  
 EE 21-JUN-1996 96US-066812d;  
 XX  
 PA (EUBW) EUBW: INST CANCER RES;  
 XX  
 PI Pfreundschuh M;  
 XX  
 XX WPI: 1996-061074/06;  
 XX  
 EE Nucleic acid and derived polypeptide markers for melanoma disease  
 EE used to identify/ing immunoreactive markers of disease  
 XX  
 ES Example 14: Page 25; 47pp; English;  
 XX  
 CC 3 peptide sequences (AAW41587-89) were found in a screening of the  
 CC deduced amino acid sequence of human malignant melanoma gene  
 CC HOM-MEL-40 (see AAW04267) for sequences which might act as  
 CC HLA-A2.1 binders/cytotoxic T lymphocyte (CTL) stimulators. These  
 CC peptides were synthesized using phase protected amino acids and used  
 CC in peptide binding assays with p2. Each peptide was seen to bind  
 CC to HLA-A2.1. HOM-MEL-40 was isolated from a human melanoma  
 CC melanoma cDNA library using a method: designated serological  
 CC fishing. Designed to identify immunoreactive markers of disease.  
 CC The new melanoma associated HOM-MEL-40 and homologs all only expressed  
 CC in melanoma, but not healthy tissues. The serological fishing  
 CC method was also used to identify a related marker (see AAW04267) of  
 CC melanoma disease.  
 XX  
 SQ Sequence 9 AA;  
 Quality Match: 36.4%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred No 9,36-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 REPK 8  
 DL III  
 DL 1 PERK 4  
 RESUL 42  
 AAW78441  
 ID AAW78441 standard: Peptide: 9 AA;  
 XX  
 AC AAW78441;  
 XX  
 DT 10 MAY 2003 (first entry)  
 XX  
 DE SSX 4 derived peptide #25;  
 XX  
 KW Cancer; SSX family; SSX 4; SSX 2; SSX 1; SSX-4; SSX-5; NY-ESO-1;  
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;  
 KW cytostatic; melanoma; synovial sarcoma;  
 XX  
 OS Homo sapiens;  
 OS W0200000824 A1;  
 XX  
 DE 26-JAN-2000  
 XX  
 EE 25-JUN-1997 97W0-US14493;  
 PF

XX  
 DT 06-JAN-2000;  
 XX  
 EE 25-JUN-1997 97W0-US14493;  
 XX  
 EE 26-JUN-1998 98US-0135839;  
 XX  
 PA (EUBW) EUBW: INST CANCER RES;  
 XX  
 PI Pfreundschuh M; Pfreundschuh M; Rammensee G; Stevanovic S;  
 PI Chen Y; Gure A; Gd LJ;  
 XX  
 XX WPI: 2000-17693715;  
 XX  
 EE Determining the possible presence of: breast, endometrial, colorectal,  
 EE Lung, Bladder or head-neck cancer;  
 XX  
 ES Example 13: Page 23; 4 pp; English;  
 XX  
 CC A method has been developed for determining the possible presence of a  
 CC cancer, which is not melanoma or synovial sarcoma. The method comprises  
 CC assaying a sample taken from the subject to determine the expression of  
 CC an SSX gene, and determining the expression as a determination of the  
 CC possible presence of cancer. Expression of SSX1 gene indicates possible  
 CC presence of breast, endometrial, colorectal, lung, bladder or head-neck  
 CC cancer. These cancers are also detected by SSX2 and SSX4 gene  
 CC expression. SSX2 gene expression additionally indicates possible presence  
 CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression  
 CC of SSX4 gene also indicates possible presence of ovarian or stomach  
 CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except  
 CC breast cancer. Determining expression of SSX gene can be used to monitor  
 CC progress of melanoma or synovial sarcoma, which is not cancer. The  
 CC SSX-derived peptide complex stimulates proliferation of cytolytic T  
 CC cells. This is useful for treating cancer, especially melanoma. AAW78464  
 CC to AAW78468 represent specifically claimed HLA binding peptides for use  
 CC in the method of the invention. AAW88452 to AAW88455 represent PCR  
 CC primers used in the isolation of SSX genes in the exemplification of the  
 CC present invention. AAW78469 to AAW78500, and AAW79684 to AAW79762  
 CC represent peptides derived from SSX proteins or NY-ESO-1, which are used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 9 AA;  
 Quality Match: 36.4%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred No 9,36-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 REPK 8  
 DL III  
 DL 1 PERK 4  
 RESUL 42  
 AAW79761  
 ID AAW79761 standard: Peptide: 9 AA;  
 XX  
 AC AAW79761;  
 XX  
 DT 10 MAY 2003 (first entry)  
 XX  
 DE SSX 4 derived peptide #25;  
 XX  
 KW Cancer; SSX family; SSX 4; SSX 2; SSX 1; SSX-4; SSX-5; NY-ESO-1;  
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;  
 KW cytostatic; melanoma; synovial sarcoma;  
 XX  
 OS Homo sapiens;  
 OS W0200000824 A1;  
 XX  
 DE 26-JAN-2000  
 XX  
 EE 25-JUN-1997 97W0-US14493;  
 PF





melanoma is a sample by assaying for expression of NY-ESO-1, SSX-2 and SSX-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGES-3 for melanoma. The expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

XX Sequence: 9 AA;

Query Match: 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8  
II  
D6 3 REK 6

RESULT 47

AAV76745  
ID: AAV76745 standard; Peptide: 9 AA;

AC AAV76745;

DC 13-APR-2000 (first entry)

XX SSX-2 HLA binding motif #14.

XX SSX-2; SSX1 gene; breast cancer; melanoma; NY-ESO-1; SCP-1; MAGES-3;  
KW diagnosis; detection; tumour rejection antigen precursor; PCR primer;  
KW HLA binding motif.

XX Homo sapiens.

IN W020000642-A1.

CU 06-JAN-2000.

XX 03-JUN-1999; 99W0-US12293.

XX 26-JUN-1998; 98US-0105907.

PA (LUDW) LODWIG INST CANCER RES.

PI Salim U., Tureci O., Chen Y., Old LJ, Pfreundschuh M;

XX WPI: 2000 147073/12.

XX Detecting breast cancer and melanoma used for diagnosis and in development of targeted therapy.

XX Example 2: Page 12; 24pp; English.

XX This sequence represents a HLA binding motif from the SSX-2 protein. The invention relates to a method for determining breast cancer or melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and SSX-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGES-3 for melanoma. The expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

XX Sequence: 9 AA;

Query Match: 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8  
II  
D6 3 REK 4

RESULT 48

AAV76745  
ID: AAV76745 standard; Peptide: 9 AA;

AC AAV76745;

DC 13-APR-2000 (first entry)

XX SSX-1 HLA binding motif #8.

XX SSX-2; SSX1 gene; breast cancer; melanoma; NY-ESO-1; SCP-1; MAGES-3;  
KW diagnosis; detection; tumour rejection antigen precursor; PCR primer;  
KW HLA binding motif.

XX Homo sapiens.

IN W020000642-A1

XX 06-JAN-2000.

XX 04-JUN-1999; 99W0-US12293.

XX 26-JUN-1998; 98US-0105907.

PA (LUDW) LODWIG INST CANCER RES.

PI Salim U., Tureci O., Chen Y., Old LJ, Pfreundschuh M;

XX WPI: 2000 147073/12

XX Detecting breast cancer and melanoma used for diagnosis and in development of targeted therapy.

XX Example 2: Page 13; 24pp; English.

XX This sequence represents a HLA binding motif from the SSX-1 protein. The invention relates to a method for determining breast cancer or melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and SSX-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGES-3 for melanoma. The expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

XX Sequence: 9 AA;

Query Match: 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8  
II  
D6 3 REK 4

RESULT 49

AAV96092  
ID: AAV96092 standard; Peptide: 9 AA;







KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL;  
 OS B-cell suppress.  
 OS Synthesized.  
 PN W0200216596 A2  
 XX 48 FEB 2002.  
 XX 22 AUG 2001: 2001W0-US26411.  
 XX 22 AUG 2001: 2001US-2270981.  
 XX 10 APR 2001: 2001US-2627490.  
 XX (AGEN-) AGENSYS INC.  
 XX Chaitin Ed DM, Hubert RS, Raitano AB, Altar DH, Levin E;  
 XX Faris M, Se W, Jakubovits A;  
 XX WPI: 2002-269357/31.  
 XX Monitoring 158PIH4 gene products in human tissue sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer.  
 XX The method comprises determining the status of 158PIH4  
 XX gene products in a tissue sample from an individual, comparing the  
 XX status to the status of 158PIH4 gene products in a normal sample, and  
 XX identifying the presence of aberrant 158PIH4 gene products in the sample.  
 XX 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 XX production. 158PIH4 polynucleotides may be used in monitoring genetic  
 XX abnormalities. The 158PIH4 proteins may be used in assessing the status  
 XX of 158PIH4 gene products in normal versus cancerous tissues and so  
 XX elucidating the malignant phenotype, in generating and characterizing  
 XX domain specific antibodies, for identifying agents or cellular factors  
 XX that bind to 158PIH4 or its particular domain, and for generating  
 XX cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 XX and prognostic assays, in treating patients with cancer, in accelerating  
 XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 XX and as immunization reagents for detecting 158PIH4-expressing cells.  
 XX The antibodies are particularly useful in bladder cancer diagnostic and  
 XX prognostic assays, and immunization methodologies. The 158PIH4 gene has been  
 XX located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
 XX the present invention has been located to chromosome 8q23. ABI50400 to  
 XX ABI50429 and AB94468 to AB94468 represent sequences used in the  
 XX exemplification of the present invention.  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 36.4%, Score 41, DP 27, Length 9;  
 XX Best Local Similarity 100.0%, Prod. No. 9, 5e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 07 7 KSKK 16  
 XX 111  
 XX 10 4 KSKK 7  
 XX 111  
 XX  
 XX RESULT 14  
 XX AB944797  
 XX 10 AB944797 Standard, Peptide: 9 AA.  
 XX AC AB944797;  
 XX  
 XX 11 17 JUN 2002 (first entry)  
 XX  
 XX 10 C110 epitope HLA peptide SEQ ID NO. 27.

XX Human: 158PIH4; chromosome 8q22-q23, 158PIH4; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL;  
 OS B-cell suppress.  
 OS Synthesized.  
 PN W0200216596 A2  
 XX 48 FEB 2002.  
 XX 22 AUG 2001: 2001W0-US26411.  
 XX 22 AUG 2001: 2001US-2270981.  
 XX 10 APR 2001: 2001US-2627490.  
 XX (AGEN-) AGENSYS INC.  
 XX Chaitin Ed DM, Hubert RS, Raitano AB, Altar DH, Levin E;  
 XX Faris M, Se W, Jakubovits A;  
 XX WPI: 2002-269357/31.  
 XX Monitoring 158PIH4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer.  
 XX The method comprises determining the status of 158PIH4  
 XX gene products in a tissue sample from an individual, comparing the  
 XX status to the status of 158PIH4 gene products in a normal sample, and  
 XX identifying the presence of aberrant 158PIH4 gene products in the sample.  
 XX 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 XX production. 158PIH4 polynucleotides may be used in monitoring genetic  
 XX abnormalities. The 158PIH4 proteins may be used in assessing the status  
 XX of 158PIH4 gene products in normal versus cancerous tissues and so  
 XX elucidating the malignant phenotype, in generating and characterizing  
 XX domain specific antibodies, for identifying agents or cellular factors  
 XX that bind to 158PIH4 or its particular domain, and for generating  
 XX cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 XX and prognostic assays, in treating patients with cancer, in accelerating  
 XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 XX and as immunization reagents for detecting 158PIH4-expressing cells.  
 XX The antibodies are particularly useful in bladder cancer diagnostic and  
 XX prognostic assays, and immunization methodologies. The 158PIH4 gene has been  
 XX located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
 XX the present invention has been located to chromosome 8q23. ABI50400 to  
 XX ABI50429 and AB94468 to AB94468 represent sequences used in the  
 XX exemplification of the present invention.  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 36.4%, Score 41, DP 23, Length 9;  
 XX Best Local Similarity 100.0%, Prod. No. 9, 5e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 07 7 KSKK 16  
 XX 111  
 XX 10 4 KSKK 4  
 XX 111  
 XX  
 XX RESULT 45  
 XX AB944867  
 XX 10 AB944867 Standard, Peptide: 9 AA.  
 XX AC AB944867;  
 XX  
 XX 11 17 JUN 2002 (first entry)  
 XX  
 XX 10 C110 epitope HLA peptide SEQ ID NO. 27.

XX C1L epitope HLA peptide SEQ ID NO:436  
 XX  
 XX  
 KW Human 158PIH4: chromosome 8q22-q24, 158PIH4: the mRNA for b22-q24 region  
 KW Bladder cancer, immune response: cytotoxic T lymphocyte, CTL, HLA  
 KW Human leukocyte antigen: helper T lymphocyte, HTL  
 XX  
 CS Homo sapiens,  
 CS Synthetic,  
 XX W020021559P A2,  
 XX 28 FEB-2002,  
 XX  
 XX 22 AUG-2001: 2001WO-0526411,  
 XX  
 XX 22 AUG-2001: 2000US-227099P,  
 XX 10 APR-2001: 2001US-282749P,  
 XX  
 XX (AGEN-) AGENSYS INC,  
 XX  
 XX Charlotte End PM, Haber, RS, Kaitano AB, Afar DEH, Levin E,  
 XX Paris M, Ge W, Jakobovits A,  
 XX WPI: 2002-264937/31,  
 XX  
 XX Monitoring 158PIH4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer,  
 XX comprises identifying presence of aberrant 158PIH4 gene products in  
 XX biological sample  
 XX  
 XX Claim 64: Page 156: 239pp: English.  
 XX  
 XX The present invention describes a method for monitoring 158PIH4 gene  
 XX products in a biological sample from a patient who has or is suspected  
 XX of having cancer. The method comprises determining the status of 158PIH4  
 XX gene products in a tissue sample from an individual, comparing the  
 XX status to the status of 158PIH4 gene products in a normal sample, and  
 XX identifying the presence of aberrant 158PIH4 gene products in the sample.  
 XX 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 XX product and 158PIH4 polynucleotides may be used in monitoring genetic  
 XX abnormalities. The 158PIH4 proteins may be used in assessing the status  
 XX of 158PIH4 gene products in normal versus cancerous tissues and so  
 XX characterizing the malignant phenotype, in generating and characterizing  
 XX domain specific antibodies, for identifying agents or cellular factors  
 XX that bind to 158PIH4 or its particular domain, and for generating  
 XX cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 XX and prognostic assays. In treating patients with cancer, in generating  
 XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 XX and as immunological reagents for detecting 158PIH4-expressing cells.  
 XX The antibodies are particularly useful in bladder cancer diagnostic and  
 XX prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
 XX located to chromosome 8q22-q24, and the 158PIH4 gene also described in  
 XX AB530429 and AB894468 to ABBAS188 represent sequences used in the  
 XX exemplification of the present invention.  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 36.4%; Score 4; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 7 RRSK 10  
 XX IIII  
 XX DL 3 RRSK 6  
 XX  
 XX RESULT 47  
 XX ABB5439P  
 XX ID ABB5439P Standard: Peptide: 9 AA.  
 XX ABB4499P  
 XX ID ABB4499P

XX 17 JUN-2002 (first entry)  
 XX  
 XX C1L epitope HLA peptide SEQ ID NO:527,  
 XX  
 XX Human 158PIH4: chromosome 8q22-q24, 158PIH4: chromosome 8q23, cancer;  
 KW Bladder cancer, immune response: cytotoxic T lymphocyte, CTL, HLA,  
 KW Human leukocyte antigen: helper T lymphocyte, HTL,  
 XX  
 CS Homo sapiens,  
 CS Synthetic,  
 XX W020021559P A2,  
 XX 28 FEB-2002,  
 XX  
 XX 22 AUG-2001: 2001WO-0526411,  
 XX  
 XX 22 AUG-2001: 2000US-227099P,  
 XX 10 APR-2001: 2001US-282749P,  
 XX  
 XX (AGEN-) AGENSYS INC,  
 XX  
 XX Charlotte End PM, Haber, RS, Kaitano AB, Afar DEH, Levin E,  
 XX Paris M, Ge W, Jakobovits A,  
 XX WPI: 2002-264937/31,  
 XX  
 XX Monitoring 158PIH4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer,  
 XX comprises identifying presence of aberrant 158PIH4 gene products in  
 XX biological sample  
 XX  
 XX Claim 64: Page 159: 239pp: English.  
 XX  
 XX The present invention describes a method for monitoring 158PIH4 gene  
 XX products in a biological sample from a patient who has or is suspected  
 XX of having cancer. The method comprises determining the status of 158PIH4  
 XX gene products in a tissue sample from an individual, comparing the  
 XX status to the status of 158PIH4 gene products in a normal sample, and  
 XX identifying the presence of aberrant 158PIH4 gene products in the sample.  
 XX 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 XX product and 158PIH4 polynucleotides may be used in monitoring genetic  
 XX abnormalities. The 158PIH4 proteins may be used in assessing the status  
 XX of 158PIH4 gene products in normal versus cancerous tissues and so  
 XX characterizing the malignant phenotype, in generating and characterizing  
 XX domain specific antibodies, for identifying agents or cellular factors  
 XX that bind to 158PIH4 or its particular domain, and for generating  
 XX cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 XX and prognostic assays. In treating patients with cancer, in generating  
 XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 XX and as immunological reagents for detecting 158PIH4-expressing cells.  
 XX The antibodies are particularly useful in bladder cancer diagnostic and  
 XX prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
 XX located to chromosome 8q22-q24, and the 158PIH4 gene also described in  
 XX AB530429 and AB894468 to ABBAS188 represent sequences used in the  
 XX exemplification of the present invention.  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 36.4%; Score 4; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 7 RRSK 10  
 XX IIII  
 XX DL 3 RRSK 6  
 XX  
 XX RESULT 47  
 XX ABB5439P  
 XX ID ABB5439P Standard: Peptide: 9 AA.



```

KW human leukocyte antigen.
XX
GS Homo sapiens.
XX
PN W020028921-A2.
XX
EC 24-007-2002.
XX
XX
PF 10-APR-2001: 2002WO-US11654.
XX
PF 10-APR-2001: 2001US-282739P.
XX
PF 10-APR-2001: 2001US-283112P.
XX
PF 25-APR-2001: 2001US-286630P.
XX
PA (AGEN ) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX WP1: 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients.
XX
XX Claim 13; Page 272; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and AB278169-AB278186). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX the genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match: 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QF 4 ITER 7
XX Db 1-11
XX 2 ITER 5
XX
XX Search completed: September 30, 2003, 10:25:13
XX Job time : 48.1667 secs

```

---

```

KW human leukocyte antigen.
XX
GS Homo sapiens.
XX
PN W020028921-A2.
XX
EC 24-007-2002.
XX
XX
PF 10-APR-2002: 2002WO-US11654.
XX
PF 10-APR-2001: 2001US-282739P.
XX
PF 10-APR-2001: 2001US-283112P.
XX
PF 25-APR-2001: 2001US-286630P.
XX
PA (AGEN ) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX WP1: 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients.
XX
XX Claim 13; Page 272; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and AB278169-AB278186). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX the genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match: 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QF 4 ITER 7
XX Db 1-11
XX 6 ITER 7
XX
XX REFSeq: Q.
XX AB278120.
XX ID AB278120.9 standard; Peptide: 9 AA
XX
XX AS278120.9.
XX
XX 19-FAY 2003 (first entry)
XX
XX Human cancer related protein 1799037 HLA peptide #243.
XX
XX Human cytotoxic T-lymphocyte antigen 1799037 HLA peptide #243.
XX
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX W020028921-A2.
XX
XX 24 OCT-2002.
XX
XX 10-APR-2002: 2002WO-US11654.
XX
XX

```











A: Accession: M4145  
A: Molecule type: Protein  
A: Residue: 1-113 MP  
A: Note: this protein is phosphorylated during stationary phase but not during export  
C: Keywords: phosphoprotein

Query Match: 27.4% Score 3: DH 2: Length 11;  
C: keywords: phosphoprotein

```

QY      3 KIR 5
      . |
L3      5 KIR 7

RESULT 6
G61497
seed protein w5-zv  winged bean (fradment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: G61497
R:Hitano, H.

```

A: Accession: *U000000000*  
A: Molecule type: protein  
A: Residues: 1-11 58-6  
C: Keywords: glycoprotein; seed

```

Query Match: 27.00; Score 3; DB 2; Length 11;
Best Local Similarity 100.00; Pred. NO. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7  
 P00034  
 dextrantransferase (EC 2.4.1.5) - Streptococcus bovis (fragment)  
 C:Species: Streptococcus bovis  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Sep-1996  
 C:Accession: P00034  
 R:Gaziano, Y., Tsumori, H., Mukasa, H.  
 submitted to JIPID, October 1993  
 A:Description: Purification and properties of glucosyltransferase synthesizing 1,6-  
 A:Reference number: P00034

Query Match 27.1% Score 3 DB 2 Length 11  
 C keywords: glycosyltransferase; hexosyltransferase

[illegible]









```

R.Yamada, M., Wasserman, R., Reichard, B.A., Shane, S., Caton, A.J., Kovera, G.
J. Exp. Med. 173: 455-467, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity
A:Reference number: P13222; MUID:91108337; PMID:1899102
A:Accession: P13134
A:Molecule type: DNA
A:Residues: 1-8 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: leletofototatmer; immunoglobulin

Query Match: 18.2% Score 2: DB 2: Length 8;
Best Local Similarity: 100.0%; Pval. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
DB 2 AR 3

RESULT 34
B45800
setum albumin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 31-Dec-1993
C:Accession: B45800
R.Carraway, K.E., Cochran, D.B., Boucher, W., Mitra, S.P.
J. Immunol. 143: 1680-1684, 1989
A>Title: Structures of histamine releasing peptides formed by the action of acid pro
A:Reference number: A45800; MUID:89343436; PMID:2474609
A:Accession: B45800
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <CAR>

Query Match: 18.2% Score 2: DB 2: Length 8;
Best Local Similarity: 100.0%; Pval. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
DB 2 AR 3

RESULT 35
P1618
14 H chain V-D-J region (clone B-less 3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: P1618
R.Iverson, D.A., Campos Torres, J., Leder, P.
J. Exp. Med. 178: 317-329, 1993
A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less
A:Reference number: P1618; MUID:93301609; PMID:8315387
A:Accession: P1618
A:Molecule type: DNA
A:Residues: 1-8 <LEV>
A:Experimental source: bone marrow pro-B lymphocyte
C:Keywords: immunoglobulin

Query Match: 18.2% Score 2: DB 2: Length 8;
Best Local Similarity: 100.0%; Pval. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
DB 2 AR 3

RESULT 36
A54824
Olfactory receptor 17 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

```

C:Accession: A54823  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 02-Aug-1996 #text\_change 17-Mar-1999  
 C:Accession: A54823  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A:Reference number: A54823; MIM:9437818; PMID:8087849  
 A:Accession: A54823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <ORF>  
 A:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

RESULT 40  
 S69145  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1998 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: S69145  
 A:Title: cDNA cloning and characterization of the rat troponin I slow gene confor tissue- and de  
 A:Reference number: S69145; MIM:94619373; PMID:8413291  
 A:Accession: S69145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ORF>  
 A:Cross references: GB:S69145; NID:q432603  
 A:Keywords: Troponin

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

RESULT 41  
 S69145  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1998 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: S69145  
 A:Title: cDNA cloning and characterization of the rat troponin I slow gene confor tissue- and de  
 A:Reference number: S69145; MIM:94619373; PMID:8413291  
 A:Accession: S69145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ORF>  
 A:Cross references: GB:S69145; NID:q432603  
 A:Keywords: Troponin

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

RESULT 42  
 S69145  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1998 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: S69145  
 A:Title: cDNA cloning and characterization of the rat troponin I slow gene confor tissue- and de  
 A:Reference number: S69145; MIM:94619373; PMID:8413291  
 A:Accession: S69145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ORF>  
 A:Cross references: GB:S69145; NID:q432603  
 A:Keywords: Troponin

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

C:Accession: A54823  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 02-Aug-1996 #text\_change 17-Mar-1999  
 C:Accession: A54823  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A:Reference number: A54823; MIM:9437818; PMID:8087849  
 A:Accession: A54823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <ORF>  
 A:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

RESULT 43  
 S69145  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1998 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: S69145  
 A:Title: cDNA cloning and characterization of the rat troponin I slow gene confor tissue- and de  
 A:Reference number: S69145; MIM:94619373; PMID:8413291  
 A:Accession: S69145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ORF>  
 A:Cross references: GB:S69145; NID:q432603  
 A:Keywords: Troponin

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

RESULT 44  
 S69145  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1998 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: S69145  
 A:Title: cDNA cloning and characterization of the rat troponin I slow gene confor tissue- and de  
 A:Reference number: S69145; MIM:94619373; PMID:8413291  
 A:Accession: S69145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ORF>  
 A:Cross references: GB:S69145; NID:q432603  
 A:Keywords: Troponin

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4

RESULT 45  
 S69145  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1998 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: S69145  
 A:Title: cDNA cloning and characterization of the rat troponin I slow gene confor tissue- and de  
 A:Reference number: S69145; MIM:94619373; PMID:8413291  
 A:Accession: S69145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ORF>  
 A:Cross references: GB:S69145; NID:q432603  
 A:Keywords: Troponin

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 II  
 DB 2 ER 4



```

RESULTS 42
S45631
Protein: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: S45631
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: S45648; M010:943327; P01:233992
A:Accession: S45631
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 43
A4346
Title: Na+-Transporting ATPase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A4346
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A4346; M010:943327; P01:233992
A:Accession: A4346
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 44
A4446
Title: Na+-Transporting ATPase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A4446
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A4446; M010:943327; P01:233992
A:Accession: A4446
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 45
A45631
Title: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A45631
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A45631; M010:943327; P01:233992
A:Accession: A45631
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

```

```

RESULTS 46
A4646
Title: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A4646
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A4646; M010:943327; P01:233992
A:Accession: A4646
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 47
A4746
Title: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A4746
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A4746; M010:943327; P01:233992
A:Accession: A4746
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 48
A4846
Title: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A4846
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A4846; M010:943327; P01:233992
A:Accession: A4846
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 49
A4946
Title: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A4946
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A4946; M010:943327; P01:233992
A:Accession: A4946
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

RESULTS 50
A5046
Title: Na+-Transporting ATP synthase (B2-36.1.1) - Accession: UniProt: (fragment)
Species: Acetabacterium woodii
Citation: 19-Mar-1997 #sequence_revision 02-Jun-1997 #text_change 02-May-1999
Accession: A5046
Ref: J. Biochem. 223: 275-283, 1994
A:Title: Purification of ATP synthase from Acetabacterium woodii and identification as a
A:Reference number: A5046; M010:943327; P01:233992
A:Accession: A5046
A:Molecule type: protein
A:Residues: 18-563
A:Keywords: hydrolase

Query Match: 18-28; Score 2; DB 2; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2 Be+05;
Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SR 10
ID 5 SR 6

```



GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: September 30, 2003, 10:07:41 Search time 6.25 Seconds  
(without alignment)  
82 717 Million cell updates/sec

Title: US-09-787-443-14

Perfect score: 11

Sequence: 1 ARKIRKRSKU 11

Scoring table: GIG9  
Gapop 60.0, Gapext 60.0

Searches: 127#63 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 737

Minimum hit seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	length	DB ID	Description
1	3	27.3	9	1	BLAK_MOUSE
2	4	27.3	11	1	TKN_ELM
3	3	27.3	11	1	UXBZ_YEAS
4	4	27.3	14	1	RYCA_MELCP
5	2	18.2	8	1	ACT_CARRA
6	2	18.2	8	1	ACT_CARRA
7	2	18.2	8	1	ACT_CARRA
8	2	18.2	8	1	NS3_MYCII
9	2	18.2	8	1	NS3_MYCII
10	2	18.2	8	1	NS3_MYCII
11	2	18.2	8	1	NS3_MYCII
12	2	18.2	9	1	HPUL_KLEAF
13	2	18.2	9	1	HPUL_KLEAF
14	2	18.2	9	1	HPUL_KLEAF
15	2	18.2	9	1	NEF_HV128
16	2	18.2	9	1	NEF_HV128
17	2	18.2	9	1	SAMP_MOUSE
18	2	18.2	9	1	THYF_PIG
19	2	18.2	10	1	CATB_SHRE
20	2	18.2	10	1	COXM_RAT
21	2	18.2	10	1	COXM_RAT
22	2	18.2	10	1	COXM_RAT
23	2	18.2	10	1	COXM_RAT
24	2	18.2	10	1	COXM_RAT
25	2	18.2	10	1	COXM_RAT
26	2	18.2	10	1	COXM_RAT
27	2	18.2	10	1	COXM_RAT
28	2	18.2	10	1	COXM_RAT
29	2	18.2	10	1	COXM_RAT
30	2	18.2	10	1	COXM_RAT
31	2	18.2	10	1	COXM_RAT
32	2	18.2	10	1	COXM_RAT
33	2	18.2	10	1	COXM_RAT

34	2	18.2	10	1	XYNB_DICB4
35	2	18.2	11	1	BRK_MEGFL
36	2	18.2	11	1	F51_RAI
37	2	18.2	11	1	MORN_HUMAN
38	2	18.2	11	1	O20A_COMTE
39	2	18.2	11	1	RR2_CONAM
40	2	18.2	11	1	RS30_ONCMY
41	2	18.2	11	1	TKN2_GPERO
42	2	18.2	11	1	TKNA_RANR1
43	2	18.2	11	1	TKND_RANCA
44	2	18.2	12	1	PAR2_PENMG
45	2	18.2	12	1	H2AX_ONCMY
46	2	18.2	12	1	H2AX_ONCMY
47	2	18.2	12	1	H2AX_ONCMY
48	2	18.2	12	1	NO40_LDTJA
49	2	18.2	12	1	NO40_SESRG
50	2	18.2	12	1	RR16_GINBI
51	2	18.2	12	1	RS19_GLYEP
52	2	18.2	12	1	RS19_ELYEP
53	2	18.2	12	1	RS19_TORBP
54	2	18.2	12	1	TKN_KASSE
55	2	18.2	12	1	V14K_WSSV
56	2	18.2	12	1	VZPY_ECOLI
57	2	18.2	13	1	BRK_PAPID
58	2	18.2	13	1	CH60_CANFA
59	2	18.2	13	1	CR81_VESCR
60	2	18.2	13	1	EP65_HUMAN
61	2	18.2	13	1	FIBB_HYLLA
62	2	18.2	13	1	FIBB_RAH11
63	2	18.2	13	1	LMAL_LOCM1
64	2	18.2	13	1	LPAA_PORGI
65	2	18.2	13	1	NEUT_BUFMA
66	2	18.2	13	1	NEUT_GAVPO
67	2	18.2	13	1	NEUT_CHICK
68	2	18.2	13	1	NEUT_RANTE
69	2	18.2	13	1	NEUT_TRIVU
70	2	18.2	13	1	NG40_PEA
71	2	18.2	13	1	NO40_VICSA
72	2	18.2	13	1	PSA2_PEA
73	2	18.2	13	1	SA2A_ONCMY
74	2	18.2	13	1	SA2B_ONCMY
75	2	18.2	13	1	TEML_RANTE
76	2	18.2	13	1	UN02_PINPS
77	2	18.2	13	1	CAL1_GALGI
78	2	18.2	14	1	CAT2_FASHE
79	2	18.2	14	1	EF10_CANFA
80	2	18.2	14	1	HY14_PIG
81	2	18.2	14	1	IF26_RAT
82	2	18.2	14	1	JAP1_RANJA
83	2	18.2	14	1	LPW_RHIME
84	2	18.2	14	1	MAST_VESBA
85	2	18.2	14	1	MY14_EISFO
86	2	18.2	14	1	RS19_PWBAP
87	2	18.2	14	1	RS19_PWBAP
88	2	18.2	14	1	SMS1_MYOSC
89	2	18.2	14	1	SMS1_MYOSC
90	2	18.2	14	1	TKN1_SCHCK
91	2	18.2	15	1	ACEA_AICLA
92	2	18.2	15	1	AF11_MALPA
93	2	18.2	15	1	AF13_MALPA
94	2	18.2	15	1	AH2_PRUSE
95	2	18.2	15	1	C10A_RAT
96	2	18.2	15	1	CKX_WHEAT
97	2	18.2	15	1	DCMM_PSECH
98	2	18.2	15	1	F1B8_ANAPL
99	2	18.2	15	1	F1B8_ALBJU
100	2	18.2	15	1	MCRA_METTE
101	2	18.2	15	1	MM01_RAT
102	2	18.2	15	1	ND03_SOLTU
103	2	18.2	15	1	ND08_SOLTU
104	2	18.2	15	1	ONC1_ONCMY
105	2	18.2	15	1	PGKH_PHYPA
106	2	18.2	15	1	RS20_BACST

P80717	dictyodolom
P12797	megascolia
P56571	rattus norv
P01163	homo sapien
P80464	comamonas t
P42341	conopholis
P83328	oncorhynch
P08616	uperoleia r
P29207	rana ridibu
P22691	rana catesb
P83322	perdeus mon
P83327	oncorhynch
Q10384	megathura c
Q22426	lotus japon
Q24369	sesbania ro
Q46207	ginkgo bilb
Q46490	clover yell
Q47881	elm yellow
Q56251	tomato big
P08611	kassina sen
P82006	white spot
P17776	escherichia
P42717	parapolybia
P49818	canis famli
P01518	vespa crabr
P54363	homo sapien
P14472	hylobates l
P14478	oryctolagus
P38496	locusta mig
P81411	porphyromon
P81796	bufo marinu
P32560	cavia porce
P13724	gallus gall
P41536	rana tempor
P31745	trichosurus
P55959	pisum sativ
P55961	vicia sativ
P17229	pisum sativ
P82238	oncorhynch
P82239	oncorhynch
P57104	rana tempor
P61667	pinus pinas
P20738	calotropis
P80342	fasciola he
P54835	canis famli
P01155	sus scrofa
P81795	rattus norv
P83305	rana japoni
P18854	rhizobium m
P21654	vespa basai
P46979	ciscenia foe
Q52093	pigeon pea
Q4160	prunus arme
P20750	myoxocephal
P31895	alligator m
P82470	schistocerc
P28467	acinetobact
P83141	malva parvi
P83137	malva parvi
P29260	prunus sero
P31730	rattus norv
P58763	trilicium ae
P19917	pseudomonas
P12801	anas platyr
P24937	albizzia ju
P22948	methanosarc
P81563	rattus norv
P80263	solanum tub
P80731	solanum tub
P83287	oncorhynch
P80659	physcomitre
Q95520	streptomyce
P59681	bacillus st

107	2	18.2	15	1	RS6_BA7ST	P59642	Bact. taur. s	180	1	9.1	9	1	BUK_CLOPA	P81337	clostridium
108	2	18.2	15	1	R032_BOVIN	P82927	Bos taurus	181	1	9.1	9	1	CCAP_CARMA	P38556	carcinus ma
109	2	18.2	13	1	ST01_RAT	P02158	Rattus norv	182	1	9.1	9	1	CONO_CONGE	P05486	conus geogr
110	2	18.2	15	1	TERM_HPM2	P29847	Escherichia	183	1	9.1	9	1	CONO_CONST	P05487	conus stri
111	2	18.2	15	1	UC16_MALZE	P80544	zea mays (m	184	1	9.1	9	1	COM_CONVE	P83047	conus ventr
112	2	18.2	15	1	UC27_MALZE	P80644	zea mays (m	185	1	9.1	9	1	COXE_THUOB	P80975	thunus obe
113	2	18.2	15	1	WAKA_KETIM	P80937	zea mays (m	186	1	9.1	9	1	DL_NEPNO	P24816	nepturus obo
114	2	18.2	15	1	YAA3_KOPPA	P82036	Chondrostoma	187	1	9.1	9	1	DNF1_LOCK1	P16339	locusta mig
115	1	9.1	8	1	AC11_HIBAL	P18641	Chondrostoma	188	1	9.1	9	1	DSIP_RAHIT	P01158	oryzotolagus
116	1	9.1	8	1	AKB2_ORYAL	P14064	gryllus tim	189	1	9.1	9	1	FAK1_CALVO	P41856	calliphora
117	1	9.1	8	1	AKB2_ORYAL	P25414	Leptothorax	190	1	9.1	9	1	FAK2_CALVO	P41857	calliphora
118	1	9.1	8	1	AKB2_ORYAL	P25414	Leptothorax	191	1	9.1	9	1	FAK2_PANRE	P41873	panagrellus
119	1	9.1	8	1	AKB2_ORYAL	P14595	Tabanus at	192	1	9.1	9	1	FAK3_CALVO	P41858	calliphora
120	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	193	1	9.1	9	1	FAK3_MACRS	P83276	macrobrachi
121	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	194	1	9.1	9	1	FAK3_PENMO	P83318	penaeus mon
122	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	195	1	9.1	9	1	FAK4_CALVO	P41859	calliphora
123	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	196	1	9.1	9	1	FAK4_PENMO	P83319	penaeus mon
124	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	197	1	9.1	9	1	FAK5_ASCSU	P43170	ascaris suu
125	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	198	1	9.1	9	1	FAK5_CALVO	P41860	calliphora
126	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	199	1	9.1	9	1	FAK5_PANRE	P82661	panagrellus
127	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	200	1	9.1	9	1	FAK5_PENMO	P83320	penaeus mon
128	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	201	1	9.1	9	1	FAK6_CALVO	P41861	calliphora
129	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	202	1	9.1	9	1	FAK6_MACRS	P83279	macrobrachi
130	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	203	1	9.1	9	1	FAK6_CALVO	P41862	calliphora
131	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	204	1	9.1	9	1	FAK9_MACRS	P83281	macrobrachi
132	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	205	1	9.1	9	1	FAK9_ASCSU	P43172	ascaris suu
133	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	206	1	9.1	9	1	FAK9_PANRE	P41865	calliphora
134	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	207	1	9.1	9	1	FAK9_CALVO	P41868	calliphora
135	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	208	1	9.1	9	1	FAK9_CALVO	P38495	calinectes
136	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	209	1	9.1	9	1	FAK9_CALVO	P19346	erythrocebu
137	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	210	1	9.1	9	1	FAK9_CALVO	P19345	macaca fusc
138	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	211	1	9.1	9	1	FAK9_CALVO	P19344	papio anubi
139	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	212	1	9.1	9	1	FAK9_CALVO	P19343	papio kamad
140	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	213	1	9.1	9	1	FAK9_CALVO	P19342	therophilhec
141	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	214	1	9.1	9	1	FAK9_CALVO	P80159	treponema h
142	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	215	1	9.1	9	1	FAK9_CALVO	P83350	sarcophaga
143	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	216	1	9.1	9	1	FAK9_CALVO	P82992	rhodopseuo
144	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	217	1	9.1	9	1	FAK9_CALVO	P42993	cyprinus ca
145	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	218	1	9.1	9	1	FAK9_CALVO	P83058	bombina var
146	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	219	1	9.1	9	1	FAK9_CALVO	P08945	litoria aur
147	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	220	1	9.1	9	1	FAK9_CALVO	P08946	phylomedus
148	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	221	1	9.1	9	1	FAK9_CALVO	P31799	locusta mig
149	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	222	1	9.1	9	1	FAK9_CALVO	P41489	locusta mig
150	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	223	1	9.1	9	1	FAK9_CALVO	P29177	bos taurus
151	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	224	1	9.1	9	1	FAK9_CALVO	P19853	clypeaster
152	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	225	1	9.1	9	1	FAK9_CALVO	P19852	clypeaster
153	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	226	1	9.1	9	1	FAK9_CALVO	P34466	cavia porce
154	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	227	1	9.1	9	1	FAK9_CALVO	P41492	sarcophaga
155	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	228	1	9.1	9	1	FAK9_CALVO	P42995	bulo requia
156	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	229	1	9.1	9	1	FAK9_CALVO	P23879	cyprinus ca
157	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	230	1	9.1	9	1	FAK9_CALVO	P42998	eisenia foe
158	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	231	1	9.1	9	1	FAK9_CALVO	P80027	octopus vul
159	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	232	1	9.1	9	1	FAK9_CALVO	P42994	raja clavet
160	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	233	1	9.1	9	1	FAK9_CALVO	P81179	diaprepes a
161	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	234	1	9.1	9	1	FAK9_CALVO	P83380	lycopersico
162	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	235	1	9.1	9	1	FAK9_CALVO	P82691	periplaneta
163	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	236	1	9.1	9	1	FAK9_CALVO	P82003	bombyx mori
164	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	237	1	9.1	9	1	FAK9_CALVO	P82075	litoria rub
165	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	238	1	9.1	9	1	FAK9_CALVO	O68936	serratia ma
166	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	239	1	9.1	9	1	FAK9_CALVO	P82926	bos taurus
167	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	240	1	9.1	9	1	FAK9_CALVO	P24047	stomopneute
168	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	241	1	9.1	9	1	FAK9_CALVO	P17440	pichia jadi
169	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	242	1	9.1	9	1	FAK9_CALVO	P17441	pichia jadi
170	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	243	1	9.1	9	1	FAK9_CALVO	P41517	calliphora
171	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	244	1	9.1	9	1	FAK9_CALVO	P16223	locusta mig
172	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	245	1	9.1	9	1	FAK9_CALVO	P81736	leucophaea
173	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	246	1	9.1	9	1	FAK9_CALVO	P38640	mus musculus
174	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	247	1	9.1	9	1	FAK9_CALVO	P40929	homo sapien
175	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	248	1	9.1	9	1	FAK9_CALVO	P31929	homo sapien
176	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	249	1	9.1	9	1	FAK9_CALVO	P31931	homo sapien
177	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	250	1	9.1	9	1	FAK9_CALVO	P31934	homo sapien
178	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	251	1	9.1	9	1	FAK9_CALVO	P81355	clostridium
179	1	9.1	8	1	ALL2_CARMA	P31814	carcinus ma	252	1	9.1	9	1	FAK9_CALVO	P30089	homo sapien

254	9.1	9.1	1	UPA5_HUMAN	P15922	homo sapien	326	1	9.1	10	1	TKL2_L10CM1	P16224	locusta miq
255	9.1	9.1	9.1	UPA7_HUMAN	P16093	homo sapien	327	1	9.1	10	1	TKL3_L10CM1	P30249	locusta miq
256	9.1	9.1	9.1	XILA_STRSQ	P17149	Streptomyces	328	1	9.1	10	1	TKL4_L10CM1	P30250	locusta miq
257	9.1	9.1	9.1	YMER_AZV1	P25425	azotobacter	329	1	9.1	10	1	TKN1_SYCA	P08608	oncorhynch
258	9.1	9.1	9.1	AEGL_AGRAE	P61465	eurocabe ae	330	1	9.1	10	1	TKNB_ONCMY	P28500	oncorhynch
259	9.1	9.1	9.1	ADXS_PUGSF	P159261	pinus sero	331	1	9.1	10	1	TKNB_RANR1	P29135	rana ridiou
260	9.1	9.1	9.1	AKHX_L10CM	P61426	locusta miq	332	1	9.1	10	1	TKN2_RANR1	P22690	rana ratiab
261	9.1	9.1	9.1	AL19_CANCA	P16422	oncorhynch	333	1	9.1	10	1	TKN3_PUG	P22690	rana ratiab
262	9.1	9.1	9.1	AMEN_BELAN	P17331	belonocystis	334	1	9.1	10	1	TKN4_PUG	P08610	phyllomedusa
263	9.1	9.1	9.1	AN31_BO1A	P20641	boia tauris	335	1	9.1	10	1	TKS1_AEDAE	P42634	aedes aegypti
264	9.1	9.1	9.1	AN32_BOVIN	P01019	bos tauris	336	1	9.1	10	1	TKS2_AEDAE	P42635	aedes aegypti
265	9.1	9.1	9.1	AN33_CHICK	P01019	gallus galli	337	1	9.1	10	1	TKU1_UREUN	P40751	urechis uni
266	9.1	9.1	9.1	AP22_BOLIA	P00473	capra hircus	338	1	9.1	10	1	TKM0_AEDAE	P19425	aedes aegypti
267	9.1	9.1	9.1	BPP_VIPAS	P10422	batrachoseps	339	1	9.1	10	1	TKP5_NICPG	P19118	nicotiana glauca
268	9.1	9.1	9.1	BRK_ONCMY	P01022	batrachoseps	340	1	9.1	10	1	TKP5_NICPG	P19118	nicotiana glauca
269	9.1	9.1	9.1	CA12_LITCI	P01022	batrachoseps	341	1	9.1	10	1	TKP6_LEUMA	P81737	leucophaea
270	9.1	9.1	9.1	CAER_LITCI	P01022	batrachoseps	342	1	9.1	10	1	TKP7_LEUMA	P81738	leucophaea
271	9.1	9.1	9.1	COXA_ONCMY	P01022	batrachoseps	343	1	9.1	10	1	TKP8_LEUMA	P81740	leucophaea
272	9.1	9.1	9.1	COXB_ONCMY	P01022	batrachoseps	344	1	9.1	10	1	TKP9_LEUMA	P81741	leucophaea
273	9.1	9.1	9.1	COXB_ONCMY	P01022	batrachoseps	345	1	9.1	10	1	TKP9_LEUMA	P81741	leucophaea
274	9.1	9.1	9.1	COXB_ONCMY	P01022	batrachoseps	346	1	9.1	10	1	TKP9_LEUMA	P81741	leucophaea
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323	9.1	9.1	9.1	COXB_ONCMY	P01022	batrachoseps	395	1	9.1	10	1	TKP9_LEUMA	P81741	leucophaea
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325	9.1	9.1	9.1	COXB_ONCMY	P01022	batrachoseps	397	1	9.1	10	1	TKP9_LEUMA	P81741	leucophaea



01 21-FEB-1986 (Rel. 01, Created)  
 02 01-FEB-1994 (Rel. 28, Last sequence update)  
 03 15-SEP-2003 (Rel. 42, Last annotation update)  
 04 Elodeaceae  
 05 Elodea nuchata (Musk octopus) (Musk octopus) and  
 06 Elodea nuchata (Musk octopus) (Musk octopus)  
 07 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 08 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 09 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 10 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 11 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 12 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 13 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 14 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 15 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
 16 Elodea nuchata (Mollusca: Cephalopoda: Nautilus)  
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Query Match: 27.3% Score: 57.00 Length: 14  
 Best Local Similarity: 100.0% Pred. No. 1.1e-03  
 Matches: 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

01 9.860 14  
 02 1.1  
 03 5.860 5

## RESULT 4

01 0X82 YEAST  
 02 0X82 YEAST  
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 20 0X82 YEAST  
 21 0X82 YEAST  
 22 0X82 YEAST  
 23 0X82 YEAST  
 24 0X82 YEAST  
 25 0X82 YEAST  
 26 0X82 YEAST  
 27 0X82 YEAST  
 28 0X82 YEAST  
 29 0X82 YEAST  
 30 0X82 YEAST

Query Match: 27.3% Score: 57.00 Length: 14  
 Best Local Similarity: 100.0% Pred. No. 1.1e-03  
 Matches: 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

01 9.860 14  
 02 1.1  
 03 5.860 5

RESULT 4  
 01 0X82 YEAST  
 02 0X82 YEAST  
 03 0X82 YEAST  
 04 0X82 YEAST  
 05 0X82 YEAST  
 06 0X82 YEAST  
 07 0X82 YEAST  
 08 0X82 YEAST  
 09 0X82 YEAST  
 10 0X82 YEAST  
 11 0X82 YEAST  
 12 0X82 YEAST  
 13 0X82 YEAST  
 14 0X82 YEAST  
 15 0X82 YEAST  
 16 0X82 YEAST  
 17 0X82 YEAST  
 18 0X82 YEAST  
 19 0X82 YEAST  
 20 0X82 YEAST  
 21 0X82 YEAST  
 22 0X82 YEAST  
 23 0X82 YEAST  
 24 0X82 YEAST  
 25 0X82 YEAST  
 26 0X82 YEAST  
 27 0X82 YEAST  
 28 0X82 YEAST  
 29 0X82 YEAST  
 30 0X82 YEAST

Query Match: 27.3% Score: 57.00 Length: 14  
 Best Local Similarity: 100.0% Pred. No. 1.1e-03  
 Matches: 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

01 7.860 9  
 02 1.1  
 03 5.860 7

## RESULT 5

01 0X82 YEAST  
 02 0X82 YEAST  
 03 0X82 YEAST  
 04 0X82 YEAST  
 05 0X82 YEAST  
 06 0X82 YEAST  
 07 0X82 YEAST  
 08 0X82 YEAST  
 09 0X82 YEAST  
 10 0X82 YEAST  
 11 0X82 YEAST  
 12 0X82 YEAST  
 13 0X82 YEAST  
 14 0X82 YEAST  
 15 0X82 YEAST  
 16 0X82 YEAST  
 17 0X82 YEAST  
 18 0X82 YEAST  
 19 0X82 YEAST  
 20 0X82 YEAST  
 21 0X82 YEAST  
 22 0X82 YEAST  
 23 0X82 YEAST  
 24 0X82 YEAST  
 25 0X82 YEAST  
 26 0X82 YEAST  
 27 0X82 YEAST  
 28 0X82 YEAST  
 29 0X82 YEAST  
 30 0X82 YEAST

Query Match: 27.3% Score: 57.00 Length: 14  
 Best Local Similarity: 100.0% Pred. No. 1.1e-03  
 Matches: 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

01 7.860 9  
 02 1.1  
 03 5.860 7

RA Gave H., Johnson A.B., Maestre J., East P.D., Thorpe A.J., Winstanley D.,  
 "Leptodoteron peptides of the allatostatin superfamily."  
 Peptides 18:1431-1435 (1997).  
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MODRES 5 R AMIDATION.  
 SQ SEQUENCE 8 AA: 676 MW: 422679;AR0566400 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AR 2  
 DE 1 II  
 1 AR 2  
 RESULT 8  
 NS\_MVTU STANDARD PFI 8 AA.  
 AC PFI152;  
 CC 15-MAY-1999 (Rel. 39, Created)  
 DI 15-MAY-1999 (Rel. 39, Last sequence update)  
 DI 15-OCT-2001 (Rel. 42, Last annotation update)  
 DE 43 kDa non-secretory protein 3 (Fragment).  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 CX NCBI\_TaxID 1774;  
 RN 1;  
 RP SEQUENCE  
 RA STRAIN H-787;  
 RA Gave H., Johnson A.B., Maestre J., East P.D., Thorpe A.J., Winstanley D.,  
 Submitted (DEC 1997) to the SWISS-PROT data bank.  
 CC CAUTION: We are unable to find this protein in the translation of  
 the genome of strain H787.  
 FT NON\_TER 1;  
 FT NON\_TER 8;  
 SQ SEQUENCE 8 AA: 619 MW: 409640H;NC0212 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FR 7  
 DE 6 ER 6  
 RESULT 4  
 RSI\_BRWB STANDARD PFI 8 AA.  
 CC RSI\_BRWB  
 AC PFI156;  
 CC 01-NOV-1994 (Rel. 39, Created)  
 DI 01-NOV-1994 (Rel. 40, Last sequence update)  
 DI 01-NOV-1995 (Rel. 42, Last annotation update)  
 DE 30S ribosomal protein S1 (Fragment).  
 OS ERWINIA chrysanthemi.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Proteobacterium.  
 CX NCBI\_TaxID 556;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA STRAIN 39x7;  
 RA Douville A., Daissac A., Farnet M.,  
 Submitted (AUG 1994) to the EMBL/GenBank/DBJ databases.  
 CC 1- FUNCTION: BINDS MRNA, THUS FACILITATING RECOGNITION OF THE  
 SHINE DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).  
 CC 1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.  
 CC

RA Gave H., Johnson A.B., Maestre J., East P.D., Thorpe A.J., Winstanley D.,  
 "Leptodoteron peptides of the allatostatin superfamily."  
 Peptides 18:1431-1435 (1997).  
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MODRES 5 R AMIDATION.  
 SQ SEQUENCE 8 AA: 676 MW: 422679;AR0566400 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AR 2  
 DE 1 II  
 1 AR 2  
 RESULT 8  
 NS\_MVTU STANDARD PFI 8 AA.  
 AC PFI152;  
 CC 15-MAY-1999 (Rel. 39, Created)  
 DI 15-MAY-1999 (Rel. 39, Last sequence update)  
 DI 15-OCT-2001 (Rel. 42, Last annotation update)  
 DE 43 kDa non-secretory protein 3 (Fragment).  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 CX NCBI\_TaxID 1774;  
 RN 1;  
 RP SEQUENCE  
 RA STRAIN H-787;  
 RA Gave H., Johnson A.B., Maestre J., East P.D., Thorpe A.J., Winstanley D.,  
 Submitted (DEC 1997) to the SWISS-PROT data bank.  
 CC CAUTION: We are unable to find this protein in the translation of  
 the genome of strain H787.  
 FT NON\_TER 1;  
 FT NON\_TER 8;  
 SQ SEQUENCE 8 AA: 619 MW: 409640H;NC0212 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FR 7  
 DE 6 ER 6  
 RESULT 4  
 RSI\_BRWB STANDARD PFI 8 AA.  
 CC RSI\_BRWB  
 AC PFI156;  
 CC 01-NOV-1994 (Rel. 39, Created)  
 DI 01-NOV-1994 (Rel. 40, Last sequence update)  
 DI 01-NOV-1995 (Rel. 42, Last annotation update)  
 DE 30S ribosomal protein S1 (Fragment).  
 OS ERWINIA chrysanthemi.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Proteobacterium.  
 CX NCBI\_TaxID 556;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA STRAIN 39x7;  
 RA Douville A., Daissac A., Farnet M.,  
 Submitted (AUG 1994) to the EMBL/GenBank/DBJ databases.  
 CC 1- FUNCTION: BINDS MRNA, THUS FACILITATING RECOGNITION OF THE  
 SHINE DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).  
 CC 1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.  
 CC



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DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT0001.S7;  
 FT NCBL TaxID 10116;  
 SQ SEQUENCE 8 AA: 517 MW: 91837.626; pI 4.97; Length 8;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KS 9  
 DB 3 KS 4  
 RESULT 10  
 ID R57\_M01T STANDARD: PRT: 8 AA  
 AC P35664  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DI 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN RPS8  
 OS Mycobacterium intracellulare  
 CC Bacteria; Actinobacteria; Actinomycetia; Actinomycetales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium  
 CC NCBL TaxID 1767;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 9119730; PubMed: 8451173;  
 RA Nair J., House D.A., Morris S.G.  
 RE "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RE Mycobacterium intracellulare."  
 RL Nucleic Acids Res. 21:1039-1049(1993)  
 FC 1- FUNCTION: one of the primary rRNA binding proteins; it binds  
 CC directly to 16S rRNA where it is located as part of the head  
 CC domain of the 30S subunit; it is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC tRNA (by similarity).  
 CC 1- SUBUNIT: part of the 30S ribosomal subunit; contacts proteins S2  
 CC and S1 (by similarity).  
 CC 1- SIMILARITY: BELONGS TO THE 27S LAMP FAMILY OF LAMPS.

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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: F0871; AAA25376.1;  
 DR DDB: S05598; S05598;  
 DR HANAP: RF\_00480; 1;  
 DR IPIR000235; Ribosomal\_S7;  
 DR PROSITE: PS00052; RIBOSOMAL\_S7; PAR:AL;  
 KW Ribosomal protein; RNA-binding; tRNA binding;  
 FT INIT\_MEL 0 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA: 850 MW: 63276.076; pI 4.19; Length 8;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 RESULT 12  
 ID HUTU\_K1EAE STANDARD: PRT: 9 AA  
 AC P12381;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucosylase hydrolase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 DE hydrolase) (Fragment).  
 GN HUTU  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella  
 CC NCBL TaxID 2845;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neukoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;  
 RE "A bidirectional promoter in the hutP region of the histidine  
 RE utilization (hut) operons from Klebsiella aerogenes.";  
 RL J. Bacteriol. 170:2240-2246(1988);  
 RN 12;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 90368611; PubMed: 2203754;  
 RA Schwacha A., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propionate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

QY 2 RK 3  
 DB 2 RK 3  
 RESULT 11  
 ID JHU9\_RAT STANDARD: PRT: 6 AA  
 AC P56575;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DI 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 15-DEC-1998 (Rel. 37, Last annotation update)  
 LE Unknown protein from 20 page of heart tissue (Spot P9) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 CC NCBL TaxID 10116;  
 RN 1;  
 RP SEQUENCE;  
 RA STRAIN-Wistar; TISSUE-Heart;  
 RA Li X.-P., Pleissner K.-P., Scheier C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;

CC Submitted (SEP 1998) to the SWISS-PROT data bank.  
 CC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 6  
 SQ SEQUENCE 8 AA: 1029 MW: 960775.604; pI 4.06; Length 8;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 RESULT 12  
 ID HUTU\_K1EAE STANDARD: PRT: 9 AA  
 AC P12381;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucosylase hydrolase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 DE hydrolase) (Fragment).  
 GN HUTU  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella  
 CC NCBL TaxID 2845;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neukoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;

CC "A bidirectional promoter in the hutP region of the histidine  
 CC utilization (hut) operons from Klebsiella aerogenes.";  
 RL J. Bacteriol. 170:2240-2246(1988);  
 RN 12;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 90368611; PubMed: 2203754;  
 RA Schwacha A., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propionate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

QY 2 RK 3  
 DB 2 RK 3  
 RESULT 11  
 ID JHU9\_RAT STANDARD: PRT: 6 AA  
 AC P56575;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DI 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 15-DEC-1998 (Rel. 37, Last annotation update)  
 LE Unknown protein from 20 page of heart tissue (Spot P9) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 CC NCBL TaxID 10116;  
 RN 1;  
 RP SEQUENCE;  
 RA STRAIN-Wistar; TISSUE-Heart;  
 RA Li X.-P., Pleissner K.-P., Scheier C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;

CC Submitted (SEP 1998) to the SWISS-PROT data bank.  
 CC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 6  
 SQ SEQUENCE 8 AA: 1029 MW: 960775.604; pI 4.06; Length 8;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 RESULT 12  
 ID HUTU\_K1EAE STANDARD: PRT: 9 AA  
 AC P12381;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucosylase hydrolase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 DE hydrolase) (Fragment).  
 GN HUTU  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella  
 CC NCBL TaxID 2845;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neukoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;

CC "A bidirectional promoter in the hutP region of the histidine  
 CC utilization (hut) operons from Klebsiella aerogenes.";  
 RL J. Bacteriol. 170:2240-2246(1988);  
 RN 12;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 90368611; PubMed: 2203754;  
 RA Schwacha A., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propionate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

QY 2 RK 3  
 DB 2 RK 3  
 RESULT 11  
 ID JHU9\_RAT STANDARD: PRT: 6 AA  
 AC P56575;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DI 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 15-DEC-1998 (Rel. 37, Last annotation update)  
 LE Unknown protein from 20 page of heart tissue (Spot P9) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 CC NCBL TaxID 10116;  
 RN 1;  
 RP SEQUENCE;  
 RA STRAIN-Wistar; TISSUE-Heart;  
 RA Li X.-P., Pleissner K.-P., Scheier C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;

CC Submitted (SEP 1998) to the SWISS-PROT data bank.  
 CC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 6  
 SQ SEQUENCE 8 AA: 1029 MW: 960775.604; pI 4.06; Length 8;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 RESULT 12  
 ID HUTU\_K1EAE STANDARD: PRT: 9 AA  
 AC P12381;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucosylase hydrolase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 DE hydrolase) (Fragment).  
 GN HUTU  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella  
 CC NCBL TaxID 2845;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neukoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;

CC "A bidirectional promoter in the hutP region of the histidine  
 CC utilization (hut) operons from Klebsiella aerogenes.";  
 RL J. Bacteriol. 170:2240-2246(1988);  
 RN 12;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 90368611; PubMed: 2203754;  
 RA Schwacha A., Bender R.A.;

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 CC J. Bacteriol. 172:5477-5481(1990).  
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 CC yl)propionate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

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DR EMBL: K09553; AAA25078.1;  
 DR EMBL: M58515; AAA2612.1;  
 DR SWAMP: ME00577;  
 DR InterPro: IPR00194; BioCase.  
 DR PROSITE: PS01243; UKCANASE; FAMILY;  
 DR BEST-ALPHABETICISM: LYSASE; NA.  
 FT NUNTER 9  
 SQ SEQUENCE 9 AA: 1140 MW: 97093.456; 55AAs; 7652As

Query Match: 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Prod. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 16  
 DL 4 SK 5

RESULT 14

1 PCA STAMM STANDARD: EPI 9 AA.  
 AC P46884;  
 DI 01-JUN-1994 (Rel. 29, Created)  
 DI 01-JUN-1994 (Rel. 29, Last sequence update)  
 DI 01-JUN-1994 (Rel. 30, Last annotation update)  
 DE Chlorophenicol resistance leader peptide  
 OS Streptococcus aureus, and  
 OS Streptococcus agalactiae  
 AC Plasmid pS56, plasmid pSCS?, Plasmid pB12, and Plasmid pB501.  
 CC Bacterial Firmicutes; Bacillales; Streptococcaceae;  
 CC NCBI TaxID: 1280, 1511;  
 RN SEQUENCE FROM N.A.  
 RP SPECIES: aureus; STRAIN 436; PLASMID: pSCS?  
 RX MEDLINE: 9227652; PubMed: 1929426;  
 RA Schwarz S., Cardoso M.;  
 RT "Nucleotide sequence and phylogeny of a chloramphenicol  
 RT acetyltransferase encoded by the plasmid pS56 from Streptococcus  
 RT aureus";  
 RL Antimicrob. Agents Chemother. 36:101 (1992);  
 RN SEQUENCE FROM N.A.  
 RP SPECIES: aureus; PLASMID: pSCS?  
 RX MEDLINE: 9226047; PubMed: 1511126;  
 RA Cardoso M., Schwarz S.;  
 RT "Nucleotide sequence and structural characterization of a  
 RT chloramphenicol acetyltransferase encoded by the plasmid pSCS from  
 RT Streptococcus aureus";  
 RL J. Appl. Bacteriol. 72:289-293 (1992);  
 RN SEQUENCE FROM N.A.  
 RP SPECIES: aureus; PLASMID: pB12;  
 RX MEDLINE: 8608179; PubMed: 3865736;  
 RA Priekker R., Matzara H.;  
 RT "Regulation of the inducible chloramphenicol acetyltransferase gene  
 RT of the Streptococcus aureus plasmid pB12";  
 RL EMBO J. 4:2295-2300 (1985);  
 RN SEQUENCE FROM N.A.  
 RP SPECIES: aqua-actiae; PLASMID: p-P501;  
 RX MEDLINE: 91098867; PubMed: 1461942;  
 SA Tricer-Gued P., de Cespedes G., Horant L.;  
 RT "Nucleotide sequence of the chloramphenicol resistance determinant of  
 RT the streptococcal plasmid p1P501";  
 RL Plasmid 26:272-276 (1992);

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: M58515; AAA2612.1;  
 DR EMBL: M58516; AAA1528.1;  
 DR EMBL: X62872; CAA2640.1;  
 DR EMBL: X60827; CAA3427.1;  
 DR EMBL: X65452; CAA36454.1;  
 DR PIR: S24362; B24352;  
 DR PIR: S30494; S30494;  
 KW Leader peptide; Antibiotic resistance; Plasmid.  
 SQ SEQUENCE 9 AA: 1074 MW: 50945.555; 5333 As; 3333 As; 3333 As

Query Match: 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Prod. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SK 9  
 DL 3 SK 4

RESULT 14

NEF\_HV128 STANDARD: EPI 9 AA.  
 DI 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DI 25-FEB-2003 (Rel. 41, Last annotation update)  
 DE Negative factor (F-protein) (3' ORF) (Fragment).  
 OS NEF.  
 CC Human immunodeficiency virus type 1 (2.84 isolate) (HIV-1).  
 CC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 CC NCBI TaxID: 11681;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 88281276; PubMed: 3395517;  
 RA Youno J., Josephs S.F., Keltz M.S., Jr., Zagury D., Wong-Staal F.,  
 RA Gallo R.C.;  
 RT "Nucleotide sequence analysis of the env gene of a new Zairian  
 RT isolate of HIV-1";  
 RL AIDS Res. Hum. Retroviruses 4:165-174 (1988).  
 CC FUNCTION: NEF has GTPase, GTP-binding and autophosphorylation  
 CC activities. It seems to down regulate the CD4(T4) antigen.  
 CC MUSCULASPROUS: THE 784 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
 CC ZAIKIAN MALE.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: J03653; AAA44687.1;  
 DR EMBL: J03654; NEFSJVI;  
 KW AIDS; Myristate; GTP-binding  
 FT CLIPD 2 2 MYRISTATE (BY SIMILARITY)  
 FT NUNTER 9  
 SQ SEQUENCE 9 AA: 967 MW: 41908.253; 33878 As; 33878 As; 33878 As

Query Match: 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Prod. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 10



Query Match 18.2% Score 23 DB 13 Length 10;  
 Best Local Similarity 100.0% Prot No. 9 RefSeq;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 25  
 CXXC\_RAB11  
 10 CXXC\_RAB11 STANDARD: PRT 10 AA  
 11 PROCEE  
 12 01-JUL-1994 (Ref. 32, Created)  
 13 01-JUL-1994 (Ref. 32, Last sequence update)  
 14 28-FEB-2003 (Ref. 41, Last annotation update)  
 15 Cytochrome c oxidase polypeptide VIII (liver/heart) (EC 1.9.3.1)  
 16 (Fragment)  
 17 P08888  
 18 CYTOCHROME C OXIDASE (Rat)  
 19 Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 20 Mammalia; Eutheria; Lagomorpha; Leporidae; Cytolagus  
 21 NCPI\_TaxID=9986;  
 22 11  
 23 SEQUENCE  
 24 TISSUE: heart, and liver  
 25 Protein R. Kadenbach, R.  
 26 Submitted (MAR-1994) to the SWISS PROT data bank  
 27 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 28 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 29 MITOCHONDRIAL ELECTRON TRANSPORT  
 30 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 31 c + 2 H(2)O  
 32 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 33 NON TER 10  
 34 SEQUENCE 10 AA: 1177 MW: 87977616 AA ID: P08888

Query Match 18.2% Score 23 DB 13 Length 10;  
 Best Local Similarity 100.0% Prot No. 9 RefSeq;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 25  
 CXXC\_RAB11  
 10 CXXC\_RAB11 STANDARD: PRT 10 AA  
 11 PROCEE  
 12 01-JUL-1994 (Ref. 32, Created)  
 13 01-JUL-1994 (Ref. 32, Last sequence update)  
 14 28-FEB-2003 (Ref. 41, Last annotation update)  
 15 Cytochrome c oxidase polypeptide VIII (liver/heart) (EC 1.9.3.1)  
 16 (Fragment)  
 17 P08888  
 18 CYTOCHROME C OXIDASE (Rat)  
 19 Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 20 Mammalia; Eutheria; Lagomorpha; Leporidae; Cytolagus  
 21 NCPI\_TaxID=9986;  
 22 11  
 23 SEQUENCE  
 24 TISSUE: heart, and liver  
 25 Protein R. Kadenbach, B.  
 26 Submitted (MAR-1994) to the SWISS PROT data bank  
 27 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 28 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 29 MITOCHONDRIAL ELECTRON TRANSPORT  
 30 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 31 c + 2 H(2)O  
 32 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 33 NON TER 10  
 34 SEQUENCE 10 AA: 1210 MW: 87977616 AA ID: P08888

Query Match 18.2% Score 23 DB 13 Length 10;  
 Best Local Similarity 100.0% Prot No. 9 RefSeq;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 25  
 CXXC\_RAB11  
 10 CXXC\_RAB11 STANDARD: PRT 10 AA  
 11 PROCEE  
 12 01-JUL-1994 (Ref. 32, Created)  
 13 01-JUL-1994 (Ref. 32, Last sequence update)  
 14 28-FEB-2003 (Ref. 41, Last annotation update)  
 15 Cytochrome c oxidase polypeptide VIII (liver/heart) (EC 1.9.3.1)  
 16 (Fragment)  
 17 P08888  
 18 CYTOCHROME C OXIDASE (Rat)  
 19 Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 20 Mammalia; Eutheria; Lagomorpha; Leporidae; Cytolagus  
 21 NCPI\_TaxID=9986;  
 22 11  
 23 SEQUENCE  
 24 TISSUE: heart, and liver  
 25 Protein R. Kadenbach, B.  
 26 Submitted (MAR-1994) to the SWISS PROT data bank  
 27 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 28 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 29 MITOCHONDRIAL ELECTRON TRANSPORT  
 30 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 31 c + 2 H(2)O  
 32 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 33 NON TER 10  
 34 SEQUENCE 10 AA: 1210 MW: 87977616 AA ID: P08888

Query Match 18.2% Score 23 DB 13 Length 10;  
 Best Local Similarity 100.0% Prot No. 9 RefSeq;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 25  
 CXXC\_RAB11  
 10 CXXC\_RAB11 STANDARD: PRT 10 AA  
 11 PROCEE  
 12 01-JUL-1994 (Ref. 32, Created)  
 13 01-JUL-1994 (Ref. 32, Last sequence update)  
 14 28-FEB-2003 (Ref. 41, Last annotation update)  
 15 Cytochrome c oxidase polypeptide VIII (liver/heart) (EC 1.9.3.1)  
 16 (Fragment)  
 17 P08888  
 18 CYTOCHROME C OXIDASE (Rat)  
 19 Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 20 Mammalia; Eutheria; Lagomorpha; Leporidae; Cytolagus  
 21 NCPI\_TaxID=9986;  
 22 11  
 23 SEQUENCE  
 24 TISSUE: heart, and liver  
 25 Protein R. Kadenbach, B.  
 26 Submitted (MAR-1994) to the SWISS PROT data bank  
 27 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 28 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 29 MITOCHONDRIAL ELECTRON TRANSPORT  
 30 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 31 c + 2 H(2)O  
 32 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 33 NON TER 10  
 34 SEQUENCE 10 AA: 1210 MW: 87977616 AA ID: P08888

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FT MEN_HER 10 10
SQ SEQUENCE 1 AA: 1027 MW: C42956A49C7633D CR 64:

Query Match:
Best Local Similarity: 100.0%, Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KI 4
DB 7 KI 8

RESULT 24
FIBR_QSER1
ID FIBR_QSER1 STANDARD: PRT: 1 AA
AC F45437
DT 01 JAN 1999 (Rel. 13, Last sequence update)
DI 01 JAN 1999 (Rel. 13, Last sequence update)
DE 24 FEB 2003 (Rel. 41, Last annotation update)
OS Fibrinogen beta chain [Contains: Fibrinogen B, (Fragment)]
GN FGB
OR Crotalaria strom (white rhizomeros) (Square tipped rhizomeros)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostei;
OC Mammalia; Eutheria; Perissodactyla; Solimovellidae; Cervidae; Cervinae;
OX NCBI TaxID 9847;
LN 111
SQ SEQUENCE 10 AA: 1097 MW: 94926203604664 64:

Query Match:
Best Local Similarity: 100.0%, Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KI 2
DB 9 KI 10

RESULT 24
MACH_KLEIN
ID MACH_KLEIN STANDARD: PRT: 10 AA
AC Q05564
DT 01 OCT 1994 (Rel. 30, Created)
DI 01 OCT 1994 (Rel. 30, Last sequence update)
DE 30 MAY 2000 (Rel. 39, Last annotation update)
OS Maltose-binding periplasmic protein (Maltose-binding protein)
GN (MBP) (Fragment)
OR Klebsiella pneumoniae
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella
OX NCBI TaxID 573;
LN 111
SQ SEQUENCE FROM N.A.
RP STRAIN-1033-5914 / KAY2026;
RX MEDLINE 93211295; PubMed 8455775;

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BA Bachelier S., Perrin D., Hofnung M., Grosz E.;
KT "Bacterial interspersed mosaic elements (BIMES) are present in the
AC genome of Klebsiella";
RC Mol. Microbiol. 7:537-544(1993).
CC -1- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEM. BASIS: TOWARD MALTO-OLIGOSACCHARIDES.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE BINDING
CC PROTEIN FAMILY 1.
CC
CC THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION
CC AT THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X68329; CAA48404.1;
DR TrEMBL: IPR006066; SBI_dcm1
DR PROSITE: PS01037; SHP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1159 MW: 8F08DC4415A6DDDA CRC64:

Query Match:
Best Local Similarity: 100.0%, Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KI 11
DB 2 KI 4

RESULT 24
SLAP_RACT3
ID SLAP_RACT3 STANDARD: PRT: 10 AA
AC P43325
DT 01-FEB-1996 (Rel. 34, Created)
DI 01-FEB-1996 (Rel. 33, Last sequence update)
DE 01-FEB-1996 (Rel. 33, Last annotation update)
OS S-layer protein (S-layer layer protein) (Fragment).
CS Bacillus thuringiensis (subsp. galleriae)
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI TaxID: 29330;
LN 111
SQ SEQUENCE
RP STRAIN-NKRL 4047;
RX MEDLINE 900781.1; PubMed-2592447;
OR Lucke et al. 1993;
KT "Characterization of a dynamic S-layer on Bacillus thuringiensis";
RC J. Bacteriol. 173:656-662(1993).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH A-BLIQUE (P2) SYMMETRY.
OR PIR: A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1080 MW: 57AB7ACAB769C7A3 CRC64:

Query Match:
Best Local Similarity: 100.0%, Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KI 4
DB 3 KI 4

RESULT 25
SP34_DJCM0

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ID SP14_P100ME STANDARD; PRI: 10 AA.
AC P14545;
DI 15-JUL-1999 (Rel. 38, Created)
DI 15-JUL-1999 (Rel. 38, Last sequence update)
DI 15-JUL-1999 (Rel. 38, Last annotation update)
DE Surface protein P14 (Fragment).
GN P14.
OS Dictyostelium discoideum (Slime mold).
OX NCBI_FaxID: 41287;
LN 11.
RP SEQUENCE.
RC STRAIN: DM-3.
RA Schreiner, S.J.
RT "Characterization of a surface protein in macrophages of early stadium
  macrophages."
RL Submitted (NCV-1498) to the SWISS PROT data bank.
CC -! FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROPHAGE PRIMARY WALL,
  WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
  REPRODUCTION.
CC -! SUBCELLULAR LOCATION: MACROPHAGE PRIMARY WALL.
KW Cell wall.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1190 MW: 185470/AA1444852 (Rel. 34)

Query Match 18.2% Score 21; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KD 11
LA 10 KD 7

RESULT 26
SP1_HAIPO STANDARD; PRI: 10 AA.
AC Q15997;
DI 01-DEC-1996 (Rel. 34, Created)
DI 01-DEC-1996 (Rel. 34, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Haemaphysalis torotzi (Sea squit).
OX Eukaryota; Metazoa; Chordata; Hemichordata; Ascidiacea;
  Stolidobranchia; Pyrosidae; Balanoglossa.
OX NCBI_FaxID: 7729;
LN 11.
RP SEQUENCE.
RC TISSUE: Hemolymph.
RA Shishikura, E.; Abe, F.; Otake, S.; Otake, T.
RT "Purification and characterization of a serine proteinase inhibitor
  inhibitor from the hemolymph of a sea squit, a chordate, Balanoglossa
  torotzi."
CC -! FUNCTION: STRONGLY INHIBITS TRYPSIN AND THROMBOLYSIN ACTIVITY.
CC -! SUBUNIT: Monomer.
CC -! SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DI InterPro: IPR002157; Serpin.
DI PROSITE: PS00284; SERPIN: PARTIAL.
KW Serpin; Serine protease inhibitor; Glycylproline plasma.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1104 MW: 422567/AA18107AA (Rel. 34)

Query Match 18.2% Score 21; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 27
SYK_CAMUP STANDARD; PRI: 10 AA.
AC Q46454;
DI 15-DEC-1996 (Rel. 37, Created)
DI 15-DEC-1996 (Rel. 37, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
  (Fragment).
GN LYSRS.
OS Campylobacter upsaliensis.
OX Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
  Campylobacteraceae; Campylobacter.
OX NCBI_FaxID: 26360;
LN 11.
RP SEQUENCE FROM N.A.
RC STRAIN: ATCC 43954.
RA MEDLINE: 97149102; PubMed: 8996110;
  Bourke, B.; Rashid, S.T.; Hindham, H.L.; Chan, V.L.;
  "Characterization of Campylobacter upsaliensis fur and its
  localization in a highly conserved region of the Campylobacter
  genome."
RL Gene 183:219-224(1996).
CC -! CATALYTIC ACTIVITY: ATP + L-lysine -> tRNA(Lys) - AMP + diphosphate
  + L-lysyl-tRNA(Lys).
CC -! COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC -! SUBUNIT: Homodimer (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: Belongs to class-11 aminocacyl-tRNA synthetase family.

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EMBL: L77076; AAR4142.1;
XMAP: MF_00252; 1.
InterPro: IPR006195; tRNA_LIGASE_11.
PROSITE: PS00862; AA_tRNA_LIGASE_11; PARTIAL.
KW Aminocacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
  Metal-binding; Magnesium.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1218 MW: 905464/AA13372B05 CRC64;

Query Match 18.2% Score 21; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KS 9
LA 11
  2 KS 3

RESULT 28
TEMK_RANTE STANDARD; PRI: 10 AA.
AC P69237;
DI 30-MAY-2000 (Rel. 39, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Terporin K.
OS Rana temporaria (European common frog).
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
  NCBI_FaxID: 8407;
LN 11.
RP SEQUENCE.
RC TISSUE: Skin secretion.
RA MEDLINE: 9715050; PubMed: 9027137;
  Simmone, M.; Mianzola, S.; Canofari, S.; Miele, R.; Mangoni, M.L.;

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RA Rana catesbeiana (Bull frog).
RT *Temporalis, antimicrobial peptides from the European red frog Rana
RT temporaria.
RT Eur. J. Biochem. 242:788-792(1996).
XX -1- FUNCTION: Has antibacterial activity against Gram-positive
XX bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the protease family.
KW Amphibian lactase peptide; Antimicrobial; Amidation.
FT MDL RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1123 MW: 3995496-4727267 (Ref. 1).

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KS 9
EB 7 KS 8

RESULT 29
TKNB_CHICK STANDARD; PRT: 10 AA.
AC P40752.
DT 01-FEB-1991 (Ref. 17, Created)
DT 01-FEB-1991 (Ref. 17, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Kankawa K, Kozawa H, Hino J, Minamoto N, Matsuo H.
OS Gallus gallus (Chicken).
CC Eukaryote; Metazoa; Chordata; Galliformes; Phasianidae; Gallinaceae;
CC Gallus.
CC Archaeosaurus; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
XX NCBI_TaxID 9081;
FN 111
RP TISSUE: Intestine;
RX MEDLINE:68204263; PubMed:24524611.
KA Gannon J.M., Katsoulis S., Schmitt W.R., Chim D.
RT *Gastrin/Substance P and neurokinin A from chicken small intestine-1;
RT Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B61033; R61033.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MDL RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1134 MW: 866845290-8668594.

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4
EB 2 KS 3

RESULT 30
TKNB_RAN_A STANDARD; PRT: 10 AA.
AC P22669;
DT 01-APR-1991 (Ref. 19, Created)
DT 01-APR-1991 (Ref. 19, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Kanatagachykinin B (R1K B).

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OS Rana catesbeiana (Bull frog).
CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
XX NCBI_TaxID-8450;
FN 111
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE:91254437; PubMed:25445443.
KA Kozawa H., Hino J., Minamoto N., Kanyawa K., Matsuo H.
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine."
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN 121
RP SEQUENCE.
RX TISSUE: Intestine;
RX MEDLINE:94024716; PubMed:840506;
KA Kanyawa K., Kozawa H., Hino J., Minamoto N., Matsuo H.
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine."
RL Regul. Pept. 46:81-88(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B61033; R61033.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MDL RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1210 MW: 917556459-917556555 (Ref. 1).

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KS 9
EB 2 KS 3

RESULT 31
TKU2_URECH STANDARD; PRT: 10 AA.
AC P40752;
DT 01-FEB-1995 (Ref. 31, Created)
DT 01-FEB-1995 (Ref. 31, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Urechis sticticus.
OS Urechis sticticus.
CC Eukaryote; Metazoa; Echinoda; Xenophenista; Urechidae; Urechis.
XX NCBI_TaxID-6432;
FN 111
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE: Ventral nerve cord;
RX MEDLINE:93236558; PubMed-847410;
KA Ikeda I., Minakata H., Numoto K., Kubota I., Muneoka Y.
RT "Two novel tachykinin related neuropeptides in the echinoid worm,
RT Urechis sticticus."
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC MUSCLE OF THE ANIMAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MDL RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 984 MW: 3F58D079C9C87698 CRC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KM Headex, anti: Vasodilation.  
 FI PEPTIDE 1 11 MFASIN-CALIXIN.  
 FI PEPTIDE 1 9 HRA-YKIN; N-LIKE PEPTIDE.  
 SL SEQUENCE 11 AA: 1274 MW: 34867490/7716978 (5662)  
 Query Match 19,28; Score 2; DB 1; Length 11.  
 Best Local Similarity 100.0%; Pred No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0  
 QY 2 SK 1  
 ID 3 SK 10  
 RESULT 38  
 Q20A\_CUMIF  
 ID Q20A\_CUMIF STANDARD; PRI 11 AA  
 AC P30464;  
 FI 01-N-V-1995 (Rel. 42, last sequence update)  
 FI 01-N-V-1995 (Rel. 40, last sequence update)  
 FI 16-06; 2501 (Rel. 46, last sequence update)  
 DE Quinoline 2-oxo-reductase, alpha chain (EC 1.3.99.17) (Fragment).  
 CS Camponotus testaceus (Pseudomyrmex testaceus).  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Camponotaceae; Comptosia.  
 CX NCBI\_TaxID:285;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN:63.  
 FX MEDLINE:96045589, PubMed:756264;  
 RA Schach S., Tsubuoka H., Fetzner S., Lingens F.  
 RI "Quinoline 2-oxo-reductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 dioxygenase from Camponotus testaceus", 63. The first two enzymes in  
 the quinoline and 3-methylquinoline degradation.  
 RL Est. J. Biochem. 232:536-544(1995).  
 CC 1- FUNCTION: CONVERTS (3-METHYL)-QUINOLINE TO (3-METHYL)-2-OXO-  
 1,2-DIHYDROQUINOLINE.  
 CC 1- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-  
 1(2H)-one + reduced acceptor.  
 CC 1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.  
 CC 1- PATHWAY: Degradation of quinoline and (3-methyl)-quinoline; first  
 step.

RP SEQUENCE.  
 RC SPECIES: A. equitissima, and H. attenuata;  
 RA Schaller H.C., Bodenmuller H.C.  
 RI "Isolation and amino acid sequence of a morphogenetic peptide from  
 Hydra".  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
 RN 31  
 RP SYNTHESIS.  
 RC MEDLINE:820580; PubMed:7297679.  
 RA Bodemuller H.C., Bodenmuller H.C., Schaller H.C.  
 RI "Synthesis of a new morphopeptide, the head activator from Hydra".  
 RL FEBS Lett. 133:317-322(1982).  
 RN 41  
 RP FUNCTION.  
 RC MEDLINE:9058924; PubMed:2581311.  
 RA Schaller H.C., Bodenmuller H.C., Bodemuller H.C.  
 RI "Head activator acts as an autocrine growth factor for NIH3T3 cells  
 in the G2/mitosis transition".  
 RL EMBO J. 8:311-318(1989).  
 CC 1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS  
 IN THE G2/MITOSIS TRANSITION.  
 CC 1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA  
 AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED  
 HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS  
 BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.  
 CC PIR: A01427; YHFI  
 CC PIR: A94966; YHXA;  
 CC PIR: R01427; YHFI;  
 CC PIR: B94966; YHFI;  
 CC PIR: G01427; YHFI;  
 CC GK: P01263;  
 KW Growth factor; cell cycle; mitosis; pyrrolidone carboxylic acid.  
 FT MZLRES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SL SEQUENCE 11 AA: 1142 MW: 37927417/3258878 CRC64;  
 Query Match 18,2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0  
 QY 9 SK 10  
 ID 6 SK 7  
 RESULT 38  
 Q20A\_CUMIF  
 ID Q20A\_CUMIF STANDARD; PRI 11 AA  
 AC P30464;  
 FI 01-N-V-1995 (Rel. 42, last sequence update)  
 FI 01-N-V-1995 (Rel. 40, last sequence update)  
 FI 16-06; 2501 (Rel. 46, last sequence update)  
 DE Quinoline 2-oxo-reductase, alpha chain (EC 1.3.99.17) (Fragment).  
 CS Camponotus testaceus (Pseudomyrmex testaceus).  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Camponotaceae; Comptosia.  
 CX NCBI\_TaxID:285;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN:63.  
 FX MEDLINE:96045589, PubMed:756264;  
 RA Schach S., Tsubuoka H., Fetzner S., Lingens F.  
 RI "Quinoline 2-oxo-reductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 dioxygenase from Camponotus testaceus", 63. The first two enzymes in  
 the quinoline and 3-methylquinoline degradation.  
 RL Est. J. Biochem. 232:536-544(1995).  
 CC 1- FUNCTION: CONVERTS (3-METHYL)-QUINOLINE TO (3-METHYL)-2-OXO-  
 1,2-DIHYDROQUINOLINE.  
 CC 1- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-  
 1(2H)-one + reduced acceptor.  
 CC 1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.  
 CC 1- PATHWAY: Degradation of quinoline and (3-methyl)-quinoline; first  
 step.



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QY 3 KT 4
DB 11
5 KT 6

RESULT 42
TKNA_RANR1
ID TKNA_RANR1 STANDARD: PRT 11 AA.
AC P29207
BT 01-DEC-1992 (rel. 24, Created)
BT 01-DEC-1992 (rel. 24, Last sequence update)
BT 15-SEP-2003 (rel. 42, Last annotation update)
DB Rankinidin (Substance-related peptide)
CS Kana Fichibunda (Catching frog) (Marsh frog)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Batrachia; Anura; Neobatrachia; Rana; Ranidae; Rana.
CX NCBI_TaxID: 8400;
RN 11
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE: 9204454; PubMed: 1656243;
RA O'Harte P., Barcher E., Iovas S., Smith L.B., Vaidya N., Carlson J.M.;
RI "Rankinidin: a novel NK1 tachykinin receptor agonist isolated with
RI rankinidin B from the brain of the frog Rana Fichibunda."
RC J. Neurochem. 57:2086-2091(1991);
BT 15-SEP-2003 (rel. 42, Last sequence update)
BT 15-SEP-2003 (rel. 42, Last annotation update)
DB Rankinidin 2 (RTK D);
CS Kana Fateshelana (Buli frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Batrachia; Anura; Neobatrachia; Rana; Ranidae; Rana.
CX NCBI_TaxID: 8400;
RN 11
RP SEQUENCE.
RC TISSUE: Intestine;
RX MEDLINE: 91254337; PubMed: 2043143;
RA Kozawa H., Hino J., Minamino N., Katsawa K., Matsuo H.;
RI "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RI brain and intestine."
RC Biochem. Biophys. Res. Commun. 177:586-595(1991)
RN 12
RP SEQUENCE.
RC TISSUE: Intestine;

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RX MEDLINE: 94023216; PubMed: 8210506;
RA Katsawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RI "Four novel tachykinins in frog (Rana catesbeiana) brain and
RI intestine."
RC Regul. Pept. 46:181-188(1993);
BT 15-SEP-2003 (rel. 42, Last sequence update)
BT 15-SEP-2003 (rel. 42, Last annotation update)
DB Rankinidin (Substance-related peptide)
CS Kana Fichibunda (Catching frog) (Marsh frog)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Batrachia; Anura; Neobatrachia; Rana; Ranidae; Rana.
CX NCBI_TaxID: 8400;
RN 11
RP SEQUENCE.
RC TISSUE: Intestine;
RX MEDLINE: 91254337; PubMed: 2043143;
RA Kozawa H., Hino J., Minamino N., Katsawa K., Matsuo H.;
RI "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RI brain and intestine."
RC Biochem. Biophys. Res. Commun. 177:586-595(1991)
RN 12
RP SEQUENCE.
RC TISSUE: Intestine;

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14 HISTONE H2A (Fragment)  
 15 neorhynchus mykiss (Rainbow trout) (Salmo gairdneri)  
 16 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 17 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 18 Proteanthopterygii; Salmoniformes; Salmonidae; neorhynchus  
 19 NCBI TaxID: 8022  
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KW Hemolymph.  
 FT NCN1ER  
 SO SEQUENCE 12 AA; 1455 MW; 288EAA44A432412 CRC64;  
 Query Match 18.4%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KS 9  
 LB 6 RS 7  
 RESULT 47  
 NOA 1471A STANDARD; PRT; 12 AA.  
 AC 142424;  
 DT 15-DEC-1998 (Rel. 47, Created)  
 DI 15-DEC-1998 (Rel. 47, Last sequence update)  
 DE 15-DEC-1998 (Rel. 47, Last annotation update)  
 EE Early nodulin 40.  
 GN EN040  
 OS Lotus japonicus.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.  
 DX NCBI TaxID: 34305;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: cv. Gifu;  
 RA Chien, R. J., Gresshoff P.M.;  
 RT "Isolation and Primary Characterization of genomic Enod40 gene from  
 RC Lotus japonicus cultivar 'Gifu'";  
 RL (in) Plant Gene Register 2007-142  
 CC 1- FUNCTION: REGULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT  
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY  
 CC SIMILARITY).  
 CC 1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE  
 CC DEVELOPMENT.  
 CC  
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 CC  
 CC EM50: APL0594; AA02785.1;  
 KW Nucleation.  
 SO SEQUENCE 12 AA; 1486 MW; 50E1E8257CB326C3 CRC64;  
 Query Match 18.4%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 KS 9  
 LB 7 KS 8  
 RESULT 48  
 NOA 1471A STANDARD; PRT; 12 AA.  
 AC 024359;  
 DT 15-DEC-1998 (Rel. 47, Created)  
 DI 15-DEC-1998 (Rel. 47, Last sequence update)  
 DE 15 DEC 1998 (Rel. 47, Last annotation update)  
 EE Early nodulin 40.  
 GN EN040  
 OS Sesbania rostrata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC

[illegible]

```

KW Ribosomal protein: Chloroplast.
FT NON_TER 12
SQ SEQUENCE 12 AA: 1488 MW: 6700EDAF9D033734 CRC64:

Query Match 14.2% Score 2: DB 1: Length 12:
Best Local Similarity 100.0%, Prod. NO. 1.1e+04;
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 PK 3
   II
LD 11 SK 12

RESULT 00
RS19_GLYEP STANDARD: FW1: 12 AA.
AC Q46460:
DT 30-MAY-2000 (Rel. 19, created)
DT 30-MAY-2000 (Rel. 19, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19 OR RPS19.
OS Clostridium yellow-edge phytoplasmata.
CC Bacteria: Firmicutes: Mollicutes: Acholeplasmales:
CC Acholeplasmales: Mollicutes: Phytoplasmata.
CC NCBI TaxID 35775;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE: 94350872; PMID: 871196.
CC Gundersen D.F., Lee J.M., Kerner S.A., Davis K.E., Kingsbury D.T.:
CC "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
CC their classification".
CC J. Bacteriol. 176:5244-5254(1994).
CC 1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC
CC EMBL 127619: AAA8943.1
CC HAMAS: MF_005432.1
CC CLUSTAL: PR000222: Ribosomal S19.
CC PROSITE: PS00323: RIBOSOMAL S19: PARTIAL.
CC Ribosomal protein. RNA binding.
CC N-TER 1
SQ SEQUENCE 12 AA: 1430 MW: 40478EF8333AA3 CRC64:

Query Match 14.2% Score 2: DB 1: Length 12:
Best Local Similarity 100.0%, Prod. NO. 1.1e+04;
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 10 KD 11
   II
LD 5 KD 6

Search completed: September 06, 2003, 10:26:05
CPU time: 17.25 secs

```

Search completed: September 10, 2003, 19:26:05  
 Job time : 7.25 secs

GenCore version 5.1.4  
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W protein: protein search, using sw model

Run date: September 30, 2003, 11:27:04 : Search time: 4.46:2.5 seconds  
(with local alignment)  
89.39 million characters/seq

Filter: US-09-787-443-14

RefSeq source: 1 ALKTRRSKU.11

Sequences: 62394

Sequences table: Gaps: 60.0 : Gapped: 6.3

Search id: 240525 seqs: 25805264 reads

Word size: 3

Total number of hits satisfying chosen parameters: 3459

Minimum E score length: 4

Maximum E score length: 15

FAST processed: Fastest first 500 summaries

- Database: 1: SPREMBL.23:\*
- 2: sp.archaea:\*
  - 3: sp.bacteria:\*
  - 4: sp.fungi:\*
  - 5: sp.human:\*
  - 6: sp.invertebrate:\*
  - 7: sp.mammal:\*
  - 8: sp.mhc:\*
  - 9: sp.orquelette:\*
  - 10: sp.phage:\*
  - 11: sp.plant:\*
  - 12: sp.rodent:\*
  - 13: sp.virus:\*
  - 14: sp.vertebrate:\*
  - 15: sp.unclassified:\*
  - 16: sp.virus:\*
  - 17: sp.bacteriophage:\*
  - 18: sp.archaea:\*

Prod. No. is the number of residues in the protein. The number in parentheses is the score quarter, that is, equal to the score of the best aligned protein.

SEQUENCE

Result No.	Score	Query Match	Length	DB ID	Accession
1	4	56.4	14	4	Q9P855
2	3	27.3	8	2	Q44563
3	4	27.3	9	4	Q93054
4	4	27.3	9	8	Q9T410
5	4	27.3	9	8	Q9T411
6	5	27.3	9	10	Q81395
7	4	27.3	9	13	Q91A14
8	4	27.3	10	2	Q5JN59
9	4	27.3	10	5	P82242
10	4	27.3	10	8	P82136
11	4	27.3	10	10	Q81395
12	4	27.3	10	10	P24134
13	4	27.3	10	12	Q84266
14	4	27.3	10	13	Q91A14
15	4	27.3	11	4	Q94785
16	4	27.3	11	4	Q94785

17	3	27.3	11	10	Q9S8X4	Q9S8X4 glycine max
18	3	27.3	11	11	Q91366	Q91366 rattus norv
19	3	27.3	12	2	Q50303	Q50303 bacillus st
20	3	27.3	12	5	Q26429	Q26429 drosophila
21	3	27.3	12	8	P82164	P82164 spinacia ol
22	3	27.3	14	10	Q81395	Q81395 zea mays (m
23	3	27.3	14	10	P82242	P82242 spinacia ol
24	3	27.3	14	10	P82247	P82247 spinacia ol
25	3	27.3	14	4	Q90C11	Q90C11 homo sapien
26	3	27.3	14	12	Q81761	Q81761 hepatitis c
27	3	27.3	14	12	Q81794	Q81794 hepatitis c
28	3	27.3	14	12	Q81784	Q81784 hepatitis c
29	3	27.3	14	12	Q81778	Q81778 hepatitis c
30	3	27.3	14	12	Q81782	Q81782 hepatitis c
31	3	27.3	14	12	Q81775	Q81775 hepatitis c
32	3	27.3	14	12	Q81767	Q81767 hepatitis c
33	3	27.3	14	12	Q81798	Q81798 hepatitis c
34	3	27.3	14	12	Q81774	Q81774 hepatitis c
35	3	27.3	14	12	Q81766	Q81766 hepatitis c
36	3	27.3	14	12	Q81793	Q81793 hepatitis c
37	3	27.3	14	12	Q81768	Q81768 hepatitis c
38	3	27.3	14	12	Q81785	Q81785 hepatitis c
39	3	27.3	14	12	Q81800	Q81800 hepatitis c
40	3	27.3	14	12	Q81765	Q81765 hepatitis c
41	3	27.3	14	12	Q81781	Q81781 hepatitis c
42	3	27.3	14	12	Q81769	Q81769 hepatitis c
43	3	27.3	14	12	Q81773	Q81773 hepatitis c
44	3	27.3	14	12	Q81799	Q81799 hepatitis c
45	3	27.3	14	12	Q81786	Q81786 hepatitis c
46	3	27.3	14	12	Q81788	Q81788 hepatitis c
47	3	27.3	14	12	Q81763	Q81763 hepatitis c
48	3	27.3	14	12	Q81764	Q81764 hepatitis c
49	3	27.3	14	12	Q81796	Q81796 hepatitis c
50	3	27.3	14	12	Q81791	Q81791 hepatitis c
51	3	27.3	14	12	Q81762	Q81762 hepatitis c
52	3	27.3	14	12	Q81790	Q81790 hepatitis c
53	3	27.3	14	12	Q81783	Q81783 hepatitis c
54	3	27.3	14	12	Q81789	Q81789 hepatitis c
55	3	27.3	14	12	Q81797	Q81797 hepatitis c
56	3	27.3	14	12	Q81795	Q81795 hepatitis c
57	3	27.3	14	12	Q81782	Q81782 hepatitis c
58	3	27.3	14	12	Q81780	Q81780 hepatitis c
59	3	27.3	14	12	Q81773	Q81773 hepatitis c
60	3	27.3	14	12	Q81779	Q81779 hepatitis c
61	3	27.3	14	12	Q81772	Q81772 hepatitis c
62	3	27.3	14	12	Q81792	Q81792 hepatitis c
63	3	27.3	14	12	Q81777	Q81777 hepatitis c
64	3	27.3	14	13	P83338	P83338 oncorhynch
65	3	27.3	14	4	Q54501	Q54501 lactobacilli
66	3	27.3	14	15	Q9SMW4	Q9SMW4 arabidopsis
67	3	27.3	14	19	Q81395	Q81395 zea mays (m
68	3	27.3	14	19	P82452	P82452 spinacia ol
69	3	27.3	14	19	P82435	P82435 nicotiana t
70	3	27.3	14	19	P82439	P82439 pisum sativ
71	3	27.3	15	2	Q46013	Q46013 caulobacter
72	3	27.3	15	2	Q54861	Q54861 streptococ
73	3	27.3	15	4	Q88947	Q88947 homo sapien
74	3	27.3	15	6	Q9TRK6	Q9TRK6 sus scrofa
75	3	27.3	15	6	Q9TRH1	Q9TRH1 bos taurus
76	3	27.3	15	6	Q8KK21	Q8KK21 bolidomonas
77	3	27.3	15	8	Q8KK22	Q8KK22 blarina hyl
78	3	27.3	15	8	P82135	P82135 spinacia ol
79	3	27.3	15	11	Q35411	Q35411 mus musculu
80	2	18.2	8	2	Q8KKX4	Q8KKX4 microcystis
81	2	18.2	8	2	Q93SR0	Q93SR0 staphylococ
82	2	18.2	8	2	Q32560	Q32560 escherichia
83	2	18.2	8	2	Q8S883	Q8S883 lactobacilli
84	2	18.2	8	2	Q87471	Q87471 haemophilus
85	2	18.2	8	2	Q56246	Q56246 thermophilu
86	2	18.2	8	2	Q989E0	Q989E0 bacillus su
87	2	18.2	8	2	Q45889	Q45889 clostridium
88	2	18.2	8	2	Q47273	Q47273 escherichia
89	2	18.2	8	2	Q9RQ57	Q9RQ57 buchneria ap

90	2	18.2	8	2	Q94V59	Q94V59	varanus ind
91	2	18.2	8	4	Q15869	Q15869	homo sapien
92	2	18.2	8	4	Q15869	Q15869	homo sapien
93	2	18.2	8	4	Q16428	Q16428	homo sapien
94	2	18.2	8	4	Q16428	Q16428	homo sapien
95	2	18.2	8	4	Q16428	Q16428	homo sapien
96	2	18.2	8	5	Q15869	Q15869	homo sapien
97	2	18.2	8	5	Q16428	Q16428	homo sapien
98	2	18.2	8	5	Q16428	Q16428	homo sapien
99	2	18.2	8	6	Q16428	Q16428	homo sapien
100	2	18.2	8	6	Q16428	Q16428	homo sapien
101	2	18.2	8	6	Q16428	Q16428	homo sapien
102	2	18.2	8	6	Q16428	Q16428	homo sapien
103	2	18.2	8	6	Q16428	Q16428	homo sapien
104	2	18.2	8	6	Q16428	Q16428	homo sapien
105	2	18.2	8	6	Q16428	Q16428	homo sapien
106	2	18.2	8	6	Q16428	Q16428	homo sapien
107	2	18.2	8	6	Q16428	Q16428	homo sapien
108	2	18.2	8	6	Q16428	Q16428	homo sapien
109	2	18.2	8	6	Q16428	Q16428	homo sapien
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112	2	18.2	8	6	Q16428	Q16428	homo sapien
113	2	18.2	8	6	Q16428	Q16428	homo sapien
114	2	18.2	8	6	Q16428	Q16428	homo sapien
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116	2	18.2	8	6	Q16428	Q16428	homo sapien
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122	2	18.2	8	6	Q16428	Q16428	homo sapien
123	2	18.2	8	6	Q16428	Q16428	homo sapien
124	2	18.2	8	6	Q16428	Q16428	homo sapien
125	2	18.2	8	6	Q16428	Q16428	homo sapien
126	2	18.2	8	6	Q16428	Q16428	homo sapien
127	2	18.2	8	6	Q16428	Q16428	homo sapien
128	2	18.2	8	6	Q16428	Q16428	homo sapien
129	2	18.2	8	6	Q16428	Q16428	homo sapien
130	2	18.2	8	6	Q16428	Q16428	homo sapien
131	2	18.2	8	6	Q16428	Q16428	homo sapien
132	2	18.2	8	6	Q16428	Q16428	homo sapien
133	2	18.2	8	6	Q16428	Q16428	homo sapien
134	2	18.2	8	6	Q16428	Q16428	homo sapien
135	2	18.2	8	6	Q16428	Q16428	homo sapien
136	2	18.2	8	6	Q16428	Q16428	homo sapien
137	2	18.2	8	6	Q16428	Q16428	homo sapien
138	2	18.2	8	6	Q16428	Q16428	homo sapien
139	2	18.2	8	6	Q16428	Q16428	homo sapien
140	2	18.2	8	6	Q16428	Q16428	homo sapien
141	2	18.2	8	6	Q16428	Q16428	homo sapien
142	2	18.2	8	6	Q16428	Q16428	homo sapien

245	2	18.2	9	8	Q952N1	Q95001 pericardium	309	2	18.2	10	5	P82217	P82217 bombyx mori
247	2	18.2	9	8	Q91NE4	Q94064 magdolia sa	310	2	18.2	10	5	P82224	P82224 bombyx mori
248	2	18.2	9	8	Q95DS6	Q95DS6 magdolia w2	311	2	18.2	10	5	P82224	P82224 bombyx mori
249	2	18.2	9	8	Q91NE6	Q91NE6 magdolia q7	312	2	18.2	10	6	Q9TRC1	Q9TRC1 bos taurus
249	2	18.2	9	8	Q91NE6	Q91NE6 magdolia q7	313	2	18.2	10	6	Q9XSE4	Q9XSE4 equus caball
241	2	18.2	9	8	Q91NE1	Q91NE1 magdolia fe	314	2	18.2	10	6	Q9M178	Q9M178 bos mutus g
242	2	18.2	9	8	Q94V84	Q94V84 rotundus gla	315	2	18.2	10	6	Q9M270	Q9M270 trichosurus
243	2	18.2	9	8	Q91ZK7	Q91ZK7 spinaria oi	316	2	18.2	10	6	P82205	P82205 ovis aries
244	2	18.2	9	8	Q94V88	Q94V88 varanus bil	317	2	18.2	10	7	Q95HE8	Q95HE8 papio anubi
245	2	18.2	9	8	Q95V13	Q95V13 magdolia fi	318	2	18.2	10	7	Q95HE9	Q95HE9 papio anubi
246	2	18.2	9	8	Q95HM3	Q95HM3 magdolia fi	319	2	18.2	10	6	Q9B4W1	Q9B4W1 triturus vu
247	2	18.2	9	8	Q95DS2	Q95DS2 magdolia fe	320	2	18.2	10	6	Q9SH26	Q9SH26 furellier be
248	2	18.2	9	8	Q94V19	Q94V19 varanus ore	321	2	18.2	10	8	Q95924	Q95924 elgaria pan
249	2	18.2	9	8	Q91AP4	Q91AP4 magdolia ma	322	2	18.2	10	8	P92616	P92616 aspidosceli
250	2	18.2	9	8	Q94V13	Q94V13 varanus ma	323	2	18.2	10	8	Q95HE9	Q95HE9 rana boylii
251	2	18.2	9	8	Q91HE3	Q91HE3 magdolia oi	324	2	18.2	10	8	Q9B4W4	Q9B4W4 pachytriton
252	2	18.2	9	8	Q91NE2	Q91NE2 magdolia sa	325	2	18.2	10	8	Q95HE2	Q95HE2 rana tempor
253	2	18.2	9	8	Q91NE5	Q91NE5 magdolia qu	326	2	18.2	10	8	Q9TGR4	Q9TGR4 diploglossu
254	2	18.2	9	8	Q91NE5	Q91NE5 magdolia ko	327	2	18.2	10	8	Q9XMR4	Q9XMR4 agalops ta
255	2	18.2	9	8	Q91NE5	Q91NE5 magdolia li	328	2	18.2	10	8	Q95HE4	Q95HE4 xantusia he
256	2	18.2	9	8	Q91NE5	Q91NE5 magdolia st	329	2	18.2	10	8	Q9TGR6	Q9TGR6 diploglossu
257	2	18.2	9	8	Q94V13	Q94V13 varanus dor	330	2	18.2	10	8	Q94VGS	Q94VGS varanus gri
258	2	18.2	9	8	Q91NE6	Q91NE6 magdolia fi	331	2	18.2	10	8	Q94VH1	Q94VH1 varanus gle
259	2	18.2	9	8	Q91HE6	Q91HE6 magdolia si	332	2	18.2	10	8	Q9TGR5	Q9TGR5 abronia oax
260	2	18.2	9	8	Q95DS4	Q95DS4 magdolia do	333	2	18.2	10	8	Q94V97	Q94V97 varanus spe
261	2	18.2	9	8	Q91NE3	Q91NE3 magdolia sh	334	2	18.2	10	8	Q9TGR5	Q9TGR5 elgaria mul
262	2	18.2	9	8	Q94V12	Q94V12 varanus ind	335	2	18.2	10	8	Q9B4V5	Q9B4V5 mertensiell
263	2	18.2	9	8	Q91NE8	Q91NE8 magdolia de	336	2	18.2	10	8	Q9TGR8	Q9TGR8 shinisaurus
264	2	18.2	9	8	Q95DS7	Q95DS7 magdolia si	337	2	18.2	10	8	P92766	P92766 varanus gri
265	2	18.2	9	8	Q91HE9	Q91HE9 magdolia fi	338	2	18.2	10	8	Q95HE8	Q95HE8 rana catesb
266	2	18.2	9	8	Q91NE6	Q91NE6 magdolia de	339	2	18.2	10	8	Q9B1W9	Q9B1W9 mertensiell
267	2	18.2	9	8	Q91NE2	Q91NE2 magdolia ta	340	2	18.2	10	8	Q94VDS	Q94VDS varanus oli
268	2	18.2	9	8	Q91HE3	Q91HE3 magdolia vi	341	2	18.2	10	8	Q9TGR0	Q9TGR0 ophiodes st
269	2	18.2	9	8	Q94V26	Q94V26 varanus pel	342	2	18.2	10	8	Q9B4U2	Q9B4U2 mertensiell
270	2	18.2	9	8	Q91NE7	Q91NE7 magdolia in	343	2	18.2	10	8	Q9TGR5	Q9TGR5 e-daria kin
271	2	18.2	9	8	Q95DS9	Q95DS9 magdolia in	344	2	18.2	10	8	Q94VCS	Q94VCS varanus pan
272	2	18.2	9	8	Q95DS8	Q95DS8 magdolia ra	345	2	18.2	10	8	Q9B4S8	Q9B4S8 mertensiell
273	2	18.2	9	8	Q94V21	Q94V21 varanus mer	346	2	18.2	10	8	Q95DS0	Q95DS0 magnolia po
274	2	18.2	9	10	Q94242	Q94242 tritium ae	347	2	18.2	10	8	Q95DS1	Q95DS1 barisia imb
275	2	18.2	9	11	Q95V14	Q95V14 mns musculo	348	2	18.2	10	8	Q95DS8	Q95DS8 saumalius
276	2	18.2	9	11	Q95V14	Q95V14 rattus norv	349	2	18.2	10	8	Q95DS8	Q95DS8 magnolia de
277	2	18.2	9	12	Q94733	Q94733 human herpe	350	2	18.2	10	8	Q95DS2	Q95DS2 acanthosau
278	2	18.2	9	12	Q95V14	Q95V14 human herpe	351	2	18.2	10	8	Q94VPS	Q94VPS varanus kin
279	2	18.2	9	12	Q91HE7	Q91HE7 hepatic is L	352	2	18.2	10	8	Q95DS9	Q95DS9 magnolia sp
280	2	18.2	9	12	Q92V12	Q92V12 avian zoon	353	2	18.2	10	8	Q91FV2	Q91FV2 teratoscinc
281	2	18.2	9	12	Q95V13	Q95V13 varanus vi	354	2	18.2	10	8	Q94W7	Q94W7 tylotriton
282	2	18.2	9	12	Q91HE9	Q91HE9 canine dist	355	2	18.2	10	8	Q95DS6	Q95DS6 rana pretio
283	2	18.2	9	12	Q94V13	Q94V13 simian vari	356	2	18.2	10	8	Q9TGA1	Q9TGA1 heloderma s
284	2	18.2	9	12	Q94V13	Q94V13 canassius a	357	2	18.2	10	8	Q95DS0	Q95DS0 rana cascad
285	2	18.2	9	15	Q94V13	Q94V13 human amni	358	2	18.2	10	8	Q95HE5	Q95HE5 rana sylvat
286	2	18.2	9	15	Q94V13	Q94V13 avian zoon	359	2	18.2	10	8	Q9B4U5	Q9B4U5 mertensiell
287	2	18.2	9	15	Q94V13	Q94V13 human amni	360	2	18.2	10	8	Q9TGR4	Q9TGR4 ophisaurus
288	2	18.2	9	15	Q94V13	Q94V13 human amni	361	2	18.2	10	8	P92771	P92771 xenosaurus
289	2	18.2	10	1	Q94V26	Q94V26 strigopod	362	2	18.2	10	8	Q94VGS	Q94VGS varanus var
290	2	18.2	10	2	Q97651	Q97651 escherichia	363	2	18.2	10	8	Q9TGR5	Q9TGR5 elgaria coe
291	2	18.2	10	2	Q9KH97	Q9KH97 crotodidm	364	2	18.2	10	8	Q9B4S0	Q9B4S0 mertensiell
292	2	18.2	10	2	Q9VNR5	Q9VNR5 helicobacte	365	2	18.2	10	8	Q95DS3	Q95DS3 rana aurora
293	2	18.2	10	2	Q9X482	Q9X482 prochloroco	366	2	18.2	10	8	Q95HE8	Q95HE8 xantusia ar
294	2	18.2	10	2	Q94745	Q94745 escherichia	367	2	18.2	10	8	Q9TGR2	Q9TGR2 ophisaurus
295	2	18.2	10	2	Q94745	Q94745 escherichia	368	2	18.2	10	8	Q9B4U8	Q9B4U8 salamandra
296	2	18.2	10	2	Q91HE2	Q91HE2 escherichia	369	2	18.2	10	8	Q95DS3	Q95DS3 magnolia me
297	2	18.2	10	2	Q94V29	Q94V29 helicobacte	370	2	18.2	10	8	Q9B4V8	Q9B4V8 chloioflossa
298	2	18.2	10	2	Q94V29	Q94V29 bacillus co	371	2	18.2	10	8	Q94V29	Q94V29 gambelia w
299	2	18.2	10	2	P82568	P82568 strigopod	372	2	18.2	10	8	Q9TGR1	Q9TGR1 crotophytus
300	2	18.2	10	2	P82568	P82568 strigopod	373	2	18.2	10	8	Q9TGR6	Q9TGR6 gerromotus
301	2	18.2	10	4	Q94V29	Q94V29 homo sapien	374	2	18.2	10	8	Q9TGR4	Q9TGR4 anguis frag
302	2	18.2	10	4	Q94V29	Q94V29 homo sapien	375	2	18.2	10	8	Q94V29	Q94V29 varanus sca
303	2	18.2	10	4	Q91HE2	Q91HE2 homo sapien	376	2	18.2	10	8	Q9B4U1	Q9B4U1 mertensiell
304	2	18.2	10	5	Q94V29	Q94V29 helicobacte	377	2	18.2	10	8	Q9TGR3	Q9TGR3 ophisaurus
305	2	18.2	10	5	Q94V29	Q94V29 helicobacte	378	2	18.2	10	8	Q9TGR2	Q9TGR2 annelia pu
306	2	18.2	10	5	Q94V29	Q94V29 helicobacte	379	2	18.2	10	8	P92576	P92576 bipes bipor
307	2	18.2	10	5	Q94V29	Q94V29 helicobacte	380	2	18.2	10	8	Q9TGR5	Q9TGR5 ophisaurus
308	2	18.2	10	5	P82568	P82568 strigopod	381	2	18.2	10	8	Q9B1X0	Q9B1X0 mertensiell





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FASTA 4
Q97220 PRELIMINARY PPT 9 AA.
AC Q97220;
CT 01-MAY-2000 (EMBL) (v. first update)
CT 01-MAY-2000 (EMBL) (v. last sequence update)
CT 01-JUN-2002 (EMBL) (v. last annotation update)
DE LHC II LIGHT-HARVESTING CHLOROPHYLL PROTEIN II (fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots;
OC Caryophyllales; Eurycotylales; Chenopodiaceae; Spinacia.
CC MBI TXID 3562;
RN 1..9
SQ
MEDLINE:G9747386 [PubMed 1894543]
RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett V.J.
RT "Fadom mass spectrometry identifies sites of three post-translational
RT modifications of spinach light-harvesting chlorophyll protein LII.
RT Proteolytic cleavage, acetylation, and phosphorylation."
J Biol Chem. 266(17):584-1759(1991);
SF 1
NSK_PER 9
NSK_TER 9
SQ SEQUENCE 9 AA: 54D9Z7634B7D3IA3 GRC64;

Query Match: 27.8% Score 3; DB 8; Length 9;
Best local Similarity 100.0%; Pred No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
Q01211
ID Q01211 PROTEIN PRIMARY PRI1 9 AA.
DI 01-MAY-2000 (ITEMBOLD) 24. (created)
DI 01-MAY-2000 (ITEMBOLD) 24. (last sequence update)
DI 01-JUN-2002 (ITEMBOLD) 24. (last annotation update)
DE LHC II (LHC) harvesting chlorophyll protein II (fragment).
CS Spinacia oleracea (Spinach).
OG chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Caryophyllales; Rhoeoideales; Spinacia
OC NERI LAXID 0062
CX NERI LAXID 0062
PN 1
PR SEQUENCE.
RX RHAELENF014734661 (EMBL) 19654-1.
RA Maeder, H., Griffin P.R., Shababowitz J.J., Hunt D.F., Bennett J.;
RE Random mass spectrometry identifies sites of three post-translational
RE modifications at Spinacia lutea harvesting chlorophyll protein II.
RE Proteomics (Glasgow), Scotland, Scotland, and phosphorylation";
RI J. Biol. Chem. 266:17564-17561(1991).
RT N_NTER 9
RT N_NTER 9
SQ SEQUENCE 9 AA: 985 MW: 34092.76 kDa: CDS: CRC64:
Query Match 27 3% Score 31 DB R: Length 9:
Best local similarity 100 100% E-val: 1e-05 No. 8.3e+05;
Matches 51 Conserved 51 Mismatches 0; Indels 0; Gaps 0;
DI 01-MAY-2000 (ITEMBOLD) 24. (created)
DI 01-MAY-2000 (ITEMBOLD) 24. (last sequence update)
DI 01-JUN-2002 (ITEMBOLD) 24. (last annotation update)
DE LHC II (LHC) harvesting chlorophyll protein II (fragment).
CS Spinacia oleracea (Spinach).
OG chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Caryophyllales; Rhoeoideales; Spinacia
OC NERI LAXID 0062
CX NERI LAXID 0062
PN 1
PR SEQUENCE.
RX RHAELENF014734661 (EMBL) 19654-1.
RA Maeder, H., Griffin P.R., Shababowitz J.J., Hunt D.F., Bennett J.;
RE Random mass spectrometry identifies sites of three post-translational
RE modifications at Spinacia lutea harvesting chlorophyll protein II.
RE Proteomics (Glasgow), Scotland, Scotland, and phosphorylation";
RI J. Biol. Chem. 266:17564-17561(1991).
RT N_NTER 9
RT N_NTER 9
SQ SEQUENCE 9 AA: 985 MW: 34092.76 kDa: CDS: CRC64:

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RESULT 13
ID Q84756 PRELIMINARY: 10 AA
AC Q84756
DT 01-NOV-1999 (TrEMBLrel. 01, Created)
DI 01-NOV-1999 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 08, Last annotation update)
DE (HIV-1) tNA (Fragment)
EN E6
OS Human papillomavirus type 11
OC Viruses: dsDNA viruses, no RNA stage; Papillomaviridae
OC Papillomavirus
CX NCBI_TaxID:13590
RN 1
RP SEQUENCE FROM N.A.
RA STEAIN Boushey
RA MEDLINE 4929475, PubMed:4545074
RA Collier S.C., Chow L.T., Kreider J.W., Probst L.S., Liu, N.L.,
RA Bower, M.K.
RT "Characterization of an HPV type 11 isolate propagated in human
RT foreskin explants is made easier."
RC Virology 171:294-297(1999)
DR EMBL:J04511; AAA66865.1
FT SEQ_FEATURE 10
FT SEQUENCE 10 AA: 1020 MW: 97895SRGHAAL25.CRC64

Query Match 27.8% Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKD 11
ID 6 SKD 5

RESULT 14
Q84757 PRELIMINARY: 10 AA
AC Q84757
DT 01-MAY-2000 (TrEMBLrel. 14, Created)
DI 01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE STEINK FEMALE attractant pheromone
OS Cynops pyrrhogaster (Japanese common toad)
OC Eukaryota; Metazoa; Chordata; Anura; Bufonidae; Bufoninae
OC Amphibia; Anura; Chordata; Salamanders; Bufonidae; Toads
CX NCBI_TaxID:8459
RN 1
RP SEQUENCE FROM N.A.
RA MEDLINE 15192714, PubMed:7890452
RA Kikuchi S., Toyoda F., Shimada Y.
RA "Isolation of female-attractant pheromone from the toad
RA Cynops pyrrhogaster."
RC ChemoSenses 1:144-154(1995)
DR EMBL:U63613; AAG17964.1
FT SEQ_FEATURE 10
FT SEQUENCE 10 AA: 1071 MW: 99578SLAA52AA.CRC64

Query Match 27.3% Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKD 11
ID 4 SKD 6

RESULT 15
Q84758 PRELIMINARY: 11 AA
AC Q84758
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Thrombospondin (Fragment)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta eudicotyledons; core eudicots; Rosidae;
OC Eurosoidae; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
CX NCBI_TaxID:4847

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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE FROM N.A.
RA Sasaki Y., Takahashi T., Nakagawa K., Okuno Y., Nakao K.
RA "Production of Thrombospondin by Human Carcinomas and Its Novel mRNA
RT Isoforms."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB014683; BAA34312.1
FT SEQ_FEATURE 11
FT SEQUENCE 11 AA: 1233 MW: 5181944B6C1A877.CRC64

Query Match 27.8% Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRE 6
ID 8 TRE 10

RESULT 16
Q84757 PRELIMINARY: 11 AA
AC Q84757
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Aquaporin-4 (Fragment)
EN AQP4
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE FROM N.A.
RA MEDLINE 97008105, PubMed:8855283
RA Li M., Lee M.B., Smith B.L., Susq J.S., Agre P., Verdink M.A.J.,
RA Borck G., RISS J.P.L., Beem P.M.T.
RA "The human AQP4 gene: definition of the locus encoding two water
RT channel polypeptides in brain."
RL Proc. Natl. Acad. Sci. U.S.A. 93:10908-10912(1996)
DR EMBL:U63613; AAG17964.1
FT SEQ_FEATURE 11
FT SEQ_FEATURE 11
FT NON_FEATURE 11
FT NON_FEATURE 11
FT SEQUENCE 11 AA: 1233 MW: 47995A331AEH737.CRC64

Query Match 27.8% Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRE 4
ID 7 TRE 9

RESULT 17
Q84758 PRELIMINARY: 11 AA
AC Q84758
DT 01-MAY-2000 (TrEMBLrel. 15, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vegetative storage protein 54 peptide 3, VSP54-LIPOXYGENASE
DE (Fragment)
OS Glycine max (Soybean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta eudicotyledons; core eudicots; Rosidae;
OC Eurosoidae; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
CX NCBI_TaxID:4847

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FT  N-NTIER 12 12
SQ  SEQUENCE 12 AA: 137% MW: 70067C90E8A6C40B CRC64:

Query Match 27.3% Score 3: DB 2: Length 12;
Best: Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RRS 7
DB 4 RRS 6

RESULT 20
Q26429 PRELIMINARY: PRT; 12 AA.
ID Q26429
AC Q26429;
DT 01-NOV-1996 (TREMBLREL: 01, Created)
DI 01-NOV-1996 (TREMBLREL: 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL: 17, Last annotation update)
DE PROBOSCIPEDIA protein (Fragment);
OS PB.
OC Drosophilina Pseudoscorpia (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neuroptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OC NCBI TaxId: 7247;
CN 11
KF SEQUENCE FROM N.A.
RX MEDLINE:9211189; PubMed:1684942;
KA Mandazzo F.M., Griggs D.L., Kaufman T.C.;
KT "Rescue and regulation of proboscipedia: a homeotic gene of the
R1 Antennapedia Complex.";
RL Development. 113:257-271(1991).
EMBL: S77929; AAB20845.1;
DR FLYBase; FBgn012734; Dpse\pb.
UNLTER 1 1
SQ SEQUENCE 12 AA: 1377 MW: 4608DH18E755A5B3 CRC64:

Query Match 27.3% Score 3: DB 5: Length 12;
Best: Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RRS 9
DB 4 RRS 6

RESULT 21
P82164 PRELIMINARY: PRT; 12 AA.
ID P82164
AC P82164;
DT 01-MAY-2000 (TREMBLREL: 13, Created)
DI 01-MAY-2000 (TREMBLREL: 13, Last sequence update)
DT 01-JUN-2001 (TREMBLREL: 17, Last annotation update)
DE Chloroplast 3S ribosomal protein S14 beta (fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OC NCBI TaxId: 3562;
CN 11
KF SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RX STRAIN-CV. ALVARO; TISSUE-Leaf;
KA MEDLINE:20435797; PubMed:10874039;
RY Yamaguchi K., von Knoblauch K., Subramanian A.R.;
R1 "The plastid ribosomal proteins. Identification of all the proteins in
R7 the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC 1-1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC 1-1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC 1-1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC 1-1- MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN PL. S14 ALPHA

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CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS.
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45685.1;
DR InterPro: IPR002522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polypeptide.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 34
Q81774
ID Q81774 PRELIMINARY; PRI: 13 AA.
AC Q81774;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN-SAL1;
RX MEDLINE:92275243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RA *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45715.1;
DR InterPro: IPR002522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polypeptide.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 35
Q81766
ID Q81766 PRELIMINARY; PRI: 13 AA.
AC Q81766;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN-BK2;
RX MEDLINE:92275243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RA *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45684.1;
DR InterPro: IPR002522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polypeptide.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1571 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 36
Q81793
ID Q81793 PRELIMINARY; PRI: 13 AA.
AC Q81793;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
KN 11

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RP SEQUENCE FROM N.A.
RC STRAIN-SAL1;
RX MEDLINE:92275243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RA *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45692.1;
DR InterPro: IPR002522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polypeptide.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 35
Q81766
ID Q81766 PRELIMINARY; PRI: 13 AA.
AC Q81766;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN-BK2;
RX MEDLINE:92275243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RA *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45684.1;
DR InterPro: IPR002522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polypeptide.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1571 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 36
Q81793
ID Q81793 PRELIMINARY; PRI: 13 AA.
AC Q81793;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
KN 11

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DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepaviruses.
CX NCBI_LinxID:11103;
EN 1;
KP SEQUENCE FROM N.A.
RA MEDLINE-92279243; PubMed 1317578;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
KL SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
EMBL: M84855; AAA45710.1;
IR InterPro: IPR002522; HCV_capsid
LR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 454797E1A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

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ID Q81768 PRELIMINARY: PRT 13 AA.
AC Q81768;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DI 01-SEP-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepaviruses.
CX NCBI_LinxID:11103;
EN 1;
KP SEQUENCE FROM N.A.
RA MEDLINE-92279243; PubMed 1317578;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
KL SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
EMBL: M84855; AAA45686.1;
IR InterPro: IPR002522; HCV_capsid.
LR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 454797E1A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

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AC Q81785;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DI 01-SEP-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepaviruses.
CX NCBI_LinxID:11103;
EN 1;
KP SEQUENCE FROM N.A.
RA MEDLINE-92279243; PubMed 1317578;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
KL SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
EMBL: M84848; AAA45702.1;
IR InterPro: IPR002522; HCV_capsid
LR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 454797E1A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

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AC Q81800;
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DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DI 01-SEP-2002 (TrEMBLrel. 22; Last annotation update)
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GN POLYPROTEIN
GS Hepatitis C virus.
CA Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepaviruses.
CX NCBI_LinxID:11103;
EN 1;
KP SEQUENCE FROM N.A.
RA MEDLINE-92279243; PubMed 1317578;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
KL SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
EMBL: M84865; AAA45717.1;
IR InterPro: IPR002522; HCV_capsid
LR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 454797E1A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;

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DE          1
SQ          9 PKT 11

Query Match:          27.3% Score 3:  DP 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
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QY          2 PKT 4
DE          1
SQ          9 PKT 11

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DI 01-NOV-1996 (FEBMRE01.01, Last sequence update)
DE 01-OCT-2002 (FEBMRE01.22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID:11103
RN SEQUENCE FROM N.A.
RS STRAIN:384
RX MEDLINE:9227424; PubMed:1317578;
RA Buch J., Purcell R.H., Miller R.H.
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC -1- SUBMIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84856; AAA45698.1
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON-TER          13
SQ SEQUENCE  13 AA: 1572 MW: 4634671A42FC7E3 16974.

Query Match:          27.3% Score 3:  DP 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches      3:  Conservative      0:  Mismatches      0:  Indels      0:  Gaps      0:
QY          2 PKT 4
DE          1
SQ          9 PKT 11

Query Match:          27.3% Score 3:  DP 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches      3:  Conservative      0:  Mismatches      0:  Indels      0:  Gaps      0:
QY          2 PKT 4
DE          1
SQ          9 PKT 11

RESULT 4:
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ID Q1774 PRELIMINARY:  PK1:  13 AA.
AC Q1774
DT 01-NOV-1996 (FEBMRE01.01, Created)
DI 01-NOV-1996 (FEBMRE01.01, Last sequence update)
DE 01-OCT-2002 (FEBMRE01.22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID:11103
RN SEQUENCE FROM N.A.
RS STRAIN:39
RX MEDLINE:9227424; PubMed:1317578;
RA Buch J., Purcell R.H., Miller R.H.
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC -1- SUBMIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84856; AAA45698.1
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON-TER          13
SQ SEQUENCE  13 AA: 1559 MW: 455405E1A42FC7E3 CRC64;

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DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON-TER          13
SQ SEQUENCE  13 AA: 1557 MW: 45405E1A42FC7E3 CRC64;

Query Match:          27.3% Score 3:  DP 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
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DE          1
SQ          9 PKT 11

Query Match:          27.3% Score 3:  DP 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches      3:  Conservative      0:  Mismatches      0:  Indels      0:  Gaps      0:
QY          2 PKT 4
DE          1
SQ          9 PKT 11

RESULT 4:
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ID Q1773 PRELIMINARY:  PK1:  13 AA.
AC Q1773
DT 01-NOV-1996 (FEBMRE01.01, Created)
DI 01-NOV-1996 (FEBMRE01.01, Last sequence update)
DE 01-OCT-2002 (FEBMRE01.22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID:11103
RN SEQUENCE FROM N.A.
RS STRAIN:39
RX MEDLINE:9227424; PubMed:1317578;
RA Buch J., Purcell R.H., Miller R.H.
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*

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Best Local Similarity: 100.00% Pred. No. 34  
Matches: 31 Conservative: 01 Mismatches: 01 Labels: 01 Gaps: 00

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111  
DL 9 R81 2

Search Completed: September 30, 2003, 11:06:54  
File Name: 06\_6667\_S005

GenCafe version 5.1.2  
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CM protein: protein search using SW model

Run on: September 30, 2003, 10:02:33, Search time: 11:03:33 seconds  
(without alignment) updates/sec  
49,411,111.6

Title: US-09-787-443-14

Perfect score: 11

Sequence: 1 ARMTREKSKD 11

Scoring table: G1G0

Gapop 66.6, Gapext 60.0

Searched: 16717 seqs, 421058 residues

Word size: 3

Total number of hits satisfying chosen parameters: 78/09

Minimum hit seq length: 8

Maximum hit seq length: 15

Post-processing: listing first 500 summaries

Database: Issued\_Patents\_AA\*

1: /cqn2\_6/ptodata/1/aa/5A/08Ms.pep\*

2: /cqn2\_6/ptodata/1/aa/5B/08Mb.pep\*

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6: /cqn2\_6/ptodata/1/aa/backres\_08b.pep\*

Prod. No. is the number of results predicted by chain 4  
Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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1	4	36.4	8	1	US-08-483-415-9	Sequence 7, Appl
2	4	36.4	8	1	US-08-483-415-9	Sequence 57, App
3	4	36.4	8	2	US-08-483-415-9	Sequence 4, Appl
4	4	36.4	8	4	US-08-483-415-9	Sequence 23, App
5	4	36.4	8	3	US-08-483-415-9	Sequence 40, App
6	4	36.4	8	3	US-08-483-415-9	Sequence 57, App
7	4	36.4	8	3	US-08-483-415-9	Sequence 57, App
8	4	36.4	8	4	US-08-483-415-9	Sequence 18, Appl
9	4	36.4	8	4	US-08-483-415-9	Sequence 39, Appl
10	4	36.4	8	4	US-08-483-415-9	Sequence 64, App
11	4	36.4	8	4	US-08-483-415-9	Sequence 91, App
12	4	36.4	8	4	US-08-483-415-9	Sequence 111, App
13	4	36.4	8	4	US-08-483-415-9	Sequence 111, App
14	4	36.4	8	6	PCT/US93/02118	Patent No. 547984
15	4	36.4	9	2	US-08-483-415-9	Sequence 10, Appl
16	4	36.4	9	2	US-08-483-415-9	Sequence 10, Appl
17	4	36.4	9	3	US-08-483-415-9	Sequence 9, Appl
18	4	36.4	9	3	US-08-483-415-9	Sequence 27, Appl
19	4	36.4	9	3	US-08-483-415-9	Sequence 44, Appl
20	4	36.4	9	3	US-08-483-415-9	Sequence 51, Appl
21	4	36.4	9	3	US-08-483-415-9	Sequence 60, Appl
22	4	36.4	9	3	US-08-483-415-9	Sequence 70, Appl
23	4	36.4	9	4	US-08-483-415-9	Sequence 41, Appl
24	4	36.4	9	4	US-08-483-415-9	Sequence 58, Appl
25	4	36.4	9	4	US-08-483-415-9	Sequence 75, Appl
26	4	36.4	9	4	US-08-483-415-9	Sequence 94, Appl
27	4	36.4	9	4	US-08-483-415-9	Sequence 112, App

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31	4	36.4	11	3	US-08-810-324-46	Sequence 16, Appl
32	4	36.4	11	3	US-08-679-006-16	Sequence 46, Appl
33	4	36.4	11	3	US-08-147-592A-41	Sequence 41, Appl
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36	4	36.4	11	4	US-08-292-694A-46	Sequence 46, Appl
37	4	36.4	11	1	US-08-495-308-2	Sequence 2, Appl
38	4	36.4	11	1	US-07-652-648-1	Sequence 1, Appl
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42	4	36.4	11	1	US-08-259-550A-35	Sequence 35, Appl
43	4	36.4	11	2	US-08-452-724A-38	Sequence 38, Appl
44	4	36.4	11	2	US-08-373-190-48	Sequence 48, Appl
45	4	36.4	11	2	US-08-481-337A-17	Sequence 17, Appl
46	4	36.4	11	2	US-08-147-777-4	Sequence 4, Appl
47	4	36.4	11	2	US-08-461-216-7	Sequence 7, Appl
48	4	36.4	11	2	US-08-350-260A-467	Sequence 467, App
49	4	36.4	11	2	US-08-438-190A-48	Sequence 48, Appl
50	4	36.4	11	2	US-08-232-539D-21	Sequence 21, Appl
51	4	36.4	11	2	US-08-696-268B-7	Sequence 7, Appl
52	4	36.4	11	2	US-08-464-025A-2	Sequence 2, Appl
53	4	36.4	11	3	US-08-350-215-48	Sequence 48, Appl
54	4	36.4	11	3	US-08-616-854-3	Sequence 3, Appl
55	4	36.4	11	3	US-08-466-151-10	Sequence 10, Appl
56	4	36.4	11	3	US-08-466-151-27	Sequence 27, Appl
57	4	36.4	11	3	US-08-925-002-21	Sequence 21, Appl
58	4	36.4	11	3	US-08-452-872-4	Sequence 4, Appl
59	4	36.4	11	3	US-08-118-055-1	Sequence 1, Appl
60	4	36.4	11	3	US-08-287-145A-48	Sequence 48, Appl
61	4	36.4	11	3	US-08-863-813A-17	Sequence 17, Appl
62	4	36.4	11	3	US-08-863-813A-28	Sequence 28, Appl
63	4	36.4	11	3	US-09-288-061-2	Sequence 2, Appl
64	4	36.4	11	3	US-08-160-604-65	Sequence 65, Appl
65	4	36.4	11	3	US-08-160-604-66	Sequence 66, Appl
66	4	36.4	11	3	US-08-160-604-67	Sequence 67, Appl
67	4	36.4	11	3	US-08-160-604-68	Sequence 68, Appl
68	4	36.4	11	3	US-08-160-604-69	Sequence 69, Appl
69	4	36.4	11	3	US-08-160-604-70	Sequence 70, Appl
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71	4	36.4	11	3	US-08-676-318A-28	Sequence 28, Appl
72	4	36.4	11	3	US-08-582-333A-87	Sequence 87, Appl
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74	4	36.4	11	3	US-09-101-649-44	Sequence 44, Appl
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76	4	36.4	11	3	US-09-556-111-48	Sequence 48, Appl
77	4	36.4	11	3	US-08-466-163B-10	Sequence 10, Appl
78	4	36.4	11	3	US-08-466-163B-27	Sequence 27, Appl
79	4	36.4	11	3	US-08-723-661B-7	Sequence 7, Appl
80	4	36.4	11	3	US-09-315-304B-815	Sequence 815, App
81	4	36.4	11	3	US-09-305-923A-6	Sequence 1545, App
82	4	36.4	11	3	US-09-451-034-1	Sequence 6, Appl
83	4	36.4	11	3	US-08-255-208A-74	Sequence 1, Appl
84	4	36.4	11	3	US-08-988-842-38	Sequence 74, Appl
85	4	36.4	11	3	US-09-670-075A-1	Sequence 38, Appl
86	4	36.4	11	3	US-09-104-333A-467	Sequence 1, Appl
87	4	36.4	11	3	US-09-101-272G-42	Sequence 42, Appl
88	4	36.4	11	3	US-09-101-272G-45	Sequence 45, Appl
89	4	36.4	11	3	US-08-695-692B-15	Sequence 15, Appl
90	4	36.4	11	3	US-08-695-692B-16	Sequence 16, Appl
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92	4	36.4	11	3	US-09-367-777-75	Sequence 75, Appl
93	4	36.4	11	3	US-09-367-777-108	Sequence 108, App
94	4	36.4	11	3	US-09-834-784-815	Sequence 815, App
95	4	36.4	11	3	US-09-308-437A-1	Sequence 1, Appl
96	4	36.4	11	3	US-08-932-411A-28	Sequence 28, Appl
97	4	36.4	11	3	US-09-367-791A-83	Sequence 83, Appl
98	4	36.4	11	3	US-09-367-791A-83	Sequence 83, Appl
99	4	36.4	11	3	PCT/US93-03985-4	Sequence 4, Appl
100	4	36.4	11	3	US-09-367-791A-83	Patent No. 5436138





247	3	27.3	16	2	US-08-436-322-79	Sequence 9, Appl	320	3	27.3	10	5	PCT US94-02531-66	Sequence 66, Appl
248	3	27.3	10	2	US-08-436-322-79	Sequence 10, Appl	321	3	27.3	10	5	PCT US95-03246-6	Sequence 6, Appl
249	3	27.3	10	2	US-08-436-322-79	Sequence 17, Appl	322	3	27.3	10	5	5168045-8	Patent No. 5168045
250	3	27.3	10	2	US-08-436-322-79	Sequence 9, Appl	323	3	27.3	10	5	517189-10	Patent No. 517189
251	3	27.3	10	2	US-08-436-322-79	Sequence 18, Appl	324	3	27.3	10	5	5182364-11	Patent No. 5182364
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253	3	27.3	10	2	US-08-436-322-79	Sequence 65, Appl	326	3	27.3	10	5	US-07-851-941-18	Sequence 18, Appl
254	3	27.3	10	2	US-08-436-322-79	Sequence 71, Appl	327	3	27.3	10	5	US-08-185-448-5	Sequence 5, Appl
255	3	27.3	10	2	US-08-436-322-79	Sequence 17, Appl	328	3	27.3	10	5	US-08-450-505-1	Sequence 1, Appl
256	3	27.3	10	2	US-08-436-322-79	Sequence 17, Appl	329	3	27.3	10	5	US-08-428-488-17	Sequence 17, Appl
257	3	27.3	10	2	US-08-436-322-79	Sequence 25, Appl	330	3	27.3	10	5	US-08-255-771-27	Sequence 27, Appl
258	3	27.3	10	2	US-08-436-322-79	Sequence 6, Appl	331	3	27.3	10	5	US-08-445-745-122	Sequence 122, Appl
259	3	27.3	10	2	US-08-436-322-79	Sequence 11, Appl	332	3	27.3	10	5	US-08-615-181-84	Sequence 84, Appl
260	3	27.3	10	2	US-08-436-322-79	Sequence 75, Appl	333	3	27.3	10	5	US-08-191-338A-33	Sequence 15, Appl
261	3	27.3	10	2	US-08-436-322-79	Sequence 22, Appl	334	3	27.3	10	5	US-08-408-604A-35	Sequence 34, Appl
262	3	27.3	10	2	US-08-436-322-79	Sequence 42, Appl	335	3	27.3	10	5	US-08-468-604A-79	Sequence 79, Appl
263	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	336	3	27.3	10	5	US-08-633-760-37	Sequence 37, Appl
264	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	337	3	27.3	10	5	US-08-181-984-31	Sequence 31, Appl
265	3	27.3	10	2	US-08-436-322-79	Sequence 20, Appl	338	3	27.3	10	5	US-08-737-085A-12	Sequence 12, Appl
266	3	27.3	10	2	US-08-436-322-79	Sequence 15, Appl	339	3	27.3	10	5	US-07-737-371E-73	Sequence 73, Appl
267	3	27.3	10	2	US-08-436-322-79	Sequence 29, Appl	340	3	27.3	10	5	US-08-466-975A-3	Sequence 3, Appl
268	3	27.3	10	2	US-08-436-322-79	Sequence 4, Appl	341	3	27.3	10	5	US-08-391-671A-3	Sequence 3, Appl
269	3	27.3	10	2	US-08-436-322-79	Sequence 1, Appl	342	3	27.3	10	5	US-08-747-137-63	Sequence 63, Appl
270	3	27.3	10	2	US-08-436-322-79	Sequence 10, Appl	343	3	27.3	10	5	US-08-482-228-200	Sequence 200, Appl
271	3	27.3	10	2	US-08-436-322-79	Sequence 69, Appl	344	3	27.3	10	5	US-08-751-767A-29	Sequence 29, Appl
272	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	345	3	27.3	10	5	US-04-115-209-74	Sequence 74, Appl
273	3	27.3	10	2	US-08-436-322-79	Sequence 8, Appl	346	3	27.3	10	5	US-08-467-902A-3	Sequence 3, Appl
274	3	27.3	10	2	US-08-436-322-79	Sequence 9, Appl	347	3	27.3	10	5	US-08-482-258-200	Sequence 200, Appl
275	3	27.3	10	2	US-08-436-322-79	Sequence 13, Appl	348	3	27.3	10	5	US-08-246-258-12	Sequence 12, Appl
276	3	27.3	10	2	US-08-436-322-79	Sequence 11, Appl	349	3	27.3	10	5	US-08-444-818-105	Sequence 105, Appl
277	3	27.3	10	2	US-08-436-322-79	Sequence 21, Appl	350	3	27.3	10	5	US-08-392-542-4	Sequence 4, Appl
278	3	27.3	10	2	US-08-436-322-79	Sequence 20, Appl	351	3	27.3	10	5	US-08-392-542-13	Sequence 13, Appl
279	3	27.3	10	2	US-08-436-322-79	Sequence 65, Appl	352	3	27.3	10	5	US-08-602-999A-283	Sequence 283, Appl
280	3	27.3	10	2	US-08-436-322-79	Sequence 75, Appl	353	3	27.3	10	5	US-08-652-877-73	Sequence 73, Appl
281	3	27.3	10	2	US-08-436-322-79	Sequence 31, Appl	354	3	27.3	10	5	US-09-208-966-3	Sequence 3, Appl
282	3	27.3	10	2	US-08-436-322-79	Sequence 29, Appl	355	3	27.3	10	5	US-08-647-405B-3	Sequence 3, Appl
283	3	27.3	10	2	US-08-436-322-79	Sequence 20, Appl	356	3	27.3	10	5	US-08-647-405B-4	Sequence 4, Appl
284	3	27.3	10	2	US-08-436-322-79	Sequence 1, Appl	357	3	27.3	10	5	US-08-647-405B-6	Sequence 5, Appl
285	3	27.3	10	2	US-08-436-322-79	Sequence 17, Appl	358	3	27.3	10	5	US-09-177-249-212	Sequence 212, Appl
286	3	27.3	10	2	US-08-436-322-79	Sequence 75, Appl	359	3	27.3	10	5	US-09-177-249-253	Sequence 253, Appl
287	3	27.3	10	2	US-08-436-322-79	Sequence 31, Appl	360	3	27.3	10	5	US-08-476-515A-73	Sequence 73, Appl
288	3	27.3	10	2	US-08-436-322-79	Sequence 20, Appl	361	3	27.3	10	5	US-08-894-327-4	Sequence 4, Appl
289	3	27.3	10	2	US-08-436-322-79	Sequence 45, Appl	362	3	27.3	10	5	US-08-894-327-14	Sequence 14, Appl
290	3	27.3	10	2	US-08-436-322-79	Sequence 1, Appl	363	3	27.3	10	5	US-09-532-105-12	Sequence 12, Appl
291	3	27.3	10	2	US-08-436-322-79	Sequence 40, Appl	364	3	27.3	10	5	US-09-275-265-4	Sequence 4, Appl
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293	3	27.3	10	2	US-08-436-322-79	Sequence 14, Appl	366	3	27.3	10	5	US-09-311-626B-30	Sequence 30, Appl
294	3	27.3	10	2	US-08-436-322-79	Sequence 58, Appl	367	3	27.3	10	5	US-09-685-027-4	Sequence 4, Appl
295	3	27.3	10	2	US-08-436-322-79	Sequence 30, Appl	368	3	27.3	10	5	US-09-685-027-14	Sequence 14, Appl
296	3	27.3	10	2	US-08-436-322-79	Sequence 25, Appl	369	3	27.3	10	5	US-09-500-124-283	Sequence 283, Appl
297	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	370	3	27.3	10	5	US-09-255-208A-77	Sequence 77, Appl
298	3	27.3	10	2	US-08-436-322-79	Sequence 31, Appl	371	3	27.3	10	5	PCT US91-08328-33	Sequence 13, Appl
299	3	27.3	10	2	US-08-436-322-79	Sequence 42, Appl	372	3	27.3	10	5	PCT US91-08328-34	Sequence 14, Appl
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301	3	27.3	10	2	US-08-436-322-79	Sequence 28, Appl	374	3	27.3	10	5	PCT US91-08328-18	Sequence 18, Appl
302	3	27.3	10	2	US-08-436-322-79	Sequence 65, Appl	375	3	27.3	10	5	PCT US91-08328-20	Sequence 20, Appl
303	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	376	3	27.3	10	5	PCT US91-08328-30	Sequence 30, Appl
304	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	377	3	27.3	10	5	US-09-941-611-3	Sequence 3, Appl
305	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	378	3	27.3	10	5	US-09-265-222-16	Sequence 16, Appl
306	3	27.3	10	2	US-08-436-322-79	Sequence 42, Appl	379	3	27.3	10	5	PCT US91-08328-33	Sequence 13, Appl
307	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	380	3	27.3	10	5	PCT US91-08328-34	Sequence 14, Appl
308	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	381	3	27.3	10	5	PCT US91-08328-16	Sequence 16, Appl
309	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	382	3	27.3	10	5	PCT US91-08328-18	Sequence 18, Appl
310	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	383	3	27.3	10	5	PCT US91-08328-20	Sequence 20, Appl
311	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	384	3	27.3	10	5	PCT US92-09070-10	Sequence 10, Appl
312	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	385	3	27.3	10	5	PCT US93-09626-33	Sequence 33, Appl
313	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	386	3	27.3	10	5	5187155-26	Patent No. 5187155
314	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	387	3	27.3	10	5	5190919-10	Patent No. 5190919
315	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	388	3	27.3	10	5	52254-12	Patent No. 52254
316	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	389	3	27.3	10	5	US-07-778-233B-35	Sequence 35, Appl
317	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	390	3	27.3	10	5	US-07-778-233B-42	Sequence 42, Appl
318	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	391	3	27.3	10	5	US-07-844-902-4	Sequence 4, Appl
319	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	392	3	27.3	10	5	US-07-964-321-35	Sequence 35, Appl
320	3	27.3	10	2	US-08-436-322-79	Sequence 76, Appl	393	3	27.3	10	5	US-07-964-321-41	Sequence 41, Appl



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1  REFERENCE/DOCKET NUMBER: 2000-050111
2  TELECOMMUNICATION INFORMATION:
3  TELEPHONE: (202) 887-1500
4  TELEFAX: (202) 887-0763
5  TELEX: 90 4030 MRSNFORBWSH
6  INFORMATION FOR SEQ ID NO: 9:
7  SEQUENCE CHARACTERISTICS:
8  LENGTH: 8 amino acids
9  TYPE: amino acid
10 STRANDEDNESS: single
11 TOPOLOGY: linear
12 JS 08-403-415-9
13
14 Query Match: 36.4%, Score 4, DB 2, Length 8;
15 Best Local Similarity: 100.0%, Pred. No. 2, Seq-ID: 9;
16 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
17
18 QY 8 KSKG 6
19 1111
20 2 KRG 5
21
22 RESULT 4:
23 US-08-978-404B-57
24 Sequence 57, Application US/08078404P
25 Patent No. 5968762
26 GENERAL INFORMATION:
27 APPLICANT: STEVENS, RICHARD L.
28 TITLE OF INVENTION: MASS CELL RELEASE AND CLEAVAGE
29 TITLE OF INVENTION: FIBRINOGEN
30 NUMBER OF SEQUENCES: 74
31 CORRESPONDENCE ADDRESS:
32 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
33 STREET: 600 Atlantic Avenue
34 CITY: Boston
35 STATE: MA
36 COUNTRY: U.S.A.
37 FILING DATE: April 22, 1994
38 COMPUTER READABLE FORM:
39 MEDIUM TYPE: Diskette
40 COMPUTER: IBM PC compatible
41 OPERATING SYSTEM: DOS
42 SOFTWARE: FASTSEQ for Windows version 2.0
43 CURRENT APPLICATION DATA:
44 APPLICATION NUMBER: US/08/978,404B
45 FILING DATE: 25-NOV-97
46 CLASSIFICATION: 435
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: 60/232,003
49 FILING DATE: 04 DEC 1996
50 ATTORNEY/AGENT INFORMATION:
51 NAME: Plomer, Elizabeth H.
52 REGISTRATION NUMBER: 36,547
53 REFERENCE/DOCKET NUMBER: 08071709
54 TELECOMMUNICATION INFORMATION:
55 TELEPHONE: 617-720-3500
56 TELEFAX: 617-720-2441
57
58 INFORMATION FOR SEQ ID NO: 57:
59 SEQUENCE CHARACTERISTICS:
60 LENGTH: 8 amino acids
61 TYPE: amino acid
62 STRANDEDNESS: single
63 TOPOLOGY: linear
64 MESSAGE TYPE: linear
65 US-08-978-404B-57
66
67 Query Match: 36.4%, Score 4, DB 2, Length 8;
68 Best Local Similarity: 100.0%, Pred. No. 2, Seq-ID: 57;
69 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
70
71 QY 7 KSKG 10
72 1111
73
74 RESULT 3:
75 US-06-318-B56A-4
76 Sequence 4, Application US/0611856A
77 Patent No. 5972451
78 GENERAL INFORMATION:
79 APPLICANT: ADRIAN V.S. HILL, et al.
80 TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I*
81 TITLE OF INVENTION: RESTRICTED CELL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAG
82 TITLE OF INVENTION: ANTIGENS (AS AMENDED)
83 NUMBER OF SEQUENCES: 86
84 CORRESPONDENCE ADDRESS:
85 ADDRESSEE: Woodstock, Lind & Ponack, L.L.P.
86 STREET: 233 K Street, N.W., Suite 900
87 CITY: Washington
88 STATE: D.C.
89 COUNTRY: U.S.A.
90 ZIP: 20006
91 COMPUTER READABLE FORM:
92 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
93 COMPUTER: IBM PC compatible
94 OPERATING SYSTEM: PC-DOS/MS-DOS
95 SOFTWARE: WordPerfect 5.11
96 CURRENT APPLICATION DATA:
97 APPLICATION NUMBER: US/06/318,856A
98 FILING DATE: October 3, 1994
99 PRIOR APPLICATION DATA:
100 APPLICATION NUMBER: 06-92-08 068,8
101 FILING DATE: April 4, 1992
102 PRIOR APPLICATION DATA:
103 APPLICATION NUMBER: 06-92-17 704,7
104 FILING DATE: August 20, 1992
105 PRIOR APPLICATION DATA:
106 APPLICATION NUMBER: WO PCT/GB93/00711
107 FILING DATE: April 9, 1994
108 ATTORNEY/AGENT INFORMATION:
109 NAME: Lee Cheng
110 REGISTRATION NUMBER: 40,549
111 REFERENCE/DOCKET NUMBER: 265 PPIR157705
112 TELECOMMUNICATION INFORMATION:
113 TELEPHONE: (202) 721-8200
114 TELEFAX: (202) 721-8250
115 INFORMATION FOR SEQ ID NO: 4:
116 SEQUENCE CHARACTERISTICS:
117 LENGTH: 8 amino acid residues
118 TYPE: amino acid
119 STRANDEDNESS: single
120 TOPOLOGY: linear
121 MESSAGE TYPE: peptide
122 ORIGINAL SOURCE:
123 ORGANISM: Plasmodium falciparum
124 US-06-318-B56A-4
125
126 Query Match: 46.4%, Score 4, DB 2, Length 8;
127 Best Local Similarity: 100.0%, Pred. No. 2, Seq-ID: 4;
128 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
129
130 QY 8 KSKG 11
131 1111
132 1 KSKD 4
133
134 RESULT 4:
135 US-09-105-B49D-25
136 Sequence 25, Application US/09105839D
137 Patent No. 6287556
138 GENERAL INFORMATION:
139 APPLICANT: Tarelli, Oreste
140 APPLICANT: Chen, Yaw-Tsong
141 APPLICANT: Sakai, Tqur
142 APPLICANT: Goto, Ali

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1 APPLICANT: Old, Lloyd J
2 APPLICANT: Freundschuh, Michael
3 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
4 TITLE REFERENCE: LUD 5556
5 CURRENT APPLICATION NUMBER: US/09/105,839D
6 PRIOR FILING DATE: 1998-06-26
7 PRIOR FILING DATE: 1997-05-05
8 NUMBER OF SEQ ID NOS: 72
9 SEQ ID NO 25
10 LENGTH: 8
11 TYPE: PRT
12 ORGANISM: Homo sapiens
13 US-09-105-839D-25

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Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KERN 8
LD 111
3 KERN 5

RESULT 5
US-09-105-839D-40
1 Sequence 40, Application US/09/105,839D
2 Patent No. 6287756
3 GENERAL INFORMATION:
4 APPLICANT: Tureci, Ozlem
5 APPLICANT: Chen, Yao-Tsong
6 APPLICANT: Sahin, Ugur
7 APPLICANT: Gure, Ali
8 APPLICANT: Old, Lloyd J
9 APPLICANT: Freundschuh, Michael
10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
11 FILE REFERENCE: LUD 5556
12 CURRENT APPLICATION NUMBER: US/09/105,839D
13 CURRENT FILING DATE: 1998-06-26
14 PRIOR FILING DATE: 1997-05-05
15 NUMBER OF SEQ ID NOS: 72
16 SEQ ID NO 40
17 LENGTH: 8
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-09-105-839D-40

Query Match: 36.4%, Score 41, DB 3, Length 8;
Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KERN 8
LD 111
3 KERN 5

RESULT 6
US-09-105-839D-57
1 Sequence 57, Application US/09/105,839D
2 Patent No. 6287756
3 GENERAL INFORMATION:
4 APPLICANT: Tureci, Ozlem
5 APPLICANT: Chen, Yao-Tsong
6 APPLICANT: Sahin, Ugur
7 APPLICANT: Gure, Ali
8 APPLICANT: Old, Lloyd J
9 APPLICANT: Freundschuh, Michael
10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
11 FILE REFERENCE: LUD 5556
12 CURRENT APPLICATION NUMBER: US/09/105,839D
13 CURRENT FILING DATE: 1998-06-26
14 PRIOR FILING DATE: 1997-05-05
15 NUMBER OF SEQ ID NOS: 72
16 SEQ ID NO 57
17 LENGTH: 8
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-09-105-839D-57

Query Match: 36.4%, Score 41, DB 3, Length 8;
Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KERN 8
LD 111
3 KERN 5

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1 CURRENT APPLICATION NUMBER: US/09/105,839D
2 CURRENT FILING DATE: 1998-06-26
3 PRIOR APPLICATION NUMBER: US 08/851,130
4 PRIOR FILING DATE: 1997-05-05
5 NUMBER OF SEQ ID NOS: 72
6 SEQ ID NO 57
7 LENGTH: 8
8 TYPE: PRT
9 ORGANISM: Homo sapiens
10 US-09-105-839D-57

Query Match: 36.4%, Score 41, DB 3, Length 8;
Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KERN 8
LD 111
3 KERN 6

RESULT 7
US-09-105-839D-69
1 Sequence 69, Application US/09/105,839D
2 Patent No. 6287756
3 GENERAL INFORMATION:
4 APPLICANT: Tureci, Ozlem
5 APPLICANT: Chen, Yao-Tsong
6 APPLICANT: Sahin, Ugur
7 APPLICANT: Gure, Ali
8 APPLICANT: Old, Lloyd J
9 APPLICANT: Freundschuh, Michael
10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Dete
11 FILE REFERENCE: LUD 5556
12 CURRENT APPLICATION NUMBER: US/09/105,839D
13 CURRENT FILING DATE: 1998-06-26
14 PRIOR APPLICATION NUMBER: US 08/851,130
15 PRIOR FILING DATE: 1997-05-05
16 NUMBER OF SEQ ID NOS: 72
17 SEQ ID NO 69
18 LENGTH: 8
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-105-839D-69

Query Match: 36.4%, Score 41, DB 3, Length 8;
Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KERN 8
LD 111
3 KERN 6

RESULT 8
US-09-105-839D-18
1 Sequence 18, Application US/08/197484
2 Patent No. 641343
3 GENERAL INFORMATION:
4 APPLICANT: Vitteillo, Maria A.
5 APPLICANT: CHESTNET, Robert W.
6 APPLICANT: SETTE, Alessandro D.
7 APPLICANT: CELIS, Esteban
8 APPLICANT: GRAY, Howard
9 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
10 NUMBER OF SEQUENCES: 153
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Townsend and Townsend Koorse and Crew
13 STREET: Stewart Street Tower, One Market Plaza
14 CITY: San Francisco
15 STATE: California
16 COUNTRY: US

```

1 ZFILE 94105-1493  
 2 COMPILER READABLE FORM:  
 3 MEDIUM TYPE: Floppy disk  
 4 OPERATING SYSTEM: PC-DOS/MS-DOS  
 5 SOFTWARE: Patent In Release 4.1.0, Version 1.1.2  
 6 CURRENT APPLICATION DATA:  
 7 APPLICATION NUMBER: US/09/144,040  
 8 FILING DATE: 16-FEB-1994  
 9 CLASSIFICATION: 424  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: US 07/744,564  
 12 FILING DATE: 26-AUG-1992  
 13 PRIOR APPLICATION DATA:  
 14 APPLICATION NUMBER: US 07/874,491  
 15 FILING DATE: 27-APR-1992  
 16 PRIOR APPLICATION DATA:  
 17 APPLICATION NUMBER: US 07/827,062  
 18 FILING DATE: 29-JAN-1992  
 19 PRIOR APPLICATION DATA:  
 20 APPLICATION NUMBER: US 07/774,564  
 21 FILING DATE: 26-AUG-1991  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: Parmelee, Steven W.  
 24 REGISTRATION NUMBER: 31,993  
 25 TELECOMMUNICATION INFORMATION:  
 26 TELEPHONE: (206) 467-9609  
 27 TELEFAX: (206) 624-6793  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 8 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: unknown  
 33 TOPOLGY: unknown  
 34 REFERENCE TYPE: peptide  
 35 US 08-177 484 18

Query Match 36.4% Score 4: DB 4: Length 8:  
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QY 8 KSKD 1:  
 DB 1 KSKD 4

RESULT 1:  
 1 US-09-344-040C-91  
 2 Sequence 9: Application US/09-44-040C  
 3 Patent No. 6548664  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureceli, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 APPLICANT: Ramensee, Hans Georg  
 9 APPLICANT: Stevanovic, Stefan  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin  
 11 TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a  
 12 TITLE OF INVENTION: Gene, and Uses Thereof  
 13 FILE REFERENCE: IUD 5556.1  
 14 CURRENT APPLICATION NUMBER: US/09/144,040C  
 15 CURRENT FILING DATE: 1999-06-25  
 16 PRIOR APPLICATION NUMBER: US 09/105,839  
 17 PRIOR FILING DATE: 1998-06-26  
 18 PRIOR APPLICATION NUMBER: US 06/851,130  
 19 PRIOR FILING DATE: 1997-05-05  
 20 NUMBER OF SEQ ID NOS: 132  
 21 SEQ ID NO 39  
 22 LENGTH: 8  
 23 TYPE: PRI  
 24 ORGANISM: Homo sapiens  
 25 US 09-344 040C-91

Query Match 36.4% Score 4: DB 4: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 5 REPK 8  
 DB 3 REPK 6  
 RESULT 1:  
 1 US-09-344-040C-91  
 2 Sequence 9: Application US/09-44-040C  
 3 Patent No. 6548664  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureceli, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 APPLICANT: Ramensee, Hans Georg  
 9 APPLICANT: Stevanovic, Stefan  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin  
 11 TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene  
 12 TITLE OF INVENTION: Gene, and Uses Thereof  
 13 FILE REFERENCE: IUD 5556.1  
 14 CURRENT APPLICATION NUMBER: US/09/144,040C  
 15 CURRENT FILING DATE: 1999-06-25  
 16 PRIOR APPLICATION NUMBER: US 09/105,839  
 17 PRIOR FILING DATE: 1998-06-26  
 18 PRIOR APPLICATION NUMBER: US 06/851,130  
 19 PRIOR FILING DATE: 1997-05-05  
 20 NUMBER OF SEQ ID NOS: 132  
 21 SEQ ID NO 64  
 22 LENGTH: 8  
 23 TYPE: PRI  
 24 ORGANISM: Homo sapiens  
 25 US 09-344-040C-91

Query Match 36.4% Score 4: DB 4: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 REPK 8  
 DB 3 REPK 6

RESULT 1:  
 1 US-09-344-040C-91  
 2 Sequence 9: Application US/09-44-040C  
 3 Patent No. 6548664  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureceli, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 APPLICANT: Ramensee, Hans Georg  
 9 APPLICANT: Stevanovic, Stefan  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin  
 11 TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene  
 12 TITLE OF INVENTION: Gene, and Uses Thereof  
 13 FILE REFERENCE: IUD 5556.1  
 14 CURRENT APPLICATION NUMBER: US/09/144,040C  
 15 CURRENT FILING DATE: 1999-06-25  
 16 PRIOR APPLICATION NUMBER: US 09/105,839  
 17 PRIOR FILING DATE: 1998-06-26  
 18 PRIOR APPLICATION NUMBER: US 06/851,130  
 19 PRIOR FILING DATE: 1997-05-05  
 20 NUMBER OF SEQ ID NOS: 132  
 21 SEQ ID NO 91  
 22 LENGTH: 8  
 23 TYPE: PRI  
 24 ORGANISM: Homo sapiens  
 25 US-09-344-040C-91







US-09-787-443-14-A 9

Query Match 36.4%, Score 4, DB 3, Length 9;  
 Best Local Similarity 100.0%, Prod. No. 2.5e+05;  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 29  
 US-09-105-8390-50  
 1 Sequence 51, Application: US/09/105-8390-50  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tsung  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for determining presence of cancer in a sample by detecting expression of an SSX gene  
 11 FILE REFERENCE: L00 5556  
 12 CURRENT APPLICATION NUMBER: US/09/105-8390  
 13 PRIOR FILING DATE: 1998-06-26  
 14 PRIOR APPLICATION NUMBER: US 08/851,140  
 15 NUMBER OF SEQ ID NOS: 72  
 16 SEQ ID NO 27  
 17 LENGTH: 9  
 18 TYPE: PRT  
 19 ORGANISM: Homo sapiens  
 20 US 09-105-8390-50

Query Match 36.4%, Score 4, DB 3, Length 9;  
 Best Local Similarity 100.0%, Prod. No. 2.5e+05;  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 29  
 US-09-105-8390-50  
 1 Sequence 44, Application: US/09/105-8390-50  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tsung  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for determining presence of cancer in a sample by detecting expression of an SSX gene  
 11 FILE REFERENCE: L00 5556  
 12 CURRENT APPLICATION NUMBER: US/09/105-8390  
 13 PRIOR FILING DATE: 1998-06-26  
 14 PRIOR APPLICATION NUMBER: US 08/851,140  
 15 NUMBER OF SEQ ID NOS: 72  
 16 SEQ ID NO 44  
 17 LENGTH: 9  
 18 TYPE: PRT  
 19 ORGANISM: Homo sapiens  
 20 US 09-105-8390-50

Query Match 36.4%, Score 4, DB 3, Length 9;  
 Best Local Similarity 100.0%, Prod. No. 2.5e+05;  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 29  
 US-09-105-8390-50  
 1 Sequence 51, Application: US/09/105-8390-50  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tsung  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for determining presence of cancer in a sample by detecting expression of an SSX gene  
 11 FILE REFERENCE: L00 5556  
 12 CURRENT APPLICATION NUMBER: US/09/105-8390  
 13 PRIOR FILING DATE: 1998-06-26  
 14 PRIOR APPLICATION NUMBER: US 08/851,140  
 15 NUMBER OF SEQ ID NOS: 72  
 16 SEQ ID NO 51  
 17 LENGTH: 9  
 18 TYPE: PRT  
 19 ORGANISM: Homo sapiens  
 20 US 09-105-8390-50

Query Match 36.4%, Score 4, DB 3, Length 9;  
 Best Local Similarity 100.0%, Prod. No. 2.5e+05;  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 21  
 US-09-105-8390-50  
 1 Sequence 60, Application: US/09/105-8390-50  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tsung  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for determining presence of cancer in a sample by detecting expression of an SSX gene  
 11 FILE REFERENCE: L00 5556  
 12 CURRENT APPLICATION NUMBER: US/09/105-8390  
 13 PRIOR FILING DATE: 1998-06-26  
 14 PRIOR APPLICATION NUMBER: US 08/851,140  
 15 NUMBER OF SEQ ID NOS: 72  
 16 SEQ ID NO 60  
 17 LENGTH: 9  
 18 TYPE: PRT  
 19 ORGANISM: Homo sapiens  
 20 US 09-105-8390-50

Query Match 36.4%, Score 4, DB 3, Length 9;  
 Best Local Similarity 100.0%, Prod. No. 2.5e+05;  
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

5 KERR B  
 11  
 3 KERR 4

```

RESULT 22
US 09-105-8350 70
: Sequence 70, Application US/091058350
: Patent No. 6287756
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Chen, Yao-Tsung
: APPLICANT: Sahin, Ugur
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Gure, Ali
: APPLICANT: Gid, David J
: APPLICANT: Pfreundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Detecting
: Expression of an SSX Gene
: FILE REFERENCE: L05 5556
: CURRENT FILING DATE: 1998-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 72
: SEQ ID NO 70
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-105-8350 70

Query Match 36.4%, Score 4, DB 4, Length 9;
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 1 PERK 4

RESULT 23
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Gure, Ali
: APPLICANT: Gid, David J
: APPLICANT: Pfreundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Detecting
: Expression of an SSX Gene
: FILE REFERENCE: L05 5556
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 75
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9;
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 1 PERK 4

RESULT 24
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Gure, Ali
: APPLICANT: Gid, David J
: APPLICANT: Pfreundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Detecting
: Expression of an SSX Gene
: FILE REFERENCE: L05 5556
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 75
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9;
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 3 PERK 6

RESULT 25
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Gure, Ali
: APPLICANT: Gid, David J
: APPLICANT: Pfreundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Detecting
: Expression of an SSX Gene
: FILE REFERENCE: L05 5556
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 75
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9;
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 3 PERK 6

RESULT 26
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Gure, Ali
: APPLICANT: Gid, David J
: APPLICANT: Pfreundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Detecting
: Expression of an SSX Gene
: FILE REFERENCE: L05 5556
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 75
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9;
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 3 PERK 6

```

```

Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Torrey, Nathan
APPLICANT: Sahli, Omar
APPLICANT: Pfreundschuh, Michael
APPLICANT: Komensec, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for determining presence of a tumor in a sample by determining
TITLE OF INVENTION: Expression of an SSX gene, peptides derived from said SSX gene a
TITLE OF INVENTION: Gene, and uses thereof
FILE REFERENCE: US 6556.1
CURRENT APPLICATION NUMBER: US/09/444,043
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/05,869
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/05,130
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 132
SEQ ID NO: 94
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US 09-444-043-94

Query Match 36.4% Score 41 Indels 0 Mismatches 0 Gaps 0
Best Local Similarity 100.0% Pred. No. 2 Seqs
Matches 4: Conservative 0 Indels 0 Gaps 0

QY 5 REK# 4
ID 1 REK# 4

RESULT 27
US-09-444-043-112
Sequence 112, Application US/09/444,043
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Torrey, Nathan
APPLICANT: Sahli, Omar
APPLICANT: Pfreundschuh, Michael
APPLICANT: Komensec, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for determining presence of a tumor in a sample by determining
TITLE OF INVENTION: Expression of an SSX gene, peptides derived from said SSX gene a
TITLE OF INVENTION: Gene, and uses thereof
FILE REFERENCE: US 6556.1
CURRENT APPLICATION NUMBER: US/09/444,043
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/05,869
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/05,130
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 132
SEQ ID NO: 112
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US 09-444-043-112

Query Match 36.4% Score 41 Indels 0 Mismatches 0 Gaps 0
Best Local Similarity 100.0% Pred. No. 2 Seqs
Matches 4: Conservative 0 Indels 0 Gaps 0

QY 5 REK# 8
ID 1 REK# 4

RESULT 28
US 09-808-277A-43
Sequence 43, Application US/98/08,277A
Patent No. 5998374

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GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT L.
APPLICANT: LEE, IN-HEE
APPLICANT: ZHANG, CHENGQUAN
TITLE OF INVENTION: GLYASPIRINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1088
COMPUTER READABLE FORM:
REGION TYPE: PRT
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,277A
FILING DATE: 2000-04-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 220002657300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-6168
TELEX:
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: Single
Topology: Linear
US-08-008-277A-43

Query Match 40.4% Score 41 DH 2 Length 10
Best Local Similarity 100.0% Pred. No. 1 Seqs
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 REK# 9
ID 1 REK# 6

RESULT 29
US-09-265-222-1
Sequence 1, Application US/09/265,222
Patent No. 6579082
GENERAL INFORMATION:
APPLICANT: Innerarity, Thomas
APPLICANT: Borer, Jan
TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING
TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
TITLE OF INVENTION: L50-PROTEOGLYCAN BINDING
FILE REFERENCE: 220002059700
CURRENT APPLICATION NUMBER: US/09/265,222
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US 60/077,618
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: MURASHIGE

```

1 LOCATION: 1  
2 OTHER INFORMATION: Missense mutation  
US-09-787-443-14

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERKS 7  
1111  
DB 4 ERKS 7

RESULT 50  
US-08-746-006-16  
1 Sequence 50; Application US/08746160  
2 Patent No. 6150500  
3 GENERAL INFORMATION:  
4 APPLICANT: Leherer, Robert L.  
5 APPLICANT: Harwig, Sylvia L.  
6 APPLICANT: Zhao, Chongquan  
7 APPLICANT: Lee, In-Hee  
8 TITLE OF INVENTION: CLAVANINS  
9 NUMBER OF SEQUENCES: 51  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: MORRISON & FORTSTER  
12 STREET: 2000 Pennsylvania Avenue, NW, Suite 1000  
13 CITY: Washington  
14 STATE: DC  
15 COUNTRY: USA  
16 ZIP: 20004-1886  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Diskette  
19 COMPUTER: IBM compatible  
20 OPERATING SYSTEM: DOS  
21 SOFTWARE: FASTSEQ for Windows Version 1.0  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/08/746-160  
24 FILING DATE: 06-NOV-1996  
25 CLASSIFICATION: 510  
26 PRIOR APPLICATION DATA:  
27 APPLICATION NUMBER:  
28 FILING DATE:  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: Morrison, Robert L.  
31 REGISTRATION NUMBER: 24,900  
32 REFERENCE/DOCKET NUMBER: 2200-2500-01  
33 TELECOMMUNICATION INFORMATION:  
34 TELEPHONE: 202-587-3500  
35 TELEFAX: 202-822-0168  
36 INDEX:  
37 INFORMATION FOR SEQ ID NO: 51:  
38 SEQUENCE CHARACTERISTICS:  
39 LENGTH: 11 amino acids  
40 TYPE: amino acid  
41 STRANDEDNESS: single  
42 TOPOLOGY: linear  
43 US-08-746-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9  
1111  
DB 4 ERKS 7

RESULT 41  
US-08-679-006-16  
1 Sequence 41; Application US/08679006  
2 Patent No. 6150500  
3 GENERAL INFORMATION:  
4 APPLICANT: Leherer, Robert L.  
5 APPLICANT: Harwig, Sylvia L.  
6 APPLICANT: Zhao, Chongquan  
7 APPLICANT: Lee, In-Hee  
8 TITLE OF INVENTION: CLAVANINS  
9 NUMBER OF SEQUENCES: 51  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: MORRISON & FORTSTER  
12 STREET: 2000 Pennsylvania Avenue, NW, Suite 1000  
13 CITY: Washington  
14 STATE: DC  
15 COUNTRY: USA  
16 ZIP: 20004-1886  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Diskette  
19 COMPUTER: IBM compatible  
20 OPERATING SYSTEM: DOS  
21 SOFTWARE: FASTSEQ for Windows Version 1.0  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/08/679-006  
24 FILING DATE: 12-JUL-1996  
25 CLASSIFICATION: 514  
26 PRIOR APPLICATION DATA:  
27 APPLICATION NUMBER:  
28 FILING DATE:  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: Brook, David E.  
31 REGISTRATION NUMBER: 24,592  
32 REFERENCE/DOCKET NUMBER: 2200-2500-01  
33 TELECOMMUNICATION INFORMATION:  
34 TELEPHONE: (617) 861-6240  
35 TELEFAX: (617) 861-9540  
36 INDEX:  
37 INFORMATION FOR SEQ ID NO: 16:  
38 SEQUENCE CHARACTERISTICS:  
39 LENGTH: 11 amino acids  
40 TYPE: amino acid  
41 STRANDEDNESS: linear  
42 TOPOLOGY: linear  
43 MOLECULE TYPE: peptide  
44 US-08-679-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9

1 APPLICANT: LEHRER, Robert L.  
2 APPLICANT: ZHAO, Chongquan  
3 APPLICANT: LEE, In-Hee  
4 APPLICANT: HAWIG, SYLVIA L.  
5 TITLE OF INVENTION: CLAVANINS  
6 FILE REFERENCE: 22000-20563-20  
7 CURRENT APPLICATION NUMBER: US/08/679-006  
8 CURRENT FILING DATE: 1997-02-28  
9 EARLIER APPLICATION NUMBER: 08/746-160  
10 EARLIER FILING DATE: 1996-11-06  
11 NUMBER OF SEQ ID NOS: 52  
12 SOFTWARE: PatentIn Ver. 2.0  
13 SEQ ID NO: 46  
14 LENGTH: 11  
15 TYPE: PRT  
16 ORGANISM: Stylota clava  
US-08-679-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9  
1111  
DB 4 ERKS 7

RESULT 42  
US-08-679-006-16  
1 Sequence 42; Application US/08679006  
2 Patent No. 6150500  
3 GENERAL INFORMATION:  
4 APPLICANT: Salernio, John C.  
5 TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF  
6 TITLE OF INVENTION: NOS ISOFORMS  
7 NUMBER OF SEQUENCES: 45  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
10 STREET: Two Millia Drive  
11 CITY: Lexington  
12 STATE: Massachusetts  
13 COUNTRY: USA  
14 ZIP: 02175  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: floppy disk  
17 COMPUTER: IBM PC compatible  
18 OPERATING SYSTEM: DOS/MS DOS  
19 SOFTWARE: PatentIn Release #1.0, Version #1.30  
20 CURRENT APPLICATION DATA:  
21 APPLICATION NUMBER: US/08/679-006  
22 FILING DATE: 12-JUL-1996  
23 CLASSIFICATION: 514  
24 ATTORNEY/AGENT INFORMATION:  
25 NAME: Brook, David E.  
26 REGISTRATION NUMBER: 24,592  
27 REFERENCE/DOCKET NUMBER: 2200-2500-01  
28 TELECOMMUNICATION INFORMATION:  
29 TELEPHONE: (617) 861-6240  
30 TELEFAX: (617) 861-9540  
31 INFORMATION FOR SEQ ID NO: 16:  
32 SEQUENCE CHARACTERISTICS:  
33 LENGTH: 11 amino acids  
34 TYPE: amino acid  
35 STRANDEDNESS: linear  
36 TOPOLOGY: linear  
37 MOLECULE TYPE: peptide  
38 US-08-679-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9

11. 111  
6 PAGES 6

RESULT 34  
US 08/147,592A 41  
Sequence 41: Application US/08/147,592A  
Patent No. 6096543  
GENERAL INFORMATION:  
APPLICANT: BELL, GRADY I  
ATTORNEY: REISNER, JERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: Optical processing methods  
FIELD OF INVENTION: Compositions and Methods  
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,592A  
FILING DATE: 05 Nov 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30 JULY 1993  
CLASSIFICATION: 435

APPLICATION NUMBER: 08/067,296  
FILING DATE: 20 MAY 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARK B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARD 143/WIR  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7977  
TELEX: N/A

INFORMATION FOR SEQUENCE 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
FUNCTION: linear  
Molecular Weight: 1600.00  
US 08/147,592A 41

Quality Match: 66.4% Score: 41 DR: 41 Length: 143  
Best Local Similarity: 100.0% Pctid: No. 190621  
Matches: 41 Conservative 0 Mismatches 0 Indels 0 Gaps 0

94 4 PAGES 7  
95 3 PAGES 6

RESULT 35  
US 08/292,654A 41  
Sequence 41: Application US/08/292,654A  
Patent No. 6119986  
GENERAL INFORMATION:  
APPLICANT: BELL, GRADY I  
ATTORNEY: REISNER, JERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: Optical processing methods  
NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,654A  
FILING DATE: August 19, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/067,296  
FILING DATE: 20 May 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30 JULY 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/147,592  
FILING DATE: 5 Nov 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US94/05747  
FILING DATE: 20 May 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARK B. WILSON  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARD 143/WIR  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 787-2679  
TELEX: 79 0924

INFORMATION FOR SEQUENCE 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
FUNCTION: linear  
Molecular Weight: 1600.00  
US 08/292,654A 41

Quality Match: 66.4% Score: 41 DR: 41 Length: 143  
Best Local Similarity: 100.0% Pctid: No. 190621  
Matches: 41 Conservative 0 Mismatches 0 Indels 0 Gaps 0

94 4 PAGES 7  
95 3 PAGES 6

RESULT 35  
US 08/292,654A 41  
Sequence 41: Application US/08/292,654A  
Patent No. 6119986  
GENERAL INFORMATION:  
APPLICANT: BELL, GRADY I  
ATTORNEY: REISNER, JERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: Optical processing methods  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
MEDIUM TYPE: Floppy disk

US 08/292,654A 41  
Sequence 41: Application US/08/292,654A  
Patent No. 6119986  
GENERAL INFORMATION:  
APPLICANT: BELL, GRADY I  
ATTORNEY: REISNER, JERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: Optical processing methods  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
MEDIUM TYPE: Floppy disk

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1  COMPUTER: IBM PC COMPATIBLE
2  OPERATING SYSTEM: PC-DOS/MS-DOS/ASNT
3  SOFTWARE: Patent Release # 100,000, Version # 1.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/07/292,694A
6  FILING DATE: August 19, 1994
7  CLASSIFICATION: 435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: 08/112,592
10 FILING DATE: 20 May 1994
11 CLASSIFICATION: 435
12 APPLICATION NUMBER: 08/112,592
13 FILING DATE: 20 May 1994
14 CLASSIFICATION: 435
15 APPLICATION NUMBER: 08/112,592
16 FILING DATE: 20 May 1994
17 CLASSIFICATION: 435
18 APPLICATION NUMBER: 08/112,592
19 FILING DATE: 20 May 1994
20 CLASSIFICATION: 435
21 ATTORNEY/AGENT INFORMATION:
22 NAME: MARK D. WILLSON
23 REGISTRATION NUMBER: 47,254
24 REFERENCE/DOCKET NUMBER: AR/112,592 / 0.01
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (612) 428-3000
27 TELEFAX: (612) 428-3000
28 REFERENCE: (612) 428-3000
29 TELEFAX: (612) 428-3000
30 REFERENCE: (612) 428-3000
31 TELEFAX: (612) 428-3000
32 INFORMATION FOR SEQ ID NO: 41:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 13 amino acids
35 TYPE: amino acids
36 TOPOLOGY: linear
37 KTYPE TYPE: protein
38 US 09 292-694A 46
39
40 Query Match:
41 Best Local Similarity: 100.0%, Score 41, DB 1, Length 13,
42 Matches: 41, Conservative 0, Mismatches 0, Indels 0, Gaps 0
43
44 QY 4 DEER 7
45 1 1
46 3 DEER 6
47
48 RESULT 46
49 US 09 292-694 46
50 Sequence 1, Application US/07/292,694
51 Patent No. 5284454
52 GENERAL INFORMATION:
53 APPLICANT: Cori, Gilbert M.
54 APPLICANT: Cori, Gilbert M.
55 TITLE OF INVENTION: Method of using amino acids
56 TITLE OF INVENTION: Method of using amino acids
57 NUMBER OF SEQUENCES: 5
58 CORRESPONDENCE ADDRESS:
59 ADDRESS: Jane Massey Licata, Esq.
60 STREET: 210 Lake Drive East, Suite 201
61 CITY: Cherry Hill
62 STATE: NJ
63 COUNTRY: USA
64 ZIP: 08002
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: DISKETTE, 3 1/2 inch, 1.44 MB
67 OPERATING SYSTEM: WINDOWS 95 WORKGROUP
68 SOFTWARE: WORDPERFECT 5.1
69 CURRENT APPLICATION DATA:
70 APPLICATION NUMBER: US/09/443-14
71 FILING DATE: November 19, 1994
72 CLASSIFICATION: 436
73 PRIOR APPLICATION DATA:
74 APPLICATION NUMBER: 08/112,592
75 FILING DATE: October 29, 1994

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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: 07/745,484
3  FILING DATE: August 14, 1991
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Jane Massey Licata
6  REGISTRATION NUMBER: 42,253
7  REFERENCE/DOCKET NUMBER: PENN-0142
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: (609) 779-2400
10 TELEFAX: (609) 779-8486
11 INFORMATION FOR SEQ ID NO: 21:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 14
14 TYPE: Amino Acid
15 TOPOLOGY: linear
16 US 09 495-128 2
17
18 Query Match:
19 Best Local Similarity: 100.0%, Score 41, DB 1, Length 14,
20 Matches: 41, Conservative 0, Mismatches 0, Indels 0, Gaps 0
21
22 QY 8 KSKO 11
23 1 111
24 3 KSKO 6
25
26 RESULT 47
27 US 09 652-648 1
28 Sequence 1, Application US/06/52448
29 Patent No. 5284454
30 GENERAL INFORMATION:
31 APPLICANT: Barstad, Paul A.
32 APPLICANT: Iverson, Gilbert M.
33 TITLE OF INVENTION: A composition for inducing humoral
34 TITLE OF INVENTION: A composition for inducing humoral
35 TITLE OF INVENTION: A composition for inducing humoral
36 TITLE OF INVENTION: A composition for inducing humoral
37 TITLE OF INVENTION: A composition for inducing humoral
38 TITLE OF INVENTION: A composition for inducing humoral
39 NUMBER OF SEQUENCES: 1
40 CORRESPONDENCE ADDRESS:
41 ADDRESS: Iverson, Gilbert M.
42 STREET: 545 Middlefield Road, Suite 200
43 CITY: Menlo Park
44 STATE: CA
45 COUNTRY: USA
46 ZIP: 94025
47 COMPUTER READABLE FORM:
48 MEDIUM TYPE: floppy disk
49 COMPUTER: IBM PC COMPATIBLE
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: Patent Release # 1.0, Version # 1.25
52 CURRENT APPLICATION DATA:
53 APPLICATION NUMBER: US/07/652,648
54 FILING DATE: 19910209
55 CLASSIFICATION: 424
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Cori, Thomas E.
58 REGISTRATION NUMBER: 21,013
59 REFERENCE/DOCKET NUMBER: 5211-0060
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (415) 327-7250
62 TELEFAX: (415) 327-2951
63 TELEX: 706141
64 INFORMATION FOR SEQ ID NO: 1:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 8 amino acids
67 TYPE: AMINO ACID
68 STRANDEDNESS: Single
69 TOPOLOGY: linear
70 US 07 652-648-1
71
72 Query Match:
73 Best Local Similarity: 100.0%, Score 41, DB 1, Length 8,
74 Matches: 41, Conservative 0, Mismatches 0, Indels 0, Gaps 0

```

```

QY      8 KSK 10
10      8 KSK 5
RESULT 00
US 08 249-087 3
Sequence 5, Application US/08249-087
Patent No. 587009
GENERAL INFORMATION:
APPLICANT: BOCHILLA, MATIAS
INVENTOR: KANG, EUN
TITLE OF INVENTION: ASSAY FOR PATENTING OF ANTIBODIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Padst
STREET: 1100 Peachtree Street, Suite 2600
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4510
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443-415
FILING DATE: 07 JUN 1995
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE R.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000 050110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 887 1500
TELEFAX: (404) 887 0764
TELEX: 90 4030 MRSNE-EPKWSH
INFORMATION FOR SEQUENCE NO. 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TAGLOGY: linear
US-08-443-415 17
Query Match 27 00, Score 5, ID 17, Length 8;
Best Local Similarity 100.00, Pred. No. 2,5e+05;
Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY      8 KSK 5
10      8 KSK 5
RESULT 00
US 08 416-855-3
Sequence 5, Application US/08016855
Patent No. 5770057
GENERAL INFORMATION:
APPLICANT: EOWAS, Angelise
INVENTOR: Ehwesang, Gilem
TITLE OF INVENTION: Method of Detecting Caprine Infection
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Piques
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616-855
FILING DATE:
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-51 1988
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPLOGY: linear  
 RECDULE TYPE: peptide  
 US-09-616-855

Query Match: 27.4% Score 31 DB 2 Length 8  
 Best Local Similarity 100.0% Pct ID No 2.5e+05  
 Matches 3 Conservative 0 Mismatches 0 Gaps 0

QY 7 RES 9  
 DL 5 RES 8

RESULT 4:  
 US-09-259-550A-35  
 Sequence 35, Application US/0826550A  
 Patent No. 5775892  
 GENERAL INFORMATION:  
 APPLICANT: GENTS, David E.  
 TITLE OF INVENTION: Anticellulimatory peptides  
 NUMBER OF SEQUENCES: 91  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & BOMERS  
 STREET: 1155 Avenue Of The Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10046-2711  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/259,550A  
 FILING DATE: 16-JUN-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MISTOCK, S. LESTIG  
 REGISTRATION NUMBER: 38,872  
 REFERENCE/BOOK NUMBER: 714, 911  
 TELEPHONE: (212) 792-9099  
 TELEFAX: (212) 869-8864/934  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 RECDULE TYPE: peptide  
 HYPERSENSIT: NO  
 ANTI-SENSE: NO  
 US-09-259-550A-35

Query Match: 27.4% Score 31 DB 2 Length 8  
 Best Local Similarity 100.0% Pct ID No 2.5e+05  
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 RES 7  
 DL 4 RES 9

RESULT 4:  
 US-09-452-724A-36

Sequence 36, Application US/08452724A  
 Patent No. 583680  
 GENERAL INFORMATION:  
 APPLICANT: Cited, Robert G.  
 TITLE OF INVENTION: Walk-Through Mutagenesis  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.  
 STREET: 2 Little Drive  
 CITY: Lexington  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02174  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452,724A  
 FILING DATE: 10-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/930,600  
 FILING DATE: 05-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US91/02362  
 FILING DATE: 05-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/905,314  
 FILING DATE: 05-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROOK ESQ., David E.  
 REGISTRATION NUMBER: 22,542  
 REFERENCE/BOOK NUMBER: 8090 01A2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-09-452-724A-36

Query Match: 27.4% Score 31 DB 2 Length 8  
 Best Local Similarity 100.0% Pct ID No 2.5e+05  
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 4 TRE 6  
 DL 5 TRE 7

RESULT 4:  
 US-09-373-190-46  
 Sequence 46, Application US/08473190  
 Patent No. 5851829  
 GENERAL INFORMATION:  
 APPLICANT: MASASCO, WAYNE  
 TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS  
 NUMBER OF SEQUENCES: 79  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRODSKIN, ROBERTS & CUSHMAN  
 STREET: 130 WATER STREET  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette



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1  COMPILED: IBM Compatible
2  OPERATING SYSTEM: DOS
3  SOFTWARE: FASTSEQ Version 1.5
4  CURRENT APPLICATION DATA
5  APPLICATION NUMBER: US/08/436,14
6  FILING DATE: 17-JAN-1995
7  CLASSIFICATION: 435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US/08/436,14
10 FILING DATE: 16-JUL-1994
11 ATTORNEY/AGENT INFORMATION:
12 NAME: RESNICK, DAVID S.
13 REGISTRATION NUMBER: 44,245
14 REFERENCE/DCKET NUMBER: 436,14
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 617-523-5400
17 TELEFAX: 617-523-6446
18 TELEX: SURE UR 2092
19 INFORMATION FOR SEQ ID NO: 435
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 8 amino acids
22 TYPE: amino acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 HYDROPHOBIC: NO
27 ANTI-SENSE: NO
28 FRAGMENT TYPE: N-terminal
29 ORIGINAL SOURCE:
30 US 08 436 14 48
31
32 Query Match: 27.4% Score 4; DB 2; Length 8;
33 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
34 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;
35
36 47 8 KSK 10
37 11
38 4 KSK 6
39
40 RESULT 44
41 US 08 436 14 48
42 1 Sequence 1; Application US/08436144
43 2 Patent No. 5813748
44 3 GENERAL INFORMATION:
45 4 APPLICANT: TEN CLIKE, Peter
46 5 APPLICANT: HELDIN, Carl Henrik
47 6 APPLICANT: MIYAZONO, Robert
48 7 APPLICANT: SAMPATH, Robert
49 8 TITLE OF INVENTION: Morphogenic factors and their function
50 9 TITLE OF INVENTION: Surface receptors and their function
51 10 NUMBER OF SEQUENCES: 18
52 11 CORRESPONDENCE ADDRESS:
53 12 ADDRESSEE: Testa, Horwitz & Chertow,
54 13 STREET: 125 High St.
55 14 CITY: Boston
56 15 STATE: MA
57 16 COUNTRY: USA
58 17 ZIP: 02110
59 18 COMPUTER READABLE FORM:
60 19 MEDIUM TYPE: Floppy disk
61 20 COMPUTER: IBM PC compatible
62 21 OPERATING SYSTEM: PC-DOS/MS-DOS
63 22 SOFTWARE: Patent Release 1.0, Version 1.0.0
64 23 CURRENT APPLICATION DATA:
65 24 APPLICATION NUMBER: US/08/436,14
66 25 FILING DATE: 02-JUN-1995
67 26 CLASSIFICATION: 435
68 27 ATTORNEY/AGENT INFORMATION:
69 28 NAME: MEYERS, Thomas G.
70 29 REGISTRATION NUMBER: 36,349
71 30 REFERENCE/DCKET NUMBER: 436,14
72 31 TELECOMMUNICATION INFORMATION:

```

```

1  TELEPHONE: (617) 248-7000
2  TELEFAX: (617) 248-7100
3  INFORMATION FOR SEQ ID NO: 17:
4  SEQUENCE CHARACTERISTICS:
5  LENGTH: 8 amino acids
6  TYPE: amino acid
7  STRANDEDNESS:
8  TOPOLOGY: linear
9  MOLECULE TYPE: peptide
10 US-08-441-147A-17
11
12 Query Match: 27.4% Score 4; DB 2; Length 8;
13 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
14 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;
15
16 49 8 KSK 10
17 11
18 5 KSK 7
19
20 RESULT 45
21 US-08-147-777-4
22 1 Sequence 4; Application US/08:47777
23 2 Patent No. 5914265
24 3 GENERAL INFORMATION:
25 4 APPLICANT: Koop, Dennis R.
26 5 APPLICANT: Rothmann, Joseph A.
27 6 APPLICANT: Greenhalgh, David A.
28 7 APPLICANT: Yuspa, Stuart H.
29 8 TITLE OF INVENTION: KERATIN K1 EXPRESSION VECTORS
30 9 TITLE OF INVENTION: AND METHODS OF USE
31 10 NUMBER OF SEQUENCES: 5
32 11 CORRESPONDENCE ADDRESS:
33 12 ADDRESSEE: LYON & LYON
34 13 STREET: 511 West Sixth Street
35 14 CITY: Los Angeles
36 15 STATE: California
37 16 COUNTRY: U.S.A.
38 17 ZIP: 90017
39 18 COMPUTER READABLE FORM:
40 19 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
41 20 COMPUTER: IBM PC compatible
42 21 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
43 22 SOFTWARE: WordPerfect (Version 5.1)
44 23 CURRENT APPLICATION DATA:
45 24 APPLICATION NUMBER: US/08/147,777
46 25 FILING DATE:
47 26 CLASSIFICATION: 800
48 27 PRIOR APPLICATION DATA: including application
49 28 PRIOR APPLICATION DATA: described below:
50 29 APPLICATION NUMBER: 07/876,289
51 30 FILING DATE: April 30, 1992
52 31 APPLICATION NUMBER: Unassigned (204/144)
53 32 FILING DATE: October 29, 1993
54 33 ATTORNEY/AGENT INFORMATION:
55 34 NAME: Warburg, Richard J.
56 35 REGISTRATION NUMBER: 32,327
57 36 REFERENCE/DCKET NUMBER: 204/153
58 37 TELECOMMUNICATION INFORMATION:
59 38 TELEPHONE: (213) 489-1600
60 39 TELEFAX: (213) 955-0440
61 40 TELEX: 67 9510
62 41 INFORMATION FOR SEQ ID NO: 4:
63 42 SEQUENCE CHARACTERISTICS:
64 43 LENGTH: 8 amino acids
65 44 TYPE: amino acid
66 45 STRANDEDNESS: single
67 46 TOPOLOGY: linear
68 47 MOLECULE TYPE: peptide
69 48 US-08-147-777-4
70
71 Query Match: 27.4% Score 4; DB 2; Length 8;

```

```

Best Local Similarity 100.0% Seed: Nucleotide
Matches 0 Conservative 0 Mismatches 0 Gaps 0

CY 2 KIS 9
  1
  1
  1 KIS 5

RESULT 46
US-09-787-443-14.oli.ra1
  Sequence 7: Application US/08/260A
  Patent No. 596883
  GENERAL INFORMATION:
  APPLICANT: Saw, A.D.
  TITLE OF INVENTION: ANIMAL MODELS + HUMAN ARYL AMIDES
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Christensen, O'Connor, Johnson and Kinross
  STREET: 1420 Fifth Avenue, Suite 2800
  CITY: Seattle
  STATE: Washington
  COUNTRY: USA
  ZIP: 98101 2347
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Disks/5.25 inch, 1.2MB storage
  COMPUTER: IBM PC/386 compatible
  OPERATING SYSTEM: MS DOS 4.01
  SOFTWARE: word for windows
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/411 216
  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/969,744
  FILING DATE: October 23, 1992
  APPLICATION NUMBER: 07/950,411
  FILING DATE: September 23, 1992
  ATTORNEY/AGENT INFORMATION:
  NAME: Bodorick, Thomas F.
  REGISTRATION NUMBER: 31,172
  REFERENCE/ROCKET NUMBER: 3 FW 1 000 0
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 1-206-682-8100; 1-206-224-9133 (1-800-
  TELEFAX: 1-206-224-2779
  ALEX: 4948023
  INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 8 amino acids
  TYPE: amino acid
  STRANDNESS: single
  TOPOLOGY: linear
  Molecule type: peptide
  DESCRIPTION: APP(324-330) (330-331) (331-332)
  US-09-787-443-14.oli.ra1
  Query Match: 27.6% Seed: Nucleotide
  Best Local Similarity 100.0% Seed: Nucleotide
  Matches 0 Conservative 0 Mismatches 0 Gaps 0

CY 5 KIS 7
  1
  1
  1 KIS 7

RESULT 47
US-09-787-443-14.oli.ra1
  Sequence 7: Application US/08/260A
  Patent No. 596883
  GENERAL INFORMATION:
  APPLICANT: Winter, Gregory Paul
  ADDRESSEE: Griffiths, Andrew Edward
  APPLICANT: Williams, Samuel Edward
  APPLICANT: Waterhouse, Peter

```

```

APPLICANT: Nissim, Abava
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 502
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Flisbach
STREET: Marshall, 10701, Dorstein, Murray & Bergin
STREET: 6500 South Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patclic Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 4.35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08-4110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08-9206318.3
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08/500,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08/500,619
FILING DATE: 15-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Florea, David W.
REGISTRATION NUMBER: 36,199
REFERENCE/ROCKET NUMBER: 2-111/5272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-434-6300
INFORMATION FOR SEQ ID NO: 467:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
US-09-787-443-14.oli.ra1
Query Match: 27.6% Seed: Nucleotide
Best Local Similarity 100.0% Seed: Nucleotide
Matches 0 Conservative 0 Mismatches 0 Gaps 0

CY 5 KIS 9
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RESULT 48
US-09-787-443-14.oli.ra1
  Sequence 7: Application US/08/260A
  Patent No. 596883
  GENERAL INFORMATION:
  APPLICANT: Nissim, Abava
  ADDRESSEE: Griffiths, Andrew Edward
  APPLICANT: Williams, Samuel Edward
  APPLICANT: Waterhouse, Peter

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1  APPLICANT: BASELINE, WILLIAM
2  TITLE OF INVENTION: METHOD OF INCREASING PROTEIN
3  FILING DATE: 14 APR 1991
4  NUMBER OF SEQUENCES: 78
5  ADDRESS: 100 WATER STREET
6  ADDRESS: CUSHMAN
7  CITY: BOSTON
8  STATE: MASSACHUSETTS
9  COUNTRY: US
10 ZIP: 02109
11 MEDIUM TYPE: floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent In Release #1.0, Version #1.0
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/438,106
17 FILING DATE:
18 CLASSIFICATION: 435
19 ATTORNEY/AGENT INFORMATION:
20 NAME: EISENSTEIN, RONALD L.
21 REGISTRATION NUMBER: 40628
22 REFERENCE/DOCKET NUMBER: 4393
23 TELEPHONE: (617) 528-3400
24 TELEFAX: (617) 528-6443
25 INFORMATION FOR SEQ ID NO: 48:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 8 amino acids
28 TYPE: amino acid
29 SUBMITTER: clinical
30 US 09-438,106-1
31 Query Match: 27.9% Score 31 100.0% Pos 2.5e-05
32 Post Local Similarity: 100.0% Pos 2.5e-05
33 Matches: 3 Conserved: 0 Mismatches: 0 Indels: 0
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27 6 KSK 10  
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3 KSK 7

Search completed: September 29, 2003 11:26 PM  
JUL 09:15 9157 SCS

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ORF protein - protein search, using sw method

Run on: September 30, 2003, 11:06:52, Search time 21.56 seconds  
(excluding alignment)

US-09-787-443-14

Perfect score: 11

Sequence: 1 AKKTKRSKD 11

Scoring table: 60x60

Search: 500494 seqs, 151467094 residues

Word size: 3

Total number of hits satisfying chosen parameters: 14887

Minimum ORF seq length: 8

Maximum ORF seq length: 15

Post processing: listing first 500 summaries

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17: /cgn2\_6/ptodata/2/pubaa/US09A\_PUB\_Ms.fpf.\*

Note: N is the number of results from this query to have a score greater than or equal to the Score of the best period found, and is derived by analysis of the total range distribution.

#### SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
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3	5	45.5	10	11	US-09-935-384-326
4	5	45.5	10	11	US-09-935-384-327
5	5	45.5	10	12	US-09-935-384-328
6	4	36.4	8	12	US-09-876-904A-452
7	4	36.4	8	12	US-09-876-904A-453
8	4	36.4	8	12	US-09-876-904A-454
9	4	36.4	8	12	US-09-876-904A-455
10	4	36.4	8	12	US-09-876-904A-456
11	4	36.4	8	12	US-09-876-904A-457
12	4	36.4	8	12	US-09-876-904A-458
13	4	36.4	8	12	US-09-876-904A-459
14	4	36.4	8	12	US-09-876-904A-460
15	4	36.4	8	12	US-09-876-904A-461

US-09-935-384-322	Sequence 322, App
US-09-935-384-326	Sequence 326, App
US-09-935-384-416	Sequence 416, App
US-09-935-384-527	Sequence 527, App
US-09-935-384-610	Sequence 610, App
US-09-833-039-41	Sequence 41, App
US-09-833-039-68	Sequence 68, App
US-09-833-039-75	Sequence 75, App
US-09-833-039-94	Sequence 94, App
US-09-833-039-112	Sequence 112, App
US-09-239-311A-195	Sequence 195, App
US-09-894-912A-21	Sequence 21, App
US-09-876-904A-391	Sequence 391, App
US-09-922-226-69	Sequence 69, App
US-09-932-165-780	Sequence 780, App
US-09-932-165-1316	Sequence 1316, App
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US-09-935-384-97	Sequence 97, App
US-09-935-384-161	Sequence 161, App
US-09-935-384-275	Sequence 275, App
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US-09-935-384-396	Sequence 396, App
US-09-935-384-593	Sequence 593, App
US-09-935-384-692	Sequence 692, App
US-10-098-238-27	Sequence 27, App
US-09-966-871-3	Sequence 3, App
US-09-876-904A-239	Sequence 239, App
US-10-039-645-3	Sequence 3, App
US-10-139-084-3	Sequence 3, App
US-10-093-958-1	Sequence 1, App
US-10-075-869-10	Sequence 10, App
US-09-876-904A-79	Sequence 79, App
US-09-876-904A-196	Sequence 196, App
US-09-876-904A-454	Sequence 454, App
US-10-158-150A-42	Sequence 42, App
US-10-174-105A-94	Sequence 94, App
US-10-174-105A-95	Sequence 95, App
US-09-802-077-10	Sequence 10, App
US-09-802-077-27	Sequence 27, App
US-09-803-096-10	Sequence 10, App
US-09-803-096-27	Sequence 27, App
US-09-910-552-21	Sequence 21, App
US-09-362-286-9	Sequence 9, App
US-09-759-130B-434	Sequence 434, App
US-09-925-179-10	Sequence 10, App
US-09-925-179-27	Sequence 27, App
US-09-953-354-105	Sequence 105, App
US-09-500-700-17	Sequence 17, App
US-09-876-904A-84	Sequence 84, App
US-09-876-904A-353	Sequence 353, App
US-09-876-904A-455	Sequence 455, App
US-09-876-904A-456	Sequence 456, App
US-09-876-904A-464	Sequence 464, App
US-09-876-904A-493	Sequence 493, App
US-09-876-904A-503	Sequence 503, App
US-09-876-904A-504	Sequence 504, App
US-09-876-904A-506	Sequence 506, App
US-09-876-904A-507	Sequence 507, App
US-09-876-904A-518	Sequence 518, App
US-09-876-904A-519	Sequence 519, App
US-09-876-904A-520	Sequence 520, App
US-09-876-904A-529	Sequence 529, App
US-09-876-904A-553	Sequence 553, App
US-10-062-587-3	Sequence 3, App
US-10-348-504-75	Sequence 75, App
US-10-348-504-108	Sequence 108, App
US-10-190-082-344	Sequence 344, App
US-10-209-187A-4	Sequence 4, App
US-10-342-103-2	Sequence 2, App
US-10-358-627-24	Sequence 24, App
US-10-358-627-26	Sequence 26, App
US-10-358-627-27	Sequence 27, App
US-10-358-627-28	Sequence 28, App













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DE      3 REK 6
111
RESULT 12
US-10-014-465A-54
: Sequence 54, Application US/2003/017596A1
: Publication No. US2003017596A1
: GENERAL INFORMATION:
: APPLICANT: Iureci, Ozlem
: APPLICANT: Sahin, Bgut
: APPLICANT: Pfrendtschuh, Michael
: TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
: FILE REFERENCE: CUB 5622.1
: CURRENT APPLICATION NUMBER: US 09/835,034
: PRIOR FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: US 09/409,456
: PRIOR FILING DATE: 1999-09-30
: PRIOR APPLICATION NUMBER: US 09/344,043
: PRIOR FILING DATE: 1999-06-25
: PRIOR APPLICATION NUMBER: US 09/135,809
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 08/851,139
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 129
: SEQ ID NO 111
: LENGTH: 8
: TYPE: PPT
: ORGANISM: Homo sapiens
US-09-014-059-111

Query Match: 46.4%; Score 4; Db 14; Length 8;
Best Local Similarity 100.0%; Pct. No. Seqs 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      5 REK 8
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DE      3 REK 6

RESULT 12
US-10-014-465A-54
: Sequence 54, Application US/190-4440A
: Publication No. US20020168684A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signalling Technology, Inc.
: APPLICANT: Zhang, Michael J.
: APPLICANT: Tan, Yi
: TITLE OF INVENTION: PROTECTION OF MOLECULAR CLAM CONTEXT INDEPENDENT ANTIBODIES
: FILE REFERENCE: CSI-138 CIP2
: CURRENT APPLICATION NUMBER: US/19/014-465A
: PRIOR FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: US 09/148,712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535,364
: PRIOR FILING DATE: 2000-04-24
: NUMBER OF SEQ ID NOS: 145
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 54
: LENGTH: 8
: TYPE: PPT
: ORGANISM: Homo sapiens
US-09-014-059-111

Query Match: 46.4%; Score 4; Db 14; Length 8;
Best Local Similarity 100.0%; Pct. No. Seqs 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      5 REK 8
111
DE      3 REK 6

RESULT 12
US-10-014-465A-54
: Sequence 54, Application US/2003/017596A1
: Publication No. US2003017596A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signalling Technology, Inc.
: APPLICANT: Zhang, Michael J.
: APPLICANT: Tan, Yi
: TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPEC
: FILE REFERENCE: CSI-138 CIP4
: CURRENT APPLICATION NUMBER: US/19/174-105A
: PRIOR FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: US 09/148,712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535,364
: PRIOR FILING DATE: 2000-04-24
: NUMBER OF SEQ ID NOS: 193
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 54
: LENGTH: 8
: TYPE: PPT
: ORGANISM: Artificial Sequence
: OTHER INFORMATION: Synthetic Peptide
: FEATURES:
: NAME/KEY: MEMORES
: LOCATION: (6)-(12)
: OTHER INFORMATION: PHOSPHORYLATION, threonine at position 6 is phosphorylated
US-10-174-105A-54

Query Match: 46.4%; Score 4; Db 15; Length 8;
Best Local Similarity 100.0%; Pct. No. Seqs 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      5 REK 8
111
DE      3 REK 4

RESULT 12
US-10-124-711-12
: Sequence 18, Application US/201-24711
: Publication No. US20030099634A1
: GENERAL INFORMATION:
: APPLICANT: VITELLO, Maria A.
: APPLICANT: CHESTNUT, Robert W.
: APPLICANT: SETTE, Alessandro D.
: APPLICANT: CELIS, Esteban
: APPLICANT: GRAY, Howard
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
: CTL IMMUNITY
: NUMBER OF SEQUENCES: 153
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Orew
: STREET: Steuart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1494
: COMPUTER PROGRAM FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

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Best Local Similarity: 100.0%, Score: 4, DB: 12, Length: 9;
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

Q7 7 RSKK 10
14 111
4 RSKK 7

RESULT 17
US-09-935-384-416
Sequence 527, Application US/99/935,384
Publication No.: US2000/0166525A1
GENERAL INFORMATION:
APPLICANT: CHALLITA-ELD, PIA
APPLICANT: HUBERT, RENE
APPLICANT: RATTANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: PARIS, MARY
APPLICANT: GE, WANGMAO
APPLICANT: JAKBOVITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
FILE REFERENCE: 51158-2003-00
CURRENT APPLICATION NUMBER: US/99/935,384
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,096
NUMBER OF SEQ ID NOS: 784
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 416
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-384-426

Query Match: 36.4%, Score: 3, DB: 12, Length: 9;
Best Local Similarity: 100.0%, Pred. No.: 50-05;
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

Q7 7 RSKK 10
14 111
4 RSKK 7

RESULT 18
US-09-935-384-416
Sequence 527, Application US/99/935,384
Publication No.: US2000/0166525A1
GENERAL INFORMATION:
APPLICANT: CHALLITA-ELD, PIA
APPLICANT: HUBERT, RENE
APPLICANT: RATTANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: PARIS, MARY
APPLICANT: GE, WANGMAO
APPLICANT: JAKBOVITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
FILE REFERENCE: 51158-2003-00
CURRENT APPLICATION NUMBER: US/99/935,384
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,096
NUMBER OF SEQ ID NOS: 784
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 416
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-384-426

Query Match: 36.4%, Score: 3, DB: 12, Length: 9;
Best Local Similarity: 100.0%, Pred. No.: 50-05;
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

Q7 7 RSKK 10
14 111
4 RSKK 7

RESULT 19
US-09-935-384-416
Sequence 527, Application US/99/935,384
Publication No.: US2000/0166525A1
GENERAL INFORMATION:
APPLICANT: CHALLITA-ELD, PIA
APPLICANT: HUBERT, RENE
APPLICANT: RATTANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: PARIS, MARY
APPLICANT: GE, WANGMAO
APPLICANT: JAKBOVITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
FILE REFERENCE: 51158-2003-00
CURRENT APPLICATION NUMBER: US/99/935,384
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,096
NUMBER OF SEQ ID NOS: 784
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 416
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-384-426

Query Match: 36.4%, Score: 4, DB: 12, Length: 9;
Best Local Similarity: 100.0%, Pred. No.: 50-05;
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

Q7 7 RSKK 10
14 111
4 RSKK 7

RESULT 20
US-09-935-384-416
Sequence 527, Application US/99/935,384
Publication No.: US2000/0166525A1
GENERAL INFORMATION:
APPLICANT: CHALLITA-ELD, PIA
APPLICANT: HUBERT, RENE
APPLICANT: RATTANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: PARIS, MARY
APPLICANT: GE, WANGMAO
APPLICANT: JAKBOVITZ, AYA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
FILE REFERENCE: 51158-2003-00
CURRENT APPLICATION NUMBER: US/99/935,384
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,096
NUMBER OF SEQ ID NOS: 784
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 416
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-384-426
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1  LENGTH: 9
2  TYPE: PRT
3  ORGANISM: Homo Sapiens
4  US 09 833 039 68

Query Match: 36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod. No. 50065,
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 7 PERK 8
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  1 PERK 4
  1 PERK 6

RESULT 21
US 09 833 039 68
1 Sequence 75, Application US/09/833 039
2 Publication No. US2003017596A1
3 GENERAL INFORMATION:
4 APPLICANT: Tumor, Ozlem
5 APPLICANT: Sahin, Dilar
6 APPLICANT: Freundschuh, Michael
7 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8 FILE REFERENCE: LID 5622.1
9 CURRENT APPLICATION NUMBER: US/09/833 039
10 PRIOR FILING DATE: 2001-04-12
11 PRIOR APPLICATION NUMBER: US 09/409,455
12 PRIOR FILING DATE: 1999-09-30
13 PRIOR APPLICATION NUMBER: US 09/444,040
14 PRIOR FILING DATE: 1999-06-25
15 PRIOR APPLICATION NUMBER: US 09/105,849
16 PRIOR FILING DATE: 1998-06-26
17 PRIOR APPLICATION NUMBER: US 08/851,130
18 PRIOR FILING DATE: 1997-05-05
19 NUMBER OF SEQ ID NOS: 129
20 SEQ ID NO: 41
21 LENGTH: 9
22 TYPE: PRT
23 ORGANISM: Homo Sapiens
24 US 09 833 039 68

Query Match: 36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod. No. 50065,
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 7 PERK 8
  1
  1 PERK 4
  1 PERK 6

RESULT 22
US 09 833 039 68
1 Sequence 75, Application US/09/833 039
2 Publication No. US2003017596A1
3 GENERAL INFORMATION:
4 APPLICANT: Tumor, Ozlem
5 APPLICANT: Sahin, Dilar
6 APPLICANT: Freundschuh, Michael
7 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8 FILE REFERENCE: LID 5622.1
9 CURRENT APPLICATION NUMBER: US/09/833 039
10 PRIOR FILING DATE: 2001-04-12
11 PRIOR APPLICATION NUMBER: US 09/409,455
12 PRIOR FILING DATE: 1999-09-30
13 PRIOR APPLICATION NUMBER: US 09/444,040
14 PRIOR FILING DATE: 1999-06-25
15 PRIOR APPLICATION NUMBER: US 09/105,849
16 PRIOR FILING DATE: 1998-06-26
17 PRIOR APPLICATION NUMBER: US 08/851,130
18 PRIOR FILING DATE: 1997-05-05
19 NUMBER OF SEQ ID NOS: 129
20 SEQ ID NO: 42
21 LENGTH: 9
22 TYPE: PRT
23 ORGANISM: Homo Sapiens
24 US 09 833 039 68

```

```

1  LENGTH: 9
2  TYPE: PRT
3  ORGANISM: Homo Sapiens
4  US 09 833 039 68

Query Match: 36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod. No. 50065,
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 7 PERK 8
  1
  1 PERK 4
  1 PERK 6

RESULT 23
US 09 833 039 68
1 Sequence 75, Application US/09/833 039
2 Publication No. US2003017596A1
3 GENERAL INFORMATION:
4 APPLICANT: Tumor, Ozlem
5 APPLICANT: Sahin, Dilar
6 APPLICANT: Freundschuh, Michael
7 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8 FILE REFERENCE: LID 5622.1
9 CURRENT APPLICATION NUMBER: US/09/833 039
10 PRIOR FILING DATE: 2001-04-12
11 PRIOR APPLICATION NUMBER: US 09/409,455
12 PRIOR FILING DATE: 1999-09-30
13 PRIOR APPLICATION NUMBER: US 09/444,040
14 PRIOR FILING DATE: 1999-06-25
15 PRIOR APPLICATION NUMBER: US 09/105,849
16 PRIOR FILING DATE: 1998-06-26
17 PRIOR APPLICATION NUMBER: US 08/851,130
18 PRIOR FILING DATE: 1997-05-05
19 NUMBER OF SEQ ID NOS: 129
20 SEQ ID NO: 75
21 LENGTH: 9
22 TYPE: PRT
23 ORGANISM: Homo Sapiens
24 US 09 833 039 68

Query Match: 36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod. No. 50065,
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 7 PERK 8
  1
  1 PERK 4
  1 PERK 6

RESULT 24
US 09 833 039 68
1 Sequence 94, Application US/09/833 039
2 Publication No. US2003019960A1
3 GENERAL INFORMATION:
4 APPLICANT: Tumor, Ozlem
5 APPLICANT: Sahin, Dilar
6 APPLICANT: Freundschuh, Michael
7 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8 FILE REFERENCE: LID 5622.1
9 CURRENT APPLICATION NUMBER: US/09/833 039
10 PRIOR FILING DATE: 2001-04-12
11 PRIOR APPLICATION NUMBER: US 09/409,455
12 PRIOR FILING DATE: 1999-09-30
13 PRIOR APPLICATION NUMBER: US 09/444,040
14 PRIOR FILING DATE: 1999-06-25
15 PRIOR APPLICATION NUMBER: US 09/105,849
16 PRIOR FILING DATE: 1998-06-26
17 PRIOR APPLICATION NUMBER: US 08/851,130
18 PRIOR FILING DATE: 1997-05-05
19 NUMBER OF SEQ ID NOS: 129
20 SEQ ID NO: 94
21 LENGTH: 9
22 TYPE: PRT
23 ORGANISM: Homo Sapiens
24 US 09 833 039 68

```

ORGANISM: Homo sapiens  
US-09-833-039-94

Query Match: 36.4% Score 4: DB 12: Length 9;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

CY 5 REK 8  
DE 1 REK 4

RESULT 25

US-09-833-039-112  
Sequence 112: Application US/09/430-09  
Publication No. US20030175960A1  
GENERAL INFORMATION:  
APPLICANT: E. J. O'Brien  
APPLICANT: E. J. O'Brien, Michael  
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof  
FILE REFERENCE: US 5622-1  
CURRENT APPLICATION NUMBER: US/09/833-039  
PRIOR FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: US/09/430-09  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: US/09/444-140  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: US/09/405-843  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: US/08/411-00  
PRIOR FILING DATE: 1997-05-05  
NUMBER OF SEQ ID NOS: 129  
SEQ ID NO 112  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-833-039-112

Query Match: 36.4% Score 4: DB 12: Length 9;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

CY 5 REK 8  
DE 1 REK 4

RESULT 26

US-09-833-039-113  
Sequence 113: Application US/09/430-113A  
Publication No. US20030175960A1  
GENERAL INFORMATION:  
APPLICANT: KINGDER - HAMOUR, CHRISTINE  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING A PLS  
TITLE OF INVENTION: N-TERMINAL A GLUCAMIC ACID OR A GLUTAMINE IN THE FORM  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/09/430-113A  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: FR 00/04711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 195  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Influenza virus

US-09-876-904A-391

Query Match: 36.4% Score 4: DB 12: Length 9;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

CY 2 REK 5  
DE 6 REK 9

RESULT 27

US-09-876-904A-21  
Sequence 21: Application US/09/430-21A  
Publication No. US20030044792A1  
GENERAL INFORMATION:  
APPLICANT: Gao et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH  
FILE REFERENCE: 28110/37260A  
CURRENT APPLICATION NUMBER: US/09/876-904A  
PRIOR FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: To be assigned  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/265,614  
PRIOR FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: 60/215,733  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 09/757,562  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: 09/543,274  
PRIOR FILING DATE: 2000-04-05  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 21  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-876-904A-21

Query Match: 36.4% Score 4: DB 11: Length 10;  
Best Local Similarity 100.0% Pred. No. 4.3e+02;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

CY 5 REK 8  
DE 4 REK 7

RESULT 28

US-09-876-904A-391  
Sequence 391: Application US/09/876904A  
Publication No. US2003007294A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
FILE REFERENCE: TB-2002-00  
CURRENT APPLICATION NUMBER: US/09/876-904A  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 391  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
FEATURE:  
OTHER INFORMATION: C. elegans Sdc 3 protein (sex-determining protein)  
US-09-876-904A-391

Query Match 36.4% Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RSKK 10  
111  
DB 2 RSKK 5

RESULT 29  
US-09-922-256-09

Sequence 654, Application US/09/572,270A  
Publication No. US20030148464A1  
GENERAL INFORMATION:  
APPLICANT: ZHANG, YI  
APPLICANT: HUBERT, SCOTT M.  
APPLICANT: XIAO, JIA BAO  
APPLICANT: KASALI, JYOTIMOY  
APPLICANT: CHANDRASEKAR, KESAVANATHAN A  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS THAT  
TITLE OF INVENTION: MODULATE BACTERIAL BIOFILM ACTIVITY  
FILE REFERENCE: P-AK 4081  
CURRENT APPLICATION NUMBER: US/09/922,226  
CURRENT FILING DATE: 2002-01-09  
PRIOR APPLICATION NUMBER: US 60/284,397  
PRIOR FILING DATE: 2001-04-18  
NUMBER OF SEQ ID NOS: 19;  
SEQ ID NO 69  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-09-922-226-09

Query Match 36.4% Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RSKK 10  
111  
DB 3 RSKK 5

RESULT 30  
US-09-932-165-166

Sequence 654, Application US/09/572,270A  
Publication No. US20030148464A1  
GENERAL INFORMATION:  
APPLICANT: RATTANOL, ARTHUR  
APPLICANT: CHALLITA-EID, PIA M.  
APPLICANT: FARIS, MARY  
APPLICANT: SAFFRAN, DOUGLAS  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: HUBERT, RENE  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKOBOWITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
TITLE OF INVENTION: DETECTION OF CANCER  
FILE REFERENCE: 51158-20014-00  
CURRENT APPLICATION NUMBER: US/09/932,166  
CURRENT FILING DATE: 2003-08-17  
PRIOR APPLICATION NUMBER: 60/226,129  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 1508  
SOFTWARE: Patentis Ver. 2.1  
SEQ ID NO 780  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-780

Query Match 36.4% Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RSKK 10  
111  
DB 7 RSKK 10

RESULT 31  
US-09-932-165-1416

Sequence 654, Application US/09/932,165  
Publication No. US20030148464A1  
GENERAL INFORMATION:  
APPLICANT: RATTANOL, ARTHUR  
APPLICANT: CHALLITA-EID, PIA M.  
APPLICANT: FARIS, MARY  
APPLICANT: SAFFRAN, DOUGLAS  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: HUBERT, RENE  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKOBOWITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
TITLE OF INVENTION: BAP2H3 AND CATEP2H11 USEFUL IN TREATMENT AND  
FILE REFERENCE: 51158-20014-00  
CURRENT APPLICATION NUMBER: US/09/932,165  
CURRENT FILING DATE: 2003-08-17  
PRIOR APPLICATION NUMBER: 60/226,129  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 1508  
SOFTWARE: Patentis Ver. 2.1  
SEQ ID NO 1316  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1316

Query Match 36.4% Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RSKK 11  
111  
DB 1 RSKK 4

RESULT 32  
US-09-572-270A-554

Sequence 654, Application US/09/572,270A  
Publication No. US20030148464A1  
GENERAL INFORMATION:  
APPLICANT: PROLEON Ltd  
TITLE OF INVENTION: Inter- complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572,270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 654  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
OTHER INFORMATION: Sequence located in Gaps OR 1347.8, at 134-208 and may  
US-09-572-270A-554



Query Match 36.4% Score 4: 08 12: Length 10:  
 Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 7 PKSK 10

RESULT 44  
 US-09-935 484-161

1 Sequence 97: Application US/09/935 64  
 2 Publication No. US20030166526A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: CHALLITA-ETC, PIA  
 5 APPLICANT: HUBERT, RENE  
 6 APPLICANT: RAITANO, ARTHUR  
 7 APPLICANT: AFAR, DANIEL  
 8 APPLICANT: LEVIN, ELANA  
 9 APPLICANT: GE, WANGMAO  
 10 APPLICANT: JAKOBOWITZ, AYA  
 11 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED "BLASDER AND  
 12 TITLE OF INVENTION: OTHER CANCERS  
 13 FILE REFERENCE: 51158-20033 00  
 14 CURRENT APPLICATION NUMBER: US/09/935 64  
 15 CURRENT FILING DATE: 2003 08 22  
 16 PRIOR APPLICATION NUMBER: 60/227,098  
 17 PRIOR FILING DATE: 2000 08 22  
 18 NUMBER OF SEQ ID NOS: 783  
 19 SOFTWARE: PatentIn Ver. 2.1  
 20 SEQ ID NO 97  
 21 LENGTH: 10  
 22 TYPE: PR1  
 23 ORGANISM: Homo sapiens  
 24 US-09-935 484-161

Query Match 36.4% Score 4: 08 12: Length 10:  
 Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 7 PKSK 10

RESULT 44  
 US-09-935 484-161

1 Sequence 97: Application US/09/935 64  
 2 Publication No. US20030166526A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: CHALLITA-ETC, PIA  
 5 APPLICANT: HUBERT, RENE  
 6 APPLICANT: RAITANO, ARTHUR  
 7 APPLICANT: AFAR, DANIEL  
 8 APPLICANT: LEVIN, ELANA  
 9 APPLICANT: GE, WANGMAO  
 10 APPLICANT: JAKOBOWITZ, AYA  
 11 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED "BLASDER AND  
 12 TITLE OF INVENTION: OTHER CANCERS  
 13 FILE REFERENCE: 51158-20033 00  
 14 CURRENT APPLICATION NUMBER: US/09/935 64  
 15 CURRENT FILING DATE: 2003 08 22  
 16 PRIOR APPLICATION NUMBER: 60/227,098  
 17 PRIOR FILING DATE: 2000 08 22  
 18 NUMBER OF SEQ ID NOS: 783  
 19 SOFTWARE: PatentIn Ver. 2.1  
 20 SEQ ID NO 10  
 21 LENGTH: 10  
 22 TYPE: PR1

1 ORGANISM: Homo sapiens  
 US-09-935 484-161

Query Match 36.4% Score 4: 08 12: Length 10:  
 Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 4 PKSK 7

RESULT 45  
 US-09-935 484-275

1 Sequence 275: Application US/09/935 384  
 2 Publication No. US20030166526A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: CHALLITA-ETC, PIA  
 5 APPLICANT: HUBERT, RENE  
 6 APPLICANT: RAITANO, ARTHUR  
 7 APPLICANT: AFAR, DANIEL  
 8 APPLICANT: LEVIN, ELANA  
 9 APPLICANT: FARIS, MARY  
 10 APPLICANT: GE, WANGMAO  
 11 APPLICANT: JAKOBOWITZ, AYA  
 12 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED "BLASDER AND  
 13 TITLE OF INVENTION: OTHER CANCERS  
 14 FILE REFERENCE: 51158-20033 00  
 15 CURRENT APPLICATION NUMBER: US/09/935 384  
 16 CURRENT FILING DATE: 2003 08 22  
 17 PRIOR APPLICATION NUMBER: 60/227,098  
 18 PRIOR FILING DATE: 2000 08 22  
 19 NUMBER OF SEQ ID NOS: 783  
 20 SOFTWARE: PatentIn Ver. 2.1  
 21 SEQ ID NO 275  
 22 LENGTH: 10  
 23 TYPE: PR1  
 24 ORGANISM: Homo sapiens  
 25 US-09-935 484-275

Query Match 36.4% Score 4: 08 12: Length 10:  
 Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 4 PKSK 7

RESULT 46  
 US-09-935 484-275

1 Sequence 275: Application US/09/935 384  
 2 Publication No. US20030166526A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: CHALLITA-ETC, PIA  
 5 APPLICANT: HUBERT, RENE  
 6 APPLICANT: RAITANO, ARTHUR  
 7 APPLICANT: AFAR, DANIEL  
 8 APPLICANT: LEVIN, ELANA  
 9 APPLICANT: FARIS, MARY  
 10 APPLICANT: GE, WANGMAO  
 11 APPLICANT: JAKOBOWITZ, AYA  
 12 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED "BLASDER AND  
 13 TITLE OF INVENTION: OTHER CANCERS  
 14 FILE REFERENCE: 51158-20033 00  
 15 CURRENT APPLICATION NUMBER: US/09/935 384  
 16 CURRENT FILING DATE: 2003 08 22  
 17 PRIOR APPLICATION NUMBER: 60/227,098  
 18 PRIOR FILING DATE: 2000 08 22  
 19 NUMBER OF SEQ ID NOS: 783  
 20 SOFTWARE: PatentIn Ver. 2.1  
 21 SEQ ID NO 275



```

1  STATES: New York
2  COUNTRY: United States of America
3  ZIP: 10022
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
6  COMPUTER: COMPAQ, PROLIMA 300 4/26
7  OPERATING SYSTEM: DOS 5.0
8  SOFTWARE: WORD POLICE 5.2
9  CURRENT APPLICATION NUMBER: US/09/096-246
10 FILING DATE: 14-Mar-2002
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US/09/119-04
13 FILING DATE: 10-Sep-1995
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Adja C. Gouffis, Esq.
16 REGISTRATION NUMBER: 29,754
17 REFERENCE/DOCKET NUMBER: 599/119600 US
18 TELEPHONE: (212) 527-7766
19 TELEFAX: (212) 753-5257
20 TELEX: 246687
21 INFORMATION FOR SEQ ID NO: 27:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 10 amino acids
24 TYPE: amino acid
25 FEATURE: unknown
26 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
27 US 10 096-246 27
28
29 Query Match 36.4% Score 4; DB 11; Length 11;
30 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
31 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
32
33 QY 5 REK 8
34 ID 111
35 DB 1 REK 11
36
37 RESULT 44
38 US 10 096-645 3
39 Sequence 3; Application US/10049645
40 Publication No. US2002047170A1
41 GENERAL INFORMATION:
42 APPLICANT: Kopin, Alan S.
43 TITLE OF INVENTION: Constitutively Active, Hypersensitive,
44 FILE REFERENCE: 60496/51002
45 CURRENT APPLICATION NUMBER: US/10/039,645
46 CURRENT FILING DATE: 2001-10-25
47 PRIOR APPLICATION NUMBER: US 60/243,550
48 PRIOR FILING DATE: 2000-10-25
49 NUMBER OF SEQ ID NOS: 87
50 SOFTWARE: FASTSEQ for Windows Version 4.0
51 SEQ ID NO: 4
52 LENGTH: 11
53 TYPE: PKT
54 ORGANISM: Homo sapiens
55 US 10 096-645 3
56
57 Query Match 36.4% Score 4; DB 14; Length 11;
58 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
59 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
60
61 QY 5 REK 8
62 ID 111
63 DB 1 REK 4
64
65 RESULT 44
66 US 10 139-084 3
67 Sequence 1; Application US/13149084
68 Publication No. US2003087313A1
69 GENERAL INFORMATION:
70 APPLICANT: Kopin, Alan S.
71 TITLE OF INVENTION: Intra-Response-Based Methods for
72 FILE REFERENCE: 60496/51002
73 CURRENT APPLICATION NUMBER: US/10/149,084
74
75 STATE: New York
76 COUNTRY: United States of America
77 ZIP: 10022
78 COMPUTER READABLE FORM:
79 MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
80 COMPUTER: COMPAQ, PROLIMA 300 4/26
81 OPERATING SYSTEM: DOS 5.0
82 SOFTWARE: WORD POLICE 5.2
83 CURRENT APPLICATION NUMBER: US/09/096-246
84 FILING DATE: 14-Mar-2002
85 PRIOR APPLICATION DATA:
86 APPLICATION NUMBER: US/09/119-04
87 FILING DATE: 10-Sep-1995
88 ATTORNEY/AGENT INFORMATION:
89 NAME: Adja C. Gouffis, Esq.
90 REGISTRATION NUMBER: 29,754
91 REFERENCE/DOCKET NUMBER: 599/119600 US
92 TELEPHONE: (212) 527-7766
93 TELEFAX: (212) 753-5257
94 TELEX: 246687
95 INFORMATION FOR SEQ ID NO: 27:
96 SEQUENCE CHARACTERISTICS:
97 LENGTH: 10 amino acids
98 TYPE: amino acid
99 FEATURE: unknown
100 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
101 US 10 096-246 27
102
103 Query Match 36.4% Score 4; DB 11; Length 11;
104 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
105 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
106
107 QY 5 REK 8
108 ID 111
109 DB 1 REK 4
110
111 RESULT 44
112 US 09 966-871-3
113 Sequence 3; Application US/09966871
114 Patent No. US2002012753A1
115 GENERAL INFORMATION:
116 APPLICANT: Kopin, Alan S.
117 TITLE OF INVENTION: Active and Inactive
118 FILE REFERENCE: 60496/51202
119 CURRENT APPLICATION NUMBER: US/09/966-871
120 CURRENT FILING DATE: 2001-09-28
121 PRIOR APPLICATION NUMBER: US 60/243,550
122 PRIOR FILING DATE: 2000-09-28
123 NUMBER OF SEQ ID NOS: 87
124 SOFTWARE: FASTSEQ for Windows Version 4.0
125 SEQ ID NO: 3
126 LENGTH: 11
127 TYPE: PKT
128 ORGANISM: Homo sapiens
129 US 09 966-871-3
130
131 Query Match 36.4% Score 4; DB 11; Length 11;
132 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
133 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
134
135 QY 5 REK 8
136 ID 111
137 DB 1 REK 4
138
139 RESULT 44
140 US 09 976-904A-239
141 Sequence 259; Application US/09876904A
142 Publication No. US20030072794A1
143 GENERAL INFORMATION:
144 APPLICANT: BOULIKAS, JENI
145 TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA LIPIDGENES TM) AND THERAPEUTIC
146 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
147 FILE REFERENCE: 14-2002-00
148 CURRENT APPLICATION NUMBER: US/09/876,904A
149 CURRENT FILING DATE: 2002-05-08
150 PRIOR APPLICATION NUMBER: US 65/219,925
151 PRIOR FILING DATE: 2000-06-09
152 NUMBER OF SEQ ID NOS: 629
153 SOFTWARE: Patent In Ver. 2.1
154 SEQ ID NO: 239
155 LENGTH: 11
156 TYPE: PKT
157 ORGANISM: Unknown organism
158 FEATURE:
159 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
160 US-09-876-904A-239
161
162 Query Match 36.4% Score 4; DB 11; Length 11;
163 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
164 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
165
166 QY 5 REK 8
167 ID 111
168 DB 1 REK 11
169
170 RESULT 44
171 US 10 039-645 3
172 Sequence 3; Application US/10049645
173 Publication No. US2002047170A1
174 GENERAL INFORMATION:
175 APPLICANT: Kopin, Alan S.
176 TITLE OF INVENTION: Constitutively Active, Hypersensitive,
177 FILE REFERENCE: 60496/51002
178 CURRENT APPLICATION NUMBER: US/10/039,645
179 CURRENT FILING DATE: 2001-10-25
180 PRIOR APPLICATION NUMBER: US 60/243,550
181 PRIOR FILING DATE: 2000-10-25
182 NUMBER OF SEQ ID NOS: 87
183 SOFTWARE: FASTSEQ for Windows Version 4.0
184 SEQ ID NO: 4
185 LENGTH: 11
186 TYPE: PKT
187 ORGANISM: Homo sapiens
188 US 10 039-645 3
189
190 Query Match 36.4% Score 4; DB 14; Length 11;
191 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
192 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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194 QY 5 REK 8
195 ID 111
196 DB 1 REK 4
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198 RESULT 44
199 US 10 139-084 3
200 Sequence 1; Application US/13149084
201 Publication No. US2003087313A1
202 GENERAL INFORMATION:
203 APPLICANT: Kopin, Alan S.
204 TITLE OF INVENTION: Intra-Response-Based Methods for
205 FILE REFERENCE: 60496/51002
206 CURRENT APPLICATION NUMBER: US/10/149,084
207
208 STATE: New York
209 COUNTRY: United States of America
210 ZIP: 10022
211 COMPUTER READABLE FORM:
212 MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
213 COMPUTER: COMPAQ, PROLIMA 300 4/26
214 OPERATING SYSTEM: DOS 5.0
215 SOFTWARE: WORD POLICE 5.2
216 CURRENT APPLICATION NUMBER: US/09/096-246
217 FILING DATE: 14-Mar-2002
218 PRIOR APPLICATION DATA:
219 APPLICATION NUMBER: US/09/119-04
220 FILING DATE: 10-Sep-1995
221 ATTORNEY/AGENT INFORMATION:
222 NAME: Adja C. Gouffis, Esq.
223 REGISTRATION NUMBER: 29,754
224 REFERENCE/DOCKET NUMBER: 599/119600 US
225 TELEPHONE: (212) 527-7766
226 TELEFAX: (212) 753-5257
227 TELEX: 246687
228 INFORMATION FOR SEQ ID NO: 27:
229 SEQUENCE CHARACTERISTICS:
230 LENGTH: 10 amino acids
231 TYPE: amino acid
232 FEATURE: unknown
233 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
234 US 10 096-246 27
235
236 Query Match 36.4% Score 4; DB 11; Length 11;
237 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
238 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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240 QY 5 REK 8
241 ID 111
242 DB 1 REK 4
243
244 RESULT 44
245 US 09 966-871-3
246 Sequence 3; Application US/09966871
247 Patent No. US2002012753A1
248 GENERAL INFORMATION:
249 APPLICANT: Kopin, Alan S.
250 TITLE OF INVENTION: Active and Inactive
251 FILE REFERENCE: 60496/51202
252 CURRENT APPLICATION NUMBER: US/09/966-871
253 CURRENT FILING DATE: 2001-09-28
254 PRIOR APPLICATION NUMBER: US 60/243,550
255 PRIOR FILING DATE: 2000-09-28
256 NUMBER OF SEQ ID NOS: 87
257 SOFTWARE: FASTSEQ for Windows Version 4.0
258 SEQ ID NO: 3
259 LENGTH: 11
260 TYPE: PKT
261 ORGANISM: Homo sapiens
262 US 09 966-871-3
263
264 Query Match 36.4% Score 4; DB 11; Length 11;
265 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
266 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
267
268 QY 5 REK 8
269 ID 111
270 DB 1 REK 4
271
272 RESULT 44
273 US 09 976-904A-239
274 Sequence 259; Application US/09876904A
275 Publication No. US20030072794A1
276 GENERAL INFORMATION:
277 APPLICANT: BOULIKAS, JENI
278 TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA LIPIDGENES TM) AND THERAPEUTIC
279 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
280 FILE REFERENCE: 14-2002-00
281 CURRENT APPLICATION NUMBER: US/09/876,904A
282 CURRENT FILING DATE: 2002-05-08
283 PRIOR APPLICATION NUMBER: US 65/219,925
284 PRIOR FILING DATE: 2000-06-09
285 NUMBER OF SEQ ID NOS: 629
286 SOFTWARE: Patent In Ver. 2.1
287 SEQ ID NO: 239
288 LENGTH: 11
289 TYPE: PKT
290 ORGANISM: Unknown organism
291 FEATURE:
292 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
293 US-09-876-904A-239
294
295 Query Match 36.4% Score 4; DB 11; Length 11;
296 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
297 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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299 QY 5 REK 8
300 ID 111
301 DB 1 REK 11
302
303 RESULT 44
304 US 10 039-645 3
305 Sequence 3; Application US/10049645
306 Publication No. US2002047170A1
307 GENERAL INFORMATION:
308 APPLICANT: Kopin, Alan S.
309 TITLE OF INVENTION: Constitutively Active, Hypersensitive,
310 FILE REFERENCE: 60496/51002
311 CURRENT APPLICATION NUMBER: US/10/039,645
312 CURRENT FILING DATE: 2001-10-25
313 PRIOR APPLICATION NUMBER: US 60/243,550
314 PRIOR FILING DATE: 2000-10-25
315 NUMBER OF SEQ ID NOS: 87
316 SOFTWARE: FASTSEQ for Windows Version 4.0
317 SEQ ID NO: 4
318 LENGTH: 11
319 TYPE: PKT
320 ORGANISM: Homo sapiens
321 US 10 039-645 3
322
323 Query Match 36.4% Score 4; DB 14; Length 11;
324 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
325 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
326
327 QY 5 REK 8
328 ID 111
329 DB 1 REK 4
330
331 RESULT 44
332 US 10 139-084 3
333 Sequence 1; Application US/13149084
334 Publication No. US2003087313A1
335 GENERAL INFORMATION:
336 APPLICANT: Kopin, Alan S.
337 TITLE OF INVENTION: Intra-Response-Based Methods for
338 FILE REFERENCE: 60496/51002
339 CURRENT APPLICATION NUMBER: US/10/149,084
340
341 STATE: New York
342 COUNTRY: United States of America
343 ZIP: 10022
344 COMPUTER READABLE FORM:
345 MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
346 COMPUTER: COMPAQ, PROLIMA 300 4/26
347 OPERATING SYSTEM: DOS 5.0
348 SOFTWARE: WORD POLICE 5.2
349 CURRENT APPLICATION NUMBER: US/09/096-246
350 FILING DATE: 14-Mar-2002
351 PRIOR APPLICATION DATA:
352 APPLICATION NUMBER: US/09/119-04
353 FILING DATE: 10-Sep-1995
354 ATTORNEY/AGENT INFORMATION:
355 NAME: Adja C. Gouffis, Esq.
356 REGISTRATION NUMBER: 29,754
357 REFERENCE/DOCKET NUMBER: 599/119600 US
358 TELEPHONE: (212) 527-7766
359 TELEFAX: (212) 753-5257
360 TELEX: 246687
361 INFORMATION FOR SEQ ID NO: 27:
362 SEQUENCE CHARACTERISTICS:
363 LENGTH: 10 amino acids
364 TYPE: amino acid
365 FEATURE: unknown
366 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
367 US 10 096-246 27
368
369 Query Match 36.4% Score 4; DB 11; Length 11;
370 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
371 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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373 QY 5 REK 8
374 ID 111
375 DB 1 REK 4
376
377 RESULT 44
378 US 09 966-871-3
379 Sequence 3; Application US/09966871
380 Patent No. US2002012753A1
381 GENERAL INFORMATION:
382 APPLICANT: Kopin, Alan S.
383 TITLE OF INVENTION: Active and Inactive
384 FILE REFERENCE: 60496/51202
385 CURRENT APPLICATION NUMBER: US/09/966-871
386 CURRENT FILING DATE: 2001-09-28
387 PRIOR APPLICATION NUMBER: US 60/243,550
388 PRIOR FILING DATE: 2000-09-28
389 NUMBER OF SEQ ID NOS: 87
390 SOFTWARE: FASTSEQ for Windows Version 4.0
391 SEQ ID NO: 3
392 LENGTH: 11
393 TYPE: PKT
394 ORGANISM: Homo sapiens
395 US 09 966-871-3
396
397 Query Match 36.4% Score 4; DB 11; Length 11;
398 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
399 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
400
401 QY 5 REK 8
402 ID 111
403 DB 1 REK 4
404
405 RESULT 44
406 US 09 976-904A-239
407 Sequence 259; Application US/09876904A
408 Publication No. US20030072794A1
409 GENERAL INFORMATION:
410 APPLICANT: BOULIKAS, JENI
411 TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA LIPIDGENES TM) AND THERAPEUTIC
412 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
413 FILE REFERENCE: 14-2002-00
414 CURRENT APPLICATION NUMBER: US/09/876,904A
415 CURRENT FILING DATE: 2002-05-08
416 PRIOR APPLICATION NUMBER: US 65/219,925
417 PRIOR FILING DATE: 2000-06-09
418 NUMBER OF SEQ ID NOS: 629
419 SOFTWARE: Patent In Ver. 2.1
420 SEQ ID NO: 239
421 LENGTH: 11
422 TYPE: PKT
423 ORGANISM: Unknown organism
424 FEATURE:
425 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
426 US-09-876-904A-239
427
428 Query Match 36.4% Score 4; DB 11; Length 11;
429 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
430 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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432 QY 5 REK 8
433 ID 111
434 DB 1 REK 11
435
436 RESULT 44
437 US 10 039-645 3
438 Sequence 3; Application US/10049645
439 Publication No. US2002047170A1
440 GENERAL INFORMATION:
441 APPLICANT: Kopin, Alan S.
442 TITLE OF INVENTION: Constitutively Active, Hypersensitive,
443 FILE REFERENCE: 60496/51002
444 CURRENT APPLICATION NUMBER: US/10/039,645
445 CURRENT FILING DATE: 2001-10-25
446 PRIOR APPLICATION NUMBER: US 60/243,550
447 PRIOR FILING DATE: 2000-10-25
448 NUMBER OF SEQ ID NOS: 87
449 SOFTWARE: FASTSEQ for Windows Version 4.0
450 SEQ ID NO: 4
451 LENGTH: 11
452 TYPE: PKT
453 ORGANISM: Homo sapiens
454 US 10 039-645 3
455
456 Query Match 36.4% Score 4; DB 14; Length 11;
457 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
458 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
459
460 QY 5 REK 8
461 ID 111
462 DB 1 REK 4
463
464 RESULT 44
465 US 10 139-084 3
466 Sequence 1; Application US/13149084
467 Publication No. US2003087313A1
468 GENERAL INFORMATION:
469 APPLICANT: Kopin, Alan S.
470 TITLE OF INVENTION: Intra-Response-Based Methods for
471 FILE REFERENCE: 60496/51002
472 CURRENT APPLICATION NUMBER: US/10/149,084
473
474 STATE: New York
475 COUNTRY: United States of America
476 ZIP: 10022
477 COMPUTER READABLE FORM:
478 MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
479 COMPUTER: COMPAQ, PROLIMA 300 4/26
480 OPERATING SYSTEM: DOS 5.0
481 SOFTWARE: WORD POLICE 5.2
482 CURRENT APPLICATION NUMBER: US/09/096-246
483 FILING DATE: 14-Mar-2002
484 PRIOR APPLICATION DATA:
485 APPLICATION NUMBER: US/09/119-04
486 FILING DATE: 10-Sep-1995
487 ATTORNEY/AGENT INFORMATION:
488 NAME: Adja C. Gouffis, Esq.
489 REGISTRATION NUMBER: 29,754
490 REFERENCE/DOCKET NUMBER: 599/119600 US
491 TELEPHONE: (212) 527-7766
492 TELEFAX: (212) 753-5257
493 TELEX: 246687
494 INFORMATION FOR SEQ ID NO: 27:
495 SEQUENCE CHARACTERISTICS:
496 LENGTH: 10 amino acids
497 TYPE: amino acid
498 FEATURE: unknown
499 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
500 US 10 096-246 27
501
502 Query Match 36.4% Score 4; DB 11; Length 11;
503 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
504 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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506 QY 5 REK 8
507 ID 111
508 DB 1 REK 4
509
510 RESULT 44
511 US 09 966-871-3
512 Sequence 3; Application US/09966871
513 Patent No. US2002012753A1
514 GENERAL INFORMATION:
515 APPLICANT: Kopin, Alan S.
516 TITLE OF INVENTION: Active and Inactive
517 FILE REFERENCE: 60496/51202
518 CURRENT APPLICATION NUMBER: US/09/966-871
519 CURRENT FILING DATE: 2001-09-28
520 PRIOR APPLICATION NUMBER: US 60/243,550
521 PRIOR FILING DATE: 2000-09-28
522 NUMBER OF SEQ ID NOS: 87
523 SOFTWARE: FASTSEQ for Windows Version 4.0
524 SEQ ID NO: 3
525 LENGTH: 11
526 TYPE: PKT
527 ORGANISM: Homo sapiens
528 US 09 966-871-3
529
530 Query Match 36.4% Score 4; DB 11; Length 11;
531 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
532 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
533
534 QY 5 REK 8
535 ID 111
536 DB 1 REK 4
537
538 RESULT 44
539 US 09 976-904A-239
540 Sequence 259; Application US/09876904A
541 Publication No. US20030072794A1
542 GENERAL INFORMATION:
543 APPLICANT: BOULIKAS, JENI
544 TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA LIPIDGENES TM) AND THERAPEUTIC
545 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
546 FILE REFERENCE: 14-2002-00
547 CURRENT APPLICATION NUMBER: US/09/876,904A
548 CURRENT FILING DATE: 2002-05-08
549 PRIOR APPLICATION NUMBER: US 65/219,925
550 PRIOR FILING DATE: 2000-06-09
551 NUMBER OF SEQ ID NOS: 629
552 SOFTWARE: Patent In Ver. 2.1
553 SEQ ID NO: 239
554 LENGTH: 11
555 TYPE: PKT
556 ORGANISM: Unknown organism
557 FEATURE:
558 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
559 US-09-876-904A-239
560
561 Query Match 36.4% Score 4; DB 11; Length 11;
562 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
563 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
564
565 QY 5 REK 8
566 ID 111
567 DB 1 REK 11
568
569 RESULT 44
570 US 10 039-645 3
571 Sequence 3; Application US/10049645
572 Publication No. US2002047170A1
573 GENERAL INFORMATION:
574 APPLICANT: Kopin, Alan S.
575 TITLE OF INVENTION: Constitutively Active, Hypersensitive,
576 FILE REFERENCE: 60496/51002
577 CURRENT APPLICATION NUMBER: US/10/039,645
578 CURRENT FILING DATE: 2001-10-25
579 PRIOR APPLICATION NUMBER: US 60/243,550
580 PRIOR FILING DATE: 2000-10-25
581 NUMBER OF SEQ ID NOS: 87
582 SOFTWARE: FASTSEQ for Windows Version 4.0
583 SEQ ID NO: 4
584 LENGTH: 11
585 TYPE: PKT
586 ORGANISM: Homo sapiens
587 US 10 039-645 3
588
589 Query Match 36.4% Score 4; DB 14; Length 11;
590 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
591 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
592
593 QY 5 REK 8
594 ID 111
595 DB 1 REK 4
596
597 RESULT 44
598 US 10 139-084 3
599 Sequence 1; Application US/13149084
600 Publication No. US2003087313A1
601 GENERAL INFORMATION:
602 APPLICANT: Kopin, Alan S.
603 TITLE OF INVENTION: Intra-Response-Based Methods for
604 FILE REFERENCE: 60496/51002
605 CURRENT APPLICATION NUMBER: US/10/149,084
606
607 STATE: New York
608 COUNTRY: United States of America
609 ZIP: 10022
610 COMPUTER READABLE FORM:
611 MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
612 COMPUTER: COMPAQ, PROLIMA 300 4/26
613 OPERATING SYSTEM: DOS 5.0
614 SOFTWARE: WORD POLICE 5.2
615 CURRENT APPLICATION NUMBER: US/09/096-246
616 FILING DATE: 14-Mar-2002
617 PRIOR APPLICATION DATA:
618 APPLICATION NUMBER: US/09/119-04
619 FILING DATE: 10-Sep-1995
620 ATTORNEY/AGENT INFORMATION:
621 NAME: Adja C. Gouffis, Esq.
622 REGISTRATION NUMBER: 29,754
623 REFERENCE/DOCKET NUMBER: 599/119600 US
624 TELEPHONE: (212) 527-7766
625 TELEFAX: (212) 753-5257
626 TELEX: 246687
627 INFORMATION FOR SEQ ID NO: 27:
628 SEQUENCE CHARACTERISTICS:
629 LENGTH: 10 amino acids
630 TYPE: amino acid
631 FEATURE: unknown
632 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
633 US 10 096-246 27
634
635 Query Match 36.4% Score 4; DB 11; Length 11;
636 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
637 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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639 QY 5 REK 8
640 ID 111
641 DB 1 REK 4
642
643 RESULT 44
644 US 09 966-871-3
645 Sequence 3; Application US/09966871
646 Patent No. US2002012753A1
647 GENERAL INFORMATION:
648 APPLICANT: Kopin, Alan S.
649 TITLE OF INVENTION: Active and Inactive
650 FILE REFERENCE: 60496/51202
651 CURRENT APPLICATION NUMBER: US/09/966-871
652 CURRENT FILING DATE: 2001-09-28
653 PRIOR APPLICATION NUMBER: US 60/243,550
654 PRIOR FILING DATE: 2000-09-28
655 NUMBER OF SEQ ID NOS: 87
656 SOFTWARE: FASTSEQ for Windows Version 4.0
657 SEQ ID NO: 3
658 LENGTH: 11
659 TYPE: PKT
660 ORGANISM: Homo sapiens
661 US 09 966-871-3
662
663 Query Match 36.4% Score 4; DB 11; Length 11;
664 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
665 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
666
667 QY 5 REK 8
668 ID 111
669 DB 1 REK 4
670
671 RESULT 44
672 US 09 976-904A-239
673 Sequence 259; Application US/09876904A
674 Publication No. US20030072794A1
675 GENERAL INFORMATION:
676 APPLICANT: BOULIKAS, JENI
677 TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA LIPIDGENES TM) AND THERAPEUTIC
678 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
679 FILE REFERENCE: 14-2002-00
680 CURRENT APPLICATION NUMBER: US/09/876,904A
681 CURRENT FILING DATE: 2002-05-08
682 PRIOR APPLICATION NUMBER: US 65/219,925
683 PRIOR FILING DATE: 2000-06-09
684 NUMBER OF SEQ ID NOS: 629
685 SOFTWARE: Patent In Ver. 2.1
686 SEQ ID NO: 239
687 LENGTH: 11
688 TYPE: PKT
689 ORGANISM: Unknown organism
690 FEATURE:
691 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
692 US-09-876-904A-239
693
694 Query Match 36.4% Score 4; DB 11; Length 11;
695 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
696 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
697
698 QY 5 REK 8
699 ID 111
700 DB 1 REK 11
701
702 RESULT 44
703 US 10 039-645 3
704 Sequence 3; Application US/10049645
705 Publication No. US2002047170A1
706 GENERAL INFORMATION:
707 APPLICANT: Kopin, Alan S.
708 TITLE OF INVENTION: Constitutively Active, Hypersensitive,
709 FILE REFERENCE: 60496/51002
710 CURRENT APPLICATION NUMBER: US/10/039,645
711 CURRENT FILING DATE: 2001-10-25
712 PRIOR APPLICATION NUMBER: US 60/243,550
713 PRIOR FILING DATE: 2000-10-25
714 NUMBER OF SEQ ID NOS: 87
715 SOFTWARE: FASTSEQ for Windows Version 4.0
716 SEQ ID NO: 4
717 LENGTH: 11
718 TYPE: PKT
719 ORGANISM: Homo sapiens
720 US 10 039-645 3
721
722 Query Match 36.4% Score 4; DB 14; Length 11;
723 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
724 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
725
726 QY 5 REK 8
727 ID 111
728 DB 1 REK 4
729
730 RESULT 44
731 US 10 139-084 3
732 Sequence 1; Application US/13149084
733 Publication No. US2003087313A1
734 GENERAL INFORMATION:
735 APPLICANT: Kopin, Alan S.
736 TITLE OF INVENTION: Intra-Response-Based Methods for
737 FILE REFERENCE: 60496/51002
738 CURRENT APPLICATION NUMBER: US/10/149,084
739
740 STATE: New York
741 COUNTRY: United States of America
742 ZIP: 10022
743 COMPUTER READABLE FORM:
744 MEDIUM TYPE: DISKETTE, 5.25 inch, 360 KB
745 COMPUTER: COMPAQ, PROLIMA 300 4/26
746 OPERATING SYSTEM: DOS 5.0
747 SOFTWARE: WORD POLICE 5.2
748 CURRENT APPLICATION NUMBER: US/09/096-246
749 FILING DATE: 14-Mar-2002
750 PRIOR APPLICATION DATA:
751 APPLICATION NUMBER: US/09/119-04
752 FILING DATE: 10-Sep-1995
753 ATTORNEY/AGENT INFORMATION:
754 NAME: Adja C. Gouffis, Esq.
755 REGISTRATION NUMBER: 29,754
756 REFERENCE/DOCKET NUMBER: 599/119600 US
757 TELEPHONE: (212) 527-7766
758 TELEFAX: (212) 753-5257
759 TELEX: 246687
760 INFORMATION FOR SEQ ID NO: 27:
761 SEQUENCE CHARACTERISTICS:
762 LENGTH: 10 amino acids
763 TYPE: amino acid
764 FEATURE: unknown
765 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
766 US 10 096-246 27
767
768 Query Match 36.4% Score 4; DB 11; Length 11;
769 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
770 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
771
772 QY 5 REK 8
773 ID 111
774 DB 1 REK 4
775
776 RESULT 44
777 US 09 966-871-3
778 Sequence 3; Application US/09966871
779 Patent No. US2002012753A1
780 GENERAL INFORMATION:
781 APPLICANT: Kopin, Alan S.
782 TITLE OF INVENTION: Active and Inactive
783 FILE REFERENCE: 60496/51202
784 CURRENT APPLICATION NUMBER: US/09/966-871
785 CURRENT FILING DATE: 2001-09-28
786 PRIOR APPLICATION NUMBER: US 60/243,550
787 PRIOR FILING DATE: 2000-09-28
788 NUMBER OF SEQ ID NOS: 87
789 SOFTWARE: FASTSEQ for Windows Version 4.0
790 SEQ ID NO: 3
791 LENGTH: 11
792 TYPE: PKT
793 ORGANISM: Homo sapiens
794 US 09 966-871-3
795
796 Query Match 36.4% Score 4; DB 11; Length 11;
797 Best Local Similarity 100.0%; Pred. No. 4, 7e-02;
798 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
799
800 QY 5 REK 8
801 ID 111
802 DB 1 REK 4
803
804 RESULT 44
805 US 09 976-904A-239
806 Sequence 259; Application US/09876904A
807 Publication No. US20030072794A1
808 GENERAL INFORMATION:
809 APPLICANT: BOULIKAS, JENI
810 TITLE OF INVENTION: ENCAPSULATION OF PLASMA-DNA LIPIDGENES TM) AND THERAPEUTIC
811 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
812 FILE REFERENCE: 14-2002-00
813 CURRENT APPLICATION NUMBER: US/09/876,904A
814 CURRENT FILING DATE: 2002-05-08
815 PRIOR APPLICATION NUMBER: US 65/219,925
816 PRIOR FILING DATE: 2000-06-09
817 NUMBER OF SEQ ID NOS: 629
818 SOFTWARE: Patent In Ver. 2.1
819 SEQ ID NO: 239
8
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1 CURRENT FILING DATE: 2002-12-24  
 2 PRIOR APPLICATION NUMBER: US 60/288,447  
 3 PRIOR FILING DATE: 2001-05-04  
 4 NUMBER OF SEQ ID NOS: 74  
 5 SOFTWARE: FASTSEQ for Windows Version 4.0  
 6 SEQ ID NO: 4  
 7 LENGTH: 11  
 8 TYPE: PPT  
 9 ORGANISM: Homo sapiens  
 10 US 10-075-884-14

Quality Match: 46.4%, Score 47, DB 15, Length 11  
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 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RRSK 8  
 10 1 5RRK 4

RESULT 45  
 US 10 093-958-1  
 1 Sequence 1: Application US/160955B  
 2 Publication No. US2004004442A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Gillies, Stephen  
 5 APPLICANT: Jeffrey, Way  
 6 TITLE OF INVENTION: Expression Testes body for Proteins Containing a Hybrid Isotype At  
 7 FILE REFERENCE: MO1074  
 8 CURRENT APPLICATION NUMBER: US/10/093-958  
 9 PRIOR FILING DATE: 2002-04-07  
 10 PRIOR APPLICATION NUMBER: US 60/274,096  
 11 PRIOR FILING DATE: 2001-04-07  
 12 NUMBER OF SEQ ID NOS: 50  
 13 SOFTWARE: Patent In version 4.0  
 14 SEQ ID NO: 1  
 15 LENGTH: 12  
 16 TYPE: PPT  
 17 ORGANISM: artificial sequence  
 18 FEATURE:  
 19 OTHER INFORMATION: IgG2 hinge sequence  
 20 US 10 093-958-1

Quality Match: 46.4%, Score 47, DB 15, Length 12  
 Best Local Similarity: 100.0%, Pred. No. 4, Seq. 4  
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 RRSK 9  
 10 1 5RRK 4

RESULT 46  
 US 10 075-884-10  
 1 Sequence 12: Application US/16075659  
 2 Publication No. US20040104622A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Robbins, Paul E.  
 5 APPLICANT: Mi, Zhibao  
 6 APPLICANT: Filizelli, Raymond  
 7 APPLICANT: Giordano, Joseph C.  
 8 APPLICANT: Gambuto, Andrea  
 9 TITLE OF INVENTION: IDENTIFICATION OF PROTEIN-DEGRADABLE  
 10 TITLE OF INVENTION: FACILITATE DEGRADATION OF PLASMIN AND/OR ANALYSE AND/OR ANALYSE  
 11 FILE REFERENCE: AP32573-AAA 072490-0-47  
 12 CURRENT APPLICATION NUMBER: US/10/075-889  
 13 CURRENT FILING DATE: 2002-02-24  
 14 PRIOR APPLICATION NUMBER: 60/151,980  
 15 PRIOR FILING DATE: 1999-09-01  
 16 PRIOR APPLICATION NUMBER: 60/288,444  
 17 PRIOR FILING DATE: 2000-04-14

1 NUMBER OF SEQ ID NOS: 99  
 2 SOFTWARE: FASTSEQ for Windows Version 4.0  
 3 SEQ ID NO: 10  
 4 LENGTH: 12  
 5 TYPE: PPT  
 6 ORGANISM: Artificial Sequence  
 7 FEATURE:  
 8 OTHER INFORMATION: Random peptide library  
 9 US 10 075-889-10

Quality Match: 46.4%, Score 47, DB 15, Length 12  
 Best Local Similarity: 100.0%, Pred. No. 5, Seq. 4  
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 RRSK 10  
 10 4 RRSK 7

RESULT 47  
 US 09 876-904A-79  
 1 Sequence 79: Application US/09876904A  
 2 Publication No. US20040072794A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: BOULIKAS, TENI  
 5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/LIPOSOEMIC PEPTIDE  
 7 FILE REFERENCE: TH-2002-00  
 8 CURRENT APPLICATION NUMBER: US/09/876,904A  
 9 CURRENT FILING DATE: 2001-06-08  
 10 PRIOR APPLICATION NUMBER: US 60/210,925  
 11 PRIOR FILING DATE: 2000-06-09  
 12 NUMBER OF SEQ ID NOS: 629  
 13 SOFTWARE: Patent In Ver. 2.1  
 14 SEQ ID NO: 79  
 15 LENGTH: 13  
 16 TYPE: PPT  
 17 ORGANISM: Artificial Sequence  
 18 FEATURE:  
 19 OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide crossli  
 20 OTHER INFORMATION: to bovine serum albumin  
 21 US 09 876 904A-79

Quality Match: 46.4%, Score 47, DB 11, Length 13  
 Best Local Similarity: 100.0%, Pred. No. 5, Seq. 4  
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARRT 4  
 10 5 ARRT 8

RESULT 48  
 US 09 876-904A-79  
 1 Sequence 196: Application US/09876904A  
 2 Publication No. US20040072794A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: BOULIKAS, TENI  
 5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/LIPOSOEMIC PEPTIDE  
 7 FILE REFERENCE: TH-2002-00  
 8 CURRENT APPLICATION NUMBER: US/09/876,904A  
 9 CURRENT FILING DATE: 2001-06-08  
 10 PRIOR APPLICATION NUMBER: US 60/210,925  
 11 PRIOR FILING DATE: 2000-06-09  
 12 NUMBER OF SEQ ID NOS: 629  
 13 SOFTWARE: Patent In Ver. 2.1  
 14 SEQ ID NO: 196  
 15 LENGTH: 14  
 16 TYPE: PPT  
 17 ORGANISM: Artificial Sequence

1 FEATURE:  
2 OTHER INFORMATION: Karyophilic peptide  
3 US-09-876-904A-19b

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QY 2 KSK 5  
II  
DB 5 KSK 8

RESULT 49  
US-09-876-904A-454  
1 Sequence 454 Application US-09-769-04A  
2 Publication No. US2003007294A1  
3 GENERAL INFORMATION:  
4 APPLICANT: BOWLEKAS, TENJ  
5 TITLE OF INVENTION: ENCAPSULATION OF PLASMI DNA (CODGENES TM) AND THERAPEUTIC  
6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PUS AGENT PEPTIDE  
7 TITLE OF INVENTION: CONJUGATES AND TARGETED LIPID-SOME COMPLEXES  
8 FILE REFERENCE: TB-2002-00  
9 CURRENT APPLICATION NUMBER: US-09-876-904A  
10 PRIORITY FILING DATE: 2001-06-08  
11 PRIOR APPLICATION NUMBER: US 60/216,925  
12 PRIOR FILING DATE: 2000-06-09  
13 NUMBER OF SEQ ID NOS: 629  
14 SOFTWARE: PatentIn Ver. 2.1  
15 SEQ ID NO: 454  
16 LENGTH: 14  
17 TYPE: PRT  
18 ORGANISM: Unknown organism  
19 FEATURE:  
20 OTHER INFORMATION: Description of Unknown organism: Mergo and human cell  
21 OTHER INFORMATION: (glucocorticoid receptor)  
22 US-09-876-904A-454

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Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 ASK 4  
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DB 2 ASK 6

RESULT 50  
US-09-108-100A-42  
1 Sequence 42 Application US/1610810A  
2 Publication No. US20030059805A1  
3 GENERAL INFORMATION:  
4 APPLICANT: RAPPOLD-HOERBRAND, GUERIN  
5 APPLICANT: KAO, FROOLE  
6 TITLE OF INVENTION: HUMAN GROWTH GENE AND SHORT SEQUENCE GENE REGION  
7 FILE REFERENCE: 108351-00004  
8 CURRENT APPLICATION NUMBER: US/16/154,100A  
9 PRIORITY FILING DATE: 2002-08-23  
10 PRIOR APPLICATION NUMBER: 09/147,699  
11 PRIOR FILING DATE: 1999-06-24  
12 PRIOR APPLICATION NUMBER: PCT/EP97/09,036  
13 PRIOR FILING DATE: 1997-09-29  
14 PCT APPLICATION NUMBER: 66/027,645  
15 PRIOR FILING DATE: 1996-10-01  
16 PRIOR APPLICATION NUMBER: EP/97100583.0  
17 PRIOR FILING DATE: 1997-01-16  
18 NUMBER OF SEQ ID NOS: 55  
19 SOFTWARE: PatentIn Ver. 2.1  
20 SEQ ID NO 42  
21 LENGTH: 15  
22 TYPE: PRT  
23 ORGANISM: Artificial Sequence  
24 FEATURE:

1 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
2 OTHER INFORMATION: peptide  
3 US-10-158-160A-42

Query Match 36.4% Score 47 DB 15 Length 15  
Best Local Similarity 100.0% Prod No. 60729  
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KSK 11  
II  
DB 2 KSK 11

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100 proteins - protein search, using sw model

Run on: September 30, 2003, 10:11:03 : Search time 21.5 seconds  
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Title: US-09-787-443-15

Perfect score: 11

Sequence: 1 ASQAKRKGP 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	5	45.5	13	10	US-09-746-170-8	Sequence 6, Appl
4	5	45.5	13	10	US-09-746-170-11	Sequence 11, Appl
5	5	45.5	13	10	US-09-746-170-14	Sequence 14, Appl
6	5	45.5	13	10	US-09-746-170-17	Sequence 17, Appl
7	5	45.5	13	10	US-09-746-170-20	Sequence 20, Appl
8	5	45.5	13	10	US-09-746-170-23	Sequence 23, Appl
9	5	45.5	13	10	US-09-746-170-26	Sequence 26, Appl
10	5	45.5	13	10	US-09-746-170-29	Sequence 29, Appl
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13	5	45.5	13	10	US-09-746-170-38	Sequence 38, Appl
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17	4	36.4	8	9	US-09-243-079-47	Sequence 47, Appl
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137	4	36.4	8	11	US 09 726 470A 174	Sequence 204, App	210	4	36.4	13	11	US 09 876 904A 433	Sequence 433, App
138	4	36.4	8	11	US 09 726 470A 174	Sequence 205, App	211	4	36.4	13	11	US 09 876 904A 434	Sequence 434, App
139	4	36.4	8	11	US 09 726 470A 174	Sequence 206, App	212	4	36.4	13	11	US 09 876 904A 435	Sequence 435, App
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142	4	36.4	8	11	US 09 726 470A 174	Sequence 209, App	215	4	36.4	13	11	US 09 876 904A 438	Sequence 438, App
143	4	36.4	8	11	US 09 726 470A 174	Sequence 210, App	216	4	36.4	13	11	US 09 876 904A 439	Sequence 439, App
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145	4	36.4	8	11	US 09 726 470A 174	Sequence 212, App	218	4	36.4	13	11	US 09 876 904A 441	Sequence 441, App
146	4	36.4	8	11	US 09 726 470A 174	Sequence 213, App	219	4	36.4	13	11	US 09 876 904A 442	Sequence 442, App
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## ALIGNMENTS

RESUME 1  
US-09-787-443-15  
Sequence 241, App  
Patient No. US200201294-1A1  
GENERAL INFORMATION  
APPLICANT: Karim, Jonathan  
APPLICANT: Walker, Stephen  
TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecular  
FILE REFERENCE: 22626/1260  
CURRENT APPLICATION NUMBER: US/09/746,170  
PRIORITY DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/131,804  
PRIOR FILING DATE: 1999-12-22  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: GATC-GENE VERSION: 3.0  
SEQ ID NO: 2  
LENGTH: 13  
TYPE: CDS  
ORGANISM: Hepatitis C Virus  
US-09-787-443-15

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Query Match          45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Prev. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KKKKG 9
QD      11 1
       7 KKKKG 11

RESULT 2
US-09-746-170-6
: Sequence 5; Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 5
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-5

Query Match          45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Prev. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KKKKG 9
QD      11 1
       7 KKKKG 11

RESULT 3
US-09-746-170-8
: Sequence 8; Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 8
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-8

Query Match          45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Prev. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KKKKG 9
QD      11 1
       7 KKKKG 11

RESULT 4
US-09-746-170-11
: Sequence 11; Application US/09746170
: Patent No. US20020127543A1

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: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 11
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-11

Query Match          45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Prev. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KKKKG 9
QD      11 1
       7 KKKKG 11

RESULT 5
US-09-746-170-14
: Sequence 14; Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-14

Query Match          45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Prev. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KKKKG 9
QD      11 1
       7 KKKKG 11

RESULT 6
US-09-746-170-17
: Sequence 17; Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 17
: LENGTH: 13

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Number of Seq ID NOS: 45	Score: 45.5%	Seq ID NOS: 45	Score: 45.5%	Seq ID NOS: 45
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3. LENGTH: 12	100.0%	100.0%	100.0%	100.0%
4. TYPE: PRI	100.0%	100.0%	100.0%	100.0%
5. ORGANISM: Hepatitis C virus	100.0%	100.0%	100.0%	100.0%
US-09-746-170-43	100.0%	100.0%	100.0%	100.0%
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Best Local Similarity	100.0%	100.0%	100.0%	100.0%
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10	4 AKRR 7	100.0%	100.0%	100.0%
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4. TYPE: PRI	100.0%	100.0%	100.0%	100.0%
5. ORGANISM: Hepatitis C virus	100.0%	100.0%	100.0%	100.0%
US-09-746-170-43	100.0%	100.0%	100.0%	100.0%
Query Match	45.5%	45.5%	45.5%	45.5%
Best Local Similarity	100.0%	100.0%	100.0%	100.0%
Matches	43	Conservative	0	Mismatches
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10	4 AKRR 7	100.0%	100.0%	100.0%
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4. TYPE: PRI	100.0%	100.0%	100.0%	100.0%
5. ORGANISM: Hepatitis C virus	100.0%	100.0%	100.0%	100.0%
US-09-746-170-43	100.0%	100.0%	100.0%	100.0%
Query Match	45.5%	45.5%	45.5%	45.5%
Best Local Similarity	100.0%	100.0%	100.0%	100.0%
Matches	43	Conservative	0	Mismatches
09	4 AKRR 7	100.0%	100.0%	100.0%
10	4 AKRR 7	100.0%	100.0%	100.0%



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RESULT 20
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1 Sequence 43, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GCI-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 PRIOR FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 43
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence
22 FEATURES:
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived
24 OTHER INFORMATION: peptide
25 US-09-726-470A-37
26 Query Match: 36.4%, Score 47, DB 11, Length 8;
27 Best Local Similarity: 100.0%, Prod. No. 5e+05;
28 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
29
30 QY 3 AKKK 7
31 1 1
32 2 AKKK 5
33
34 RESULT 21
US-09-726-470A-40
1 Sequence 40, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GCI-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 PRIOR FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 40
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence
22 FEATURES:
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived
24 OTHER INFORMATION: peptide
25 OTHER INFORMATION: Synthesised with free amino terminus and as the
26 OTHER INFORMATION: C-terminal carboxamide
27 US-09-726-470A-40
28 Query Match: 36.4%, Score 47, DB 11, Length 8;
29 Best Local Similarity: 100.0%, Prod. No. 5e+05;
30 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

```

```

QY 4 AKKK 7
1 1
2 AKKK 5
3
4 RESULT 22
US-09-726-470A-42
1 Sequence 42, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GCI-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 CURRENT FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 42
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence
22 FEATURES:
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived
24 OTHER INFORMATION: peptide
25 OTHER INFORMATION: Synthesised with free amino terminus and as the
26 OTHER INFORMATION: C-terminal carboxamide
27 US-09-726-470A-42
28 Query Match: 36.4%, Score 47, DB 11, Length 8;
29 Best Local Similarity: 100.0%, Prod. No. 5e+05;
30 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
31
32 QY 4 AKKK 7
33 1 1
34 2 AKKK 5
35
36 RESULT 23
US-09-726-470A-43
1 Sequence 43, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GCI-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 CURRENT FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 43
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence

```

1 FEATURE:  
 2 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 3 OTHER INFORMATION: peptide  
 4 FEATURE:  
 5 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 6 OTHER INFORMATION: C-terminal carboxamide  
 7 FEATURE:  
 8 NAME/KEY: SITE  
 9 LOCATION: (1)  
 10 OTHER INFORMATION: Xaa - 2 Thionylamino  
 11 US-09-726-470A-43

Query Match 36.4% Score 41 IP 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AKRR 7  
 III  
 2 AKRR 5

RESULT 24  
 US-09-726-470A-44  
 1 Sequence 44, Application: US/09726470A  
 2 Publication No. US2003046628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela 1  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McIntus, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 FILE REFERENCE: 014  
 11 CURRENT APPLICATION NUMBER: US/09726470A  
 12 PRIOR FILING DATE: 2000-11-29  
 13 PRIOR APPLICATION NUMBER: GB 9928423.6  
 14 PRIOR FILING DATE: 1999-11-30  
 15 NUMBER OF SEQ ID NOS: 275  
 16 SOFTWARE: Patent In Ver. 2.1  
 17 SEQ ID NO: 44  
 18 LENGTH: 8  
 19 TYPE: PPT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 23 OTHER INFORMATION: peptide  
 24 FEATURE:  
 25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 26 OTHER INFORMATION: C-terminal carboxamide  
 27 NAME/KEY: SITE  
 28 LOCATION: (1)  
 29 OTHER INFORMATION: Xaa - Histosettine  
 30 US-09-726-470A-44

Query Match 36.4% Score 41 IP 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AKRR 7  
 III  
 2 AKRR 5

RESULT 25  
 US-09-726-470A-45  
 1 Sequence 45, Application: US/09726470A  
 2 Publication No. US2003046628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela 1  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McIntus, Campbell

7 APPLICANT: Andrews, Martin J1  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 TITLE OF INVENTION: p21 Peptides  
 11 FILE REFERENCE: 014  
 12 CURRENT APPLICATION NUMBER: US/09726470A  
 13 PRIOR FILING DATE: 2000-11-29  
 14 PRIOR APPLICATION NUMBER: GB 9928423.6  
 15 PRIOR FILING DATE: 1999-11-30  
 16 NUMBER OF SEQ ID NOS: 275  
 17 SOFTWARE: Patent In Ver. 2.1  
 18 SEQ ID NO: 45  
 19 LENGTH: 8  
 20 TYPE: PPT  
 21 ORGANISM: Artificial Sequence  
 22 FEATURE:  
 23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 24 OTHER INFORMATION: peptide  
 25 FEATURE:  
 26 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 27 OTHER INFORMATION: C-terminal carboxamide  
 28 US-09-726-470A-45

Query Match 36.4% Score 41 IP 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AKRR 7  
 III  
 2 AKRR 5

RESULT 26  
 US-09-726-470A-46  
 1 Sequence 46, Application: US/09726470A  
 2 Publication No. US2003046628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela 1  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McIntus, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 TITLE OF INVENTION: p21 Peptides  
 11 FILE REFERENCE: 014  
 12 CURRENT APPLICATION NUMBER: US/09726470A  
 13 PRIOR FILING DATE: 2000-11-29  
 14 PRIOR APPLICATION NUMBER: GB 9928423.6  
 15 PRIOR FILING DATE: 1999-11-30  
 16 NUMBER OF SEQ ID NOS: 275  
 17 SOFTWARE: Patent In Ver. 2.1  
 18 SEQ ID NO: 46  
 19 LENGTH: 8  
 20 TYPE: PPT  
 21 ORGANISM: Artificial Sequence  
 22 FEATURE:  
 23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 24 OTHER INFORMATION: peptide  
 25 FEATURE:  
 26 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 27 OTHER INFORMATION: C-terminal carboxamide  
 28 NAME/KEY: SITE  
 29 LOCATION: (1)  
 30 OTHER INFORMATION: Xaa - L-L-Glutamyl-L-proline acid  
 31 US-09-726-470A-46

Query Match 36.4% Score 41 IP 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AKRR 7  
 III

DB 2 AKR 5

RESULT 27  
US 09-726-470A-75  
; Sequence 75, Application US/09726475A  
; Publication No. US2003036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; FILE REFERENCE: CCI 014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09-726 470A-75

Query Match 36.4% Score 4: DB 11: Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

QY 4 AKR 7  
DB 2 AKR 5

RESULT 28  
US 09-726-470A-75  
; Sequence 75, Application US/09726475A  
; Publication No. US2003036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; FILE REFERENCE: CCI-014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09 726 470A-75

Query Match 36.4% Score 4: DB 11: Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

QY 4 AKR 7  
DB 2 AKR 5

RESULT 29  
US 09-726-470A-75  
; Sequence 75, Application US/09726475A  
; Publication No. US2003036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; FILE REFERENCE: CCI 014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 76  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09-726-470A-76

Query Match 36.4% Score 4: DB 11: Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

QY 4 AKR 7  
DB 2 AKR 5

RESULT 30  
US 09-726-470A-77  
; Sequence 77, Application US/09726477A  
; Publication No. US2003036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; FILE REFERENCE: CCI-014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 77  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09 726 470A-77



1 FEATURE:  
2 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
3  
4 OTHER INFORMATION: peptide  
5  
6 FEATURE:  
7  
8 OTHER INFORMATION: Synthesised with free amino terminus and as the  
9  
10 OTHER INFORMATION: C-terminal carboxamide  
11  
12 FEATURE:  
13  
14 NAME/KEY: SITE  
15  
16 LOCATION: (6)  
17  
18 OTHER INFORMATION: Xaa - D Leu  
19  
20 US-09-726-470A-77

Query Match: 36.4% Score 47: DB 11: Length 8:  
Best Local Similarity: 100.0%: Pred. No. 5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 AKRR 7  
111  
DB 2 AKRR 5

RESULT 42  
US-09-726-470A-78  
1 Sequence 79: Application US/09726470A  
2 Publication No. US2003036628A1  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Zheleva, Daniela I  
6 APPLICANT: Fischer, Peter M  
7 APPLICANT: McInnes, Campbell  
8 APPLICANT: Andrews, Martin JI  
9 APPLICANT: Chan, Weng C  
10 APPLICANT: Atkinson, Gail E  
11  
12 TITLE OF INVENTION: p21 Peptides  
13  
14 FILE REFERENCED: 071-014  
15  
16 CURRENT APPLICATION NUMBER: US/09726470A  
17  
18 PRIOR FILING DATE: 2000-11-29  
19  
20 PRIOR FILING DATE: 1999-11-30  
21  
22 NUMBER OF SEQ ID NOS: 275  
23  
24 SOFTWARE: Patent. Ver. 2.1  
25  
26 SEQ ID NO 78  
27  
28 LENGTH: 8  
29  
30 TYPE: PRI  
31  
32 ORGANISM: Artificial Sequence  
33  
34 FEATURE:  
35  
36 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
37  
38 OTHER INFORMATION: peptide  
39  
40 FEATURE:  
41  
42 OTHER INFORMATION: Synthesised with free amino terminus and as the  
43  
44 OTHER INFORMATION: C-terminal carboxamide  
45  
46 US-09-726-470A-78

Query Match: 36.4% Score 47: DB 11: Length 8:  
Best Local Similarity: 100.0%: Pred. No. 5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 AKRR 7  
111  
DB 2 AKRR 5

RESULT 43  
US-09-726-470A-79  
1 Sequence 79: Application US/09726470A  
2 Publication No. US2003036628A1  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Zheleva, Daniela I  
6 APPLICANT: Fischer, Peter M  
7 APPLICANT: McInnes, Campbell  
8 APPLICANT: Andrews, Martin JI  
9 APPLICANT: Chan, Weng C  
10 APPLICANT: Atkinson, Gail E  
11  
12 TITLE OF INVENTION: p21 Peptides

1 FILE REFERENCED: 071-014  
2  
3 CURRENT APPLICATION NUMBER: US/09726470A  
4  
5 CURRENT FILING DATE: 2000-11-29  
6  
7 PRIOR APPLICATION NUMBER: GB 9928323.6  
8  
9 PRIOR FILING DATE: 1999-11-30  
10  
11 NUMBER OF SEQ ID NOS: 275  
12  
13 SOFTWARE: Patent. Ver. 2.1  
14  
15 SEQ ID NO 79  
16  
17 LENGTH: 8  
18  
19 TYPE: PRI  
20  
21 ORGANISM: Artificial Sequence  
22  
23 FEATURE:  
24  
25 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
26  
27 OTHER INFORMATION: peptide  
28  
29 FEATURE:  
30  
31 OTHER INFORMATION: Synthesised with free amino terminus and as the  
32  
33 OTHER INFORMATION: C-terminal carboxamide  
34  
35 US-09-726-470A-79

Query Match: 36.4% Score 47: DB 11: Length 8:  
Best Local Similarity: 100.0%: Pred. No. 5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 AKRR 7  
111  
DB 2 AKRR 5

RESULT 44  
US-09-726-470A-80  
1 Sequence 80: Application US/09726470A  
2 Publication No. US2003036628A1  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Zheleva, Daniela I  
6 APPLICANT: Fischer, Peter M  
7 APPLICANT: McInnes, Campbell  
8 APPLICANT: Andrews, Martin JI  
9 APPLICANT: Chan, Weng C  
10 APPLICANT: Atkinson, Gail E  
11  
12 TITLE OF INVENTION: p21 Peptides  
13  
14 FILE REFERENCED: 071-014  
15  
16 CURRENT APPLICATION NUMBER: US/09726470A  
17  
18 CURRENT FILING DATE: 2000-11-29  
19  
20 PRIOR APPLICATION NUMBER: GB 9928323.6  
21  
22 PRIOR FILING DATE: 1999-11-30  
23  
24 NUMBER OF SEQ ID NOS: 275  
25  
26 SOFTWARE: Patent. Ver. 2.1  
27  
28 SEQ ID NO 80  
29  
30 LENGTH: 8  
31  
32 TYPE: PRI  
33  
34 ORGANISM: Artificial Sequence  
35  
36 FEATURE:  
37  
38 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
39  
40 OTHER INFORMATION: peptide  
41  
42 FEATURE:  
43  
44 OTHER INFORMATION: Synthesised with free amino terminus and as the  
45  
46 OTHER INFORMATION: C-terminal carboxamide  
47  
48 FEATURE:  
49  
50 NAME/KEY: MODSFS  
51  
52 LOCATION: (6)  
53  
54 OTHER INFORMATION: Nle  
55  
56 US-09-726-470A-80

Query Match: 36.4% Score 47: DB 11: Length 8:  
Best Local Similarity: 100.0%: Pred. No. 5e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 AKRR 7  
111  
DB 2 AKRR 5

RESULT 44

US 09-726-470A-B2  
 ? Sequence B1: Application US/09/726-470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell I  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: 021-014  
 ? CURRENT APPLICATION NUMBER: US/09/726-470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423-6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 8:  
 ? LENGTH: 8  
 ? TYPE: P21  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: Synthesized with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:  
 ? NAME/KEY: SEQ\_RES  
 ? LOCATION: 63  
 ? OTHER INFORMATION: Nva  
 ? US 09-726-470A-B1

Query Match: 36.4% Score 41: 100.0% Length 8:  
 Best Local Similarity: 100.0%: Pred. No. 50-05:  
 Matches: 4: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 4 AKRR 7  
 ILL  
 DE 2 AKRR 5

US 09-726-470A-B2  
 ? Sequence B2: Application US/09/726-470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell I  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: 021-014  
 ? CURRENT APPLICATION NUMBER: US/09/726-470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423-6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 82  
 ? LENGTH: 8  
 ? TYPE: P21  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: Synthesized with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:

NAME/KEY: SITE  
 ? LOCATION: 63  
 ? OTHER INFORMATION: Nva - C-terminal carboxamide  
 ? US 09-726-470A-B2  
 Query Match: 36.4% Score 41: 100.0% Length 8:  
 Best Local Similarity: 100.0%: Pred. No. 50-05:  
 Matches: 4: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 4 AKRR 7  
 ILL  
 DE 2 AKRR 5

US 09-726-470A-B1  
 ? Sequence B3: Application US/09/726-470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell I  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: 021-014  
 ? CURRENT APPLICATION NUMBER: US/09/726-470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423-6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 83  
 ? LENGTH: 8  
 ? TYPE: P21  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: Synthesized with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:  
 ? NAME/KEY: SEQ\_RES  
 ? LOCATION: 63  
 ? OTHER INFORMATION: Nva  
 ? US 09-726-470A-B3

Query Match: 36.4% Score 41: 100.0% Length 8:  
 Best Local Similarity: 100.0%: Pred. No. 50-05:  
 Matches: 4: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 4 AKRR 7  
 ILL  
 DE 2 AKRR 5

US 09-726-470A-B4  
 ? Sequence B4: Application US/09/726-470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell I  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: 021-014  
 ? CURRENT APPLICATION NUMBER: US/09/726-470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423-6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1

```

1 SEQ ID NO: 64
2 LENGTH: 8
3 TYPE: PPT
4 ORGANISM: Artificial Sequence
5 FEATURE:
6 OTHER INFORMATION: Described with free amino terminus and as the
7 OTHER INFORMATION: C-terminal catboxamide
8 FEATURE:
9 OTHER INFORMATION: Synthesized with free amino terminus and as the
10 OTHER INFORMATION: C-terminal catboxamide
11 NAME/KEY: SITE
12 LOCATION: 64
13 OTHER INFORMATION: Xaa 1-Naphthylalanine
14 US-09-726-470A-84
15
16 Query Match
17 Best Local Similarity: 36.4%, Score 4; DB 11; Length 8;
18 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19
20 QY 4 AKRP 7
21 III
22 2 AKRP 5
23
24 RESULT 44
25 US-09-726-470A-85
26 Sequence 86, Application US/09726470A
27 Publication No. US20030036628A1
28 GENERAL INFORMATION:
29 APPLICANT: Zheleva, Daniela I
30 APPLICANT: Fischer, Peter M
31 APPLICANT: McIntosh, Campbell I
32 APPLICANT: Andrews, Martin J
33 APPLICANT: Chao, Weng C
34 APPLICANT: Alkimos, Gal E
35 TITLE OF INVENTION: p21 Peptides
36 FILE REFERENCE: 021 014
37 CURRENT APPLICATION NUMBER: US/09726470A
38 PRIORITY FILING DATE: 2000 11 29; 726-470A
39 PRIOR APPLICATION NUMBER: 09-728-275
40 NUMBER OF SEQ ID NOS: 275
41 SOFTWARE: Patent In Ver. 2.1
42 SEQ ID NO: 65
43 LENGTH: 8
44 TYPE: PPT
45 ORGANISM: Artificial Sequence
46 FEATURE:
47 OTHER INFORMATION: Described with free amino terminus and as the
48 OTHER INFORMATION: C-terminal catboxamide
49 FEATURE:
50 OTHER INFORMATION: Synthesized with free amino terminus and as the
51 OTHER INFORMATION: C-terminal catboxamide
52 US-09-726-470A-85
53
54 Query Match
55 Best Local Similarity: 36.4%, Score 4; DB 11; Length 8;
56 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
57
58 QY 4 AKRP 7
59 III
60 2 AKRP 5
61
62 RESULT 45
63 US-09-726-470A-86
64 Sequence 86, Application US/09726470A
65 Publication No. US20030036628A1
66 GENERAL INFORMATION:
67 APPLICANT: Zheleva, Daniela I
68 APPLICANT: Fischer, Peter M
69 APPLICANT: McIntosh, Campbell I
70 APPLICANT: Andrews, Martin J
71 APPLICANT: Chao, Weng C
72 APPLICANT: Alkimos, Gal E
73 TITLE OF INVENTION: p21 Peptides
74 FILE REFERENCE: 021 014
75 CURRENT APPLICATION NUMBER: US/09726470A
76 PRIORITY FILING DATE: 2000 11 29; 726-470A
77 PRIOR APPLICATION NUMBER: 09-728-275
78 NUMBER OF SEQ ID NOS: 275
79 SOFTWARE: Patent In Ver. 2.1
80 SEQ ID NO: 66
81 LENGTH: 8
82 TYPE: PPT
83 ORGANISM: Artificial Sequence
84 FEATURE:
85 OTHER INFORMATION: Described with free amino terminus and as the
86 OTHER INFORMATION: C-terminal catboxamide
87 FEATURE:
88 OTHER INFORMATION: Synthesized with free amino terminus and as the
89 OTHER INFORMATION: C-terminal catboxamide
90 US-09-726-470A-86
91
92 Query Match
93 Best Local Similarity: 36.4%, Score 4; DB 11; Length 8;
94 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
95
96 QY 4 AKRP 7
97 III
98 2 AKRP 5
99
100 RESULT 46
101 US-09-726-470A-87
102 Sequence 87, Application US/09726470A
103 Publication No. US20030036628A1
104 GENERAL INFORMATION:
105 APPLICANT: Zheleva, Daniela I
106 APPLICANT: Fischer, Peter M
107 APPLICANT: McIntosh, Campbell I
108 APPLICANT: Andrews, Martin J
109 APPLICANT: Chao, Weng C
110 APPLICANT: Alkimos, Gal E
111 TITLE OF INVENTION: p21 Peptides
112 FILE REFERENCE: 021 014
113 CURRENT APPLICATION NUMBER: US/09726470A
114 PRIORITY FILING DATE: 2000 11 29; 726-470A
115 PRIOR APPLICATION NUMBER: 09-728-275
116 NUMBER OF SEQ ID NOS: 275
117 SOFTWARE: Patent In Ver. 2.1
118 SEQ ID NO: 67
119 LENGTH: 8
120 TYPE: PPT
121 ORGANISM: Artificial Sequence
122 FEATURE:
123 OTHER INFORMATION: Described with free amino terminus and as the
124 OTHER INFORMATION: C-terminal catboxamide
125 FEATURE:
126 OTHER INFORMATION: Synthesized with free amino terminus and as the
127 OTHER INFORMATION: C-terminal catboxamide
128 US-09-726-470A-87
129
130 Query Match
131 Best Local Similarity: 36.4%, Score 4; DB 11; Length 8;
132 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
133
134 QY 4 AKRP 7
135 III
136 2 AKRP 5
137
138 RESULT 47
139 US-09-726-470A-88
140 Sequence 86, Application US/09726470A
141 Publication No. US20030036628A1
142 GENERAL INFORMATION:
143 APPLICANT: Zheleva, Daniela I
144 APPLICANT: Fischer, Peter M
145 APPLICANT: McIntosh, Campbell I

```

US-09-726-470A-88  
 ? Sequence 88, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIORITY FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 88  
 ? LENGTH: 8  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? NAME/KEY: M40-RES  
 ? LOCATION: (7)  
 ? OTHER INFORMATION: Nie  
 US-09-726-470A-88

Query Match 36.4%, Score 4, DB 11, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7  
 111  
 DB 2 AKKR 5

RESULT 42  
 US-09-726-470A-89  
 ? Sequence 89, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIORITY FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 89  
 ? LENGTH: 8  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? NAME/KEY: M40-RES  
 ? LOCATION: (7)  
 ? OTHER INFORMATION: Nie

? NAME/KEY: M40-RES  
 ? LOCATION: (7)  
 ? OTHER INFORMATION: Nie  
 US-09-726-470A-89

Query Match 36.4%, Score 4, DB 11, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7  
 111  
 DB 2 AKKR 5

RESULT 43  
 US-09-726-470A-90  
 ? Sequence 90, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIORITY FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 90  
 ? LENGTH: 8  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? NAME/KEY: M40-RES  
 ? LOCATION: (7)  
 ? OTHER INFORMATION: Nie  
 US-09-726-470A-90

Query Match 36.4%, Score 4, DB 11, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7  
 111  
 DB 2 AKKR 5

RESULT 44  
 US-09-726-470A-91  
 ? Sequence 91, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIORITY FILING DATE: 2000-11-29

1 PRIOR APPLICATION NUMBER: GB 9928325.6  
 2 PRIOR FILING DATE: 1999-11-30  
 3 NUMBER OF SEQ ID NOS: 275  
 4 SOFTWARE: PatentIn Ver. 2.1  
 5 SEQ ID NO 91  
 6 LENGTH: 8  
 7 TYPE: PPT  
 8 ORGANISM: Artificial Sequence  
 9 FEATURE:  
 10 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 11  
 12 FEATURES:  
 13 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 14 OTHER INFORMATION: C-terminal carboxamide  
 15 US-09-726-470A-91

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
 111  
 LE 2 AKRR 5

RESULT 46  
 US-09-726-470A-92  
 1 Sequence 92; Application US/09726470A  
 2 Publication No. US20030036628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela I  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McInnes, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 TITLE OF INVENTION: p21 Peptides  
 11 FILE REFERENCE: COT 014  
 12 CURRENT APPLICATION NUMBER: US/09/726-470A  
 13 PRIOR FILING DATE: 2003-11-29  
 14 PRIOR APPLICATION NUMBER: GB 9928325.6  
 15 NUMBER OF SEQ ID NOS: 275  
 16 SOFTWARE: PatentIn Ver. 2.1  
 17 SEQ ID NO 92  
 18 LENGTH: 8  
 19 TYPE: PPT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 23  
 24 FEATURES:  
 25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 26 OTHER INFORMATION: C-terminal carboxamide  
 27 US-09-726-470A-92

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
 111  
 LE 2 AKRR 5

RESULT 46  
 US-09-726-470A-14  
 1 Sequence 94; Application US/09726470A  
 2 Publication No. US20030036628A1

3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela I  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McInnes, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 TITLE OF INVENTION: p21 Peptides  
 11 FILE REFERENCE: COT 014  
 12 CURRENT APPLICATION NUMBER: US/09/726-470A  
 13 PRIOR FILING DATE: 2003-11-29  
 14 PRIOR APPLICATION NUMBER: GB 9928325.6  
 15 NUMBER OF SEQ ID NOS: 275  
 16 SOFTWARE: PatentIn Ver. 2.1  
 17 SEQ ID NO 94  
 18 LENGTH: 8  
 19 TYPE: PPT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
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 24 FEATURES:  
 25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 26 OTHER INFORMATION: C-terminal carboxamide  
 27 US-09-726-470A-94

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
 111  
 LE 2 AKRR 5

RESULT 47  
 US-09-726-470A-95  
 1 Sequence 95; Application US/09726470A  
 2 Publication No. US20030036628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela I  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McInnes, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 TITLE OF INVENTION: p21 Peptides  
 11 FILE REFERENCE: COT 014  
 12 CURRENT APPLICATION NUMBER: US/09/726-470A  
 13 PRIOR FILING DATE: 2003-11-29  
 14 PRIOR APPLICATION NUMBER: GB 9928325.6  
 15 NUMBER OF SEQ ID NOS: 275  
 16 SOFTWARE: PatentIn Ver. 2.1  
 17 SEQ ID NO 95  
 18 LENGTH: 8  
 19 TYPE: PPT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 23  
 24 FEATURES:  
 25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 26 OTHER INFORMATION: C-terminal carboxamide  
 27 US-09-726-470A-95

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
 111

10 2 AKKR 5

RESULT 4b  
US-09-726-470A-98  
Sequence 98, Application US/09/726470A  
Publication No. US2003036628A1  
GENERAL INFORMATION:  
APPLICANT: Zieleva, Daniela I  
APPLICANT: Fischer, Peter M  
APPLICANT: McInnes, Campbell J  
APPLICANT: Andrews, Martin J  
APPLICANT: Chan, Weng C  
APPLICANT: Atkinson, Gail E  
TITLE OF INVENTION: p21 Peptides  
FILE REFERENCE: CCI 014  
CURRENT APPLICATION NUMBER: US/09/726-470A  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: GB 9928324.6  
NUMBER OF SEQ ID NOS: 275  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 96  
LENGTH: 8  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
FEATURE:  
OTHER INFORMATION: peptide  
OTHER INFORMATION: Synthesised with free amino terminus and as the  
OTHER INFORMATION: C-terminal carboxamide  
US-09-726-470A-98

Query Match 36.4%, Score 4, DB 11, Length 8;  
Best Local Similarity 100.0%, Prod. No. 5e+05,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 4 AKKR 7  
11  
10 2 AKKR 5

RESULT 4c  
US-09-726-470A-97  
Sequence 97, Application US/09/726470A  
Publication No. US2003036628A1  
GENERAL INFORMATION:  
APPLICANT: Zieleva, Daniela I  
APPLICANT: Fischer, Peter M  
APPLICANT: McInnes, Campbell J  
APPLICANT: Andrews, Martin J  
APPLICANT: Chan, Weng C  
APPLICANT: Atkinson, Gail E  
TITLE OF INVENTION: p21 Peptides  
FILE REFERENCE: CCI-014  
CURRENT APPLICATION NUMBER: US/09/726-470A  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: GB 9928324.6  
NUMBER OF SEQ ID NOS: 275  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 97  
LENGTH: 8  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: p21 derived

OTHER INFORMATION: peptide

FEATURE:  
OTHER INFORMATION: Synthesised with free amino terminus and as the  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (8)  
OTHER INFORMATION: Xaa Homophenylalanine  
US-09-726-470A-97

Query Match 36.4%, Score 4, DB 11, Length 8;  
Best Local Similarity 100.0%, Prod. No. 5e+05,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 4 AKKR 7  
11  
10 2 AKKR 5

RESULT 50  
US-09-726-470A-98  
Sequence 98, Application US/09/726470A  
Publication No. US2003036628A1  
GENERAL INFORMATION:  
APPLICANT: Zieleva, Daniela I  
APPLICANT: Fischer, Peter M  
APPLICANT: McInnes, Campbell J  
APPLICANT: Andrews, Martin J  
APPLICANT: Chan, Weng C  
APPLICANT: Atkinson, Gail E  
TITLE OF INVENTION: p21 Peptides  
FILE REFERENCE: CCI 014  
CURRENT APPLICATION NUMBER: US/09/726-470A  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: GB 9928324.6  
NUMBER OF SEQ ID NOS: 275  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 98  
LENGTH: 8  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
FEATURE:  
OTHER INFORMATION: peptide  
FEATURE:  
OTHER INFORMATION: Synthesised with free amino terminus and as the  
OTHER INFORMATION: C-terminal carboxamide  
US-09-726-470A-98

Query Match 36.4%, Score 4, DB 11, Length 8;  
Best Local Similarity 100.0%, Prod. No. 5e+05,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 4 AKKR 7  
11  
10 2 AKKR 5

Search completed: September 30, 2003, 10:31:03  
Job time : 21.5 secs

us-09-787-443-15

Genome version 5.1.0  
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us-09-787-443-15

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Total number of hits satisfying chosen parameters: 28369

Minimum hit seq length: 9

Maximum hit seq length: 15

Post processing: Listing first 500 summaries

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3: /cqn2.6/prodata/1/aa/AA\_1Ms.fpf.\*  
4: /cqn2.6/prodata/1/aa/AA\_0.5Ms.fpf.\*  
5: /cqn2.6/prodata/1/aa/AA\_0.2Ms.fpf.\*  
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Pred. No. is the number of results predicted by database  
score greater than or equal to the score of the result being plotted,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	45.5	13	4	US-09-726-601-24	4	Sequence 4, Appl
5	45.5	13	4	US-09-726-601-24	5	Sequence 5, Appl
6	45.5	13	4	US-09-726-601-24	6	Sequence 6, Appl
7	45.5	13	4	US-09-726-601-24	7	Sequence 7, Appl
8	45.5	13	4	US-09-726-601-24	8	Sequence 8, Appl
9	45.5	13	4	US-09-726-601-24	9	Sequence 9, Appl
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39	45.5	13	4	US-09-726-601-24	39	Sequence 39, Appl
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42	45.5	13	4	US-09-726-601-24	42	Sequence 42, Appl
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55	45.5	13	4	US-09-726-601-24	55	Sequence 55, Appl
56	45.5	13	4	US-09-726-601-24	56	Sequence 56, Appl
57	45.5	13	4	US-09-726-601-24	57	Sequence 57, Appl
58	45.5	13	4	US-09-726-601-24	58	Sequence 58, Appl
59	45.5	13	4	US-09-726-601-24	59	Sequence 59, Appl
60	45.5	13	4	US-09-726-601-24	60	Sequence 60, Appl
61	45.5	13	4	US-09-726-601-24	61	Sequence 61, Appl
62	45.5	13	4	US-09-726-601-24	62	Sequence 62, Appl
63	45.5	13	4	US-09-726-601-24	63	Sequence 63, Appl
64	45.5	13	4	US-09-726-601-24	64	Sequence 64, Appl
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71	45.5	13	4	US-09-726-601-24	71	Sequence 71, Appl
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73	45.5	13	4	US-09-726-601-24	73	Sequence 73, Appl
74	45.5	13	4	US-09-726-601-24	74	Sequence 74, Appl
75	45.5	13	4	US-09-726-601-24	75	Sequence 75, Appl
76	45.5	13	4	US-09-726-601-24	76	Sequence 76, Appl
77	45.5	13	4	US-09-726-601-24	77	Sequence 77, Appl
78	45.5	13	4	US-09-726-601-24	78	Sequence 78, Appl
79	45.5	13	4	US-09-726-601-24	79	Sequence 79, Appl
80	45.5	13	4	US-09-726-601-24	80	Sequence 80, Appl
81	45.5	13	4	US-09-726-601-24	81	Sequence 81, Appl
82	45.5	13	4	US-09-726-601-24	82	Sequence 82, Appl
83	45.5	13	4	US-09-726-601-24	83	Sequence 83, Appl
84	45.5	13	4	US-09-726-601-24	84	Sequence 84, Appl
85	45.5	13	4	US-09-726-601-24	85	Sequence 85, Appl
86	45.5	13	4	US-09-726-601-24	86	Sequence 86, Appl
87	45.5	13	4	US-09-726-601-24	87	Sequence 87, Appl
88	45.5	13	4	US-09-726-601-24	88	Sequence 88, Appl
89	45.5	13	4	US-09-726-601-24	89	Sequence 89, Appl
90	45.5	13	4	US-09-726-601-24	90	Sequence 90, Appl
91	45.5	13	4	US-09-726-601-24	91	Sequence 91, Appl
92	45.5	13	4	US-09-726-601-24	92	Sequence 92, Appl
93	45.5	13	4	US-09-726-601-24	93	Sequence 93, Appl
94	45.5	13	4	US-09-726-601-24	94	Sequence 94, Appl
95	45.5	13	4	US-09-726-601-24	95	Sequence 95, Appl
96	45.5	13	4	US-09-726-601-24	96	Sequence 96, Appl
97	45.5	13	4	US-09-726-601-24	97	Sequence 97, Appl
98	45.5	13	4	US-09-726-601-24	98	Sequence 98, Appl
99	45.5	13	4	US-09-726-601-24	99	Sequence 99, Appl
100	45.5	13	4	US-09-726-601-24	100	Sequence 100, Appl

101	4	36.4	15	1	US-08-729-042-10	Sequence 10, Appl	174	3	27.3	8	1	US-09-042-107-257	Sequence 257, Appl
102	4	36.4	15	1	US-08-415-666-16	Sequence 10, Appl	175	3	27.3	8	1	US-08-817-895-4	Sequence 4, Appl11
103	4	36.4	15	1	US-08-702-801A-10	Sequence 10, Appl	176	3	27.3	8	1	US-09-026-904-7	Sequence 7, Appl11
104	4	36.4	15	1	US-08-709-606-10	Sequence 10, Appl	177	3	27.3	8	1	US-08-412-697-11	Sequence 11, Appl
105	4	36.4	15	1	US-08-711-176-10	Sequence 10, Appl	178	3	27.3	8	1	US-09-263-975-25	Sequence 25, Appl
106	4	36.4	15	1	US-08-408-252-43	Sequence 25, Appl	179	3	27.3	8	1	US-09-263-975-26	Sequence 26, Appl
107	4	36.4	15	2	US-08-083-610A-09	Sequence 29, Appl	180	3	27.3	8	1	US-09-263-975-30	Sequence 30, Appl
108	4	36.4	15	2	US-08-530-131-29	Sequence 29, Appl	181	3	27.3	8	1	US-09-435-098A-10	Sequence 10, Appl
109	4	36.4	15	3	US-08-181-339-23	Sequence 23, Appl	182	3	27.3	8	1	US-08-406-248-11	Sequence 11, Appl
110	4	36.4	15	1	US-07-747-747-35	Sequence 35, Appl	183	3	27.3	8	1	US-08-981-392-58	Sequence 58, Appl
111	4	36.4	8	1	US-08-273-663-89	Sequence 89, Appl	184	3	27.3	8	1	US-09-531-521-14	Sequence 14, Appl
112	4	36.4	8	1	US-08-436-503-35	Sequence 15, Appl	185	3	27.3	8	1	US-09-385-740B-10	Sequence 10, Appl
113	4	36.4	8	1	US-08-439-563-19	Sequence 15, Appl	186	3	27.3	8	1	US-09-444-827A-8	Sequence 8, Appl11
114	4	36.4	8	1	US-08-453-243A-14	Sequence 14, Appl	187	3	27.3	8	1	US-09-444-827A-12	Sequence 12, Appl
115	4	36.4	8	1	US-08-243-322A-15	Sequence 15, Appl	188	3	27.3	8	1	US-09-444-827A-14	Sequence 14, Appl
116	4	36.4	8	1	US-08-444-792-15	Sequence 15, Appl	189	3	27.3	8	1	US-09-444-827A-15	Sequence 15, Appl
117	4	36.4	8	1	US-07-445-342-15	Sequence 15, Appl	190	3	27.3	8	1	US-09-444-827A-15	Sequence 15, Appl
118	4	36.4	8	1	US-08-482-880-34	Sequence 34, Appl	191	3	27.3	8	1	US-08-467-602-15	Sequence 15, Appl
119	4	36.4	8	1	US-08-429-820-24	Sequence 24, Appl	192	3	27.3	8	1	US-09-659-786-104	Sequence 104, Appl
120	4	36.4	8	1	US-08-429-820-24	Sequence 24, Appl	193	3	27.3	8	1	US-09-104-337A-468	Sequence 468, Appl
121	4	36.4	8	1	US-08-429-820-24	Sequence 24, Appl	194	3	27.3	8	1	US-09-129-192C-25	Sequence 25, Appl
122	4	36.4	8	1	US-08-429-820-24	Sequence 24, Appl	195	3	27.3	8	1	US-09-129-192C-30	Sequence 30, Appl
123	4	36.4	8	1	US-08-416-855-35	Sequence 35, Appl	196	3	27.3	8	1	US-09-619-68	Sequence 68, Appl
124	4	36.4	8	1	US-08-459-555A-06	Sequence 06, Appl	197	3	27.3	8	1	US-09-344-219-8	Sequence 8, Appl11
125	4	36.4	8	1	US-08-459-555A-06	Sequence 06, Appl	198	3	27.3	8	1	US-09-445-327A-27	Sequence 27, Appl
126	4	36.4	8	1	US-08-463-520A-35	Sequence 35, Appl	199	3	27.3	8	1	US-09-467-486-53	Sequence 53, Appl
127	4	36.4	8	2	US-08-534-265B-30	Sequence 30, Appl	200	3	27.3	8	1	US-09-467-777-76	Sequence 76, Appl
128	4	36.4	8	2	US-08-463-622-11	Sequence 11, Appl	201	3	27.3	8	1	US-09-467-777-77	Sequence 77, Appl
129	4	36.4	8	2	US-08-473-273-34	Sequence 34, Appl	202	3	27.3	8	1	US-09-467-777-78	Sequence 78, Appl
130	4	36.4	8	2	US-07-566-509H-7	Sequence 7, Appl	203	3	27.3	8	1	US-09-467-777-79	Sequence 79, Appl
131	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	204	3	27.3	8	1	US-09-467-777-110	Sequence 110, Appl
132	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	205	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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134	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	207	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
135	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	208	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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137	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	210	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
138	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	211	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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146	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	219	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
147	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	220	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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149	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	222	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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151	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	224	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
152	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	225	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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163	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	236	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
164	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	237	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
165	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	238	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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167	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	240	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
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171	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	244	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
172	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	245	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl
173	4	36.4	8	2	US-08-734-617A-10	Sequence 10, Appl	246	3	27.3	8	1	US-09-467-777-10	Sequence 10, Appl



247	9	1	US-08-240-514-43	Sequence 13, Appl	320	9	3	27.3	9	3	US-08-897-924A-18	Sequence 18, Appl
248	9	1	US-08-349-902B-28	Sequence 28, Appl	321	9	3	27.3	9	3	US-08-167-641C-57	Sequence 57, Appl
249	9	1	US-08-345-333-44	Sequence 44, Appl	322	9	3	27.3	9	3	US-08-159-339A-221	Sequence 221, Appl
250	9	1	US-08-687-226-47	Sequence 47, Appl	323	9	3	27.3	9	3	US-08-159-339A-241	Sequence 241, Appl
251	9	1	US-08-454-207A-67	Sequence 57, Appl	324	9	3	27.3	9	3	US-08-159-339A-243	Sequence 243, Appl
252	9	1	US-08-454-207A-68	Sequence 58, Appl	325	9	3	27.3	9	3	US-08-159-339A-273	Sequence 273, Appl
253	9	1	US-08-454-207A-69	Sequence 59, Appl	326	9	3	27.3	9	3	US-08-159-339A-425	Sequence 425, Appl
254	9	1	US-08-454-207A-69	Sequence 59, Appl	327	9	3	27.3	9	3	US-08-159-339A-439	Sequence 439, Appl
255	9	1	US-08-454-207A-69	Sequence 59, Appl	328	9	3	27.3	9	3	US-08-159-339A-541	Sequence 541, Appl
256	9	1	US-08-595-719A-65	Sequence 5, Appl	329	9	3	27.3	9	3	US-08-159-339A-782	Sequence 782, Appl
257	9	1	US-08-467-083-12	Sequence 12, Appl	330	9	3	27.3	9	3	US-08-159-339A-796	Sequence 796, Appl
258	9	1	US-08-486-013-1	Sequence 5, Appl	331	9	3	27.3	9	3	US-08-159-339A-801	Sequence 801, Appl
259	9	1	US-08-329-820-24	Sequence 24, Appl	332	9	3	27.3	9	3	US-08-159-339A-808	Sequence 808, Appl
260	9	1	US-08-329-820-78	Sequence 78, Appl	333	9	3	27.3	9	3	US-08-159-339A-813	Sequence 813, Appl
261	9	1	US-08-465-167A-5	Sequence 5, Appl	334	9	3	27.3	9	3	US-08-159-339A-818	Sequence 818, Appl
262	9	1	US-08-465-167A-36	Sequence 36, Appl	335	9	3	27.3	9	3	US-08-159-339A-819	Sequence 819, Appl
263	9	1	US-08-615-181-94	Sequence 34, Appl	336	9	3	27.3	9	3	US-08-159-339A-821	Sequence 821, Appl
264	9	1	US-08-542-255-12	Sequence 12, Appl	337	9	3	27.3	9	3	US-08-159-339A-824	Sequence 824, Appl
265	9	1	US-08-642-255-15	Sequence 15, Appl	338	9	3	27.3	9	3	US-08-159-339A-881	Sequence 881, Appl
266	9	1	US-08-787-547-52	Sequence 52, Appl	339	9	3	27.3	9	3	US-08-718-904-26	Sequence 26, Appl
267	9	1	US-08-475-583-1	Sequence 1, Appl	340	9	3	27.3	9	3	US-08-718-904-30	Sequence 30, Appl
268	9	1	US-08-475-583-2	Sequence 2, Appl	341	9	3	27.3	9	3	US-09-015-968-5	Sequence 5, Appl
269	9	1	US-08-434-417B-12	Sequence 12, Appl	342	9	3	27.3	9	3	US-08-667-725B-47	Sequence 47, Appl
270	9	2	US-08-632-760-7	Sequence 7, Appl	343	9	3	27.3	9	3	US-08-466-800B-12	Sequence 12, Appl
271	9	2	US-08-632-762A-13	Sequence 13, Appl	344	9	3	27.3	9	3	US-08-785-831-47	Sequence 47, Appl
272	9	2	US-08-612-322A-13	Sequence 13, Appl	345	9	3	27.3	9	3	US-08-993-235-3	Sequence 9, Appl
273	9	2	US-08-378-709-1	Sequence 1, Appl	346	9	3	27.3	9	3	US-09-007-748-47	Sequence 47, Appl
274	9	2	US-08-378-709-1	Sequence 1, Appl	347	9	3	27.3	9	3	US-08-460-971A-57	Sequence 57, Appl
275	9	2	US-08-378-709-5	Sequence 5, Appl	348	9	3	27.3	9	3	US-08-564-164A-10	Sequence 10, Appl
276	9	2	US-08-378-709-6	Sequence 6, Appl	349	9	3	27.3	9	3	US-08-723-425A-224	Sequence 224, Appl
277	9	2	US-08-378-709-7	Sequence 7, Appl	350	9	3	27.3	9	3	US-08-723-425A-225	Sequence 225, Appl
278	9	2	US-08-378-709-8	Sequence 8, Appl	351	9	3	27.3	9	3	US-08-723-425A-226	Sequence 226, Appl
279	9	2	US-08-378-709-9	Sequence 9, Appl	352	9	3	27.3	9	3	US-08-723-425A-227	Sequence 227, Appl
280	9	2	US-08-378-709-10	Sequence 10, Appl	353	9	3	27.3	9	3	US-08-723-425A-228	Sequence 228, Appl
281	9	2	US-08-378-709-12	Sequence 12, Appl	354	9	3	27.3	9	3	US-08-723-425A-229	Sequence 229, Appl
282	9	2	US-08-442-4610-57	Sequence 19, Appl	355	9	3	27.3	9	3	US-08-723-425A-230	Sequence 230, Appl
283	9	2	US-08-582-279-5	Sequence 5, Appl	356	9	3	27.3	9	3	US-08-974-549A-150	Sequence 150, Appl
284	9	2	US-08-342-268-5	Sequence 5, Appl	357	9	3	27.3	9	3	US-09-258-754-145	Sequence 145, Appl
285	9	2	US-08-486-349A-12	Sequence 12, Appl	358	9	3	27.3	9	3	US-08-485-355B-29	Sequence 29, Appl
286	9	2	US-08-528-057-25	Sequence 25, Appl	359	9	3	27.3	9	3	US-08-485-355B-31	Sequence 31, Appl
287	9	2	US-08-239-187A-9	Sequence 9, Appl	360	9	3	27.3	9	3	US-08-485-355B-33	Sequence 33, Appl
288	9	2	US-08-621-801-203	Sequence 203, Appl	361	9	3	27.3	9	3	US-08-462-040-57	Sequence 57, Appl
289	9	2	US-08-621-259A-176	Sequence 176, Appl	362	9	3	27.3	9	3	US-08-915-314-90	Sequence 90, Appl
290	9	2	US-08-624-838B-44	Sequence 44, Appl	363	9	3	27.3	9	3	US-09-113-921-4	Sequence 4, Appl
291	9	2	US-08-624-838B-46	Sequence 46, Appl	364	9	3	27.3	9	3	US-09-202-812-8	Sequence 8, Appl
292	9	2	US-08-704-556-11	Sequence 11, Appl	365	9	3	27.3	9	3	US-09-183-931-28	Sequence 28, Appl
293	9	2	US-08-368-549B-12	Sequence 12, Appl	366	9	3	27.3	9	3	US-09-183-931-45	Sequence 35, Appl
294	9	2	US-08-373-273A-22	Sequence 22, Appl	367	9	3	27.3	9	3	US-09-183-931-38	Sequence 38, Appl
295	9	2	US-08-146-028-229	Sequence 24, Appl	368	9	3	27.3	9	3	US-09-112-206-224	Sequence 224, Appl
296	9	2	US-08-146-028-230	Sequence 25, Appl	369	9	3	27.3	9	3	US-09-112-206-225	Sequence 225, Appl
297	9	2	US-08-146-028-231	Sequence 26, Appl	370	9	3	27.3	9	3	US-09-112-206-227	Sequence 227, Appl
298	9	2	US-08-146-028-232	Sequence 27, Appl	371	9	3	27.3	9	3	US-09-112-206-228	Sequence 228, Appl
299	9	2	US-08-146-028-233	Sequence 28, Appl	372	9	3	27.3	9	3	US-09-112-206-229	Sequence 229, Appl
300	9	2	US-08-146-028-234	Sequence 29, Appl	373	9	3	27.3	9	3	US-09-112-206-230	Sequence 230, Appl
301	9	2	US-08-146-028-235	Sequence 30, Appl	374	9	3	27.3	9	3	US-09-642-107-145	Sequence 145, Appl
302	9	2	US-08-146-028-236	Sequence 31, Appl	375	9	3	27.3	9	3	US-08-605-430-49	Sequence 49, Appl
303	9	2	US-08-893-853-4	Sequence 4, Appl	376	9	3	27.3	9	3	US-09-183-706-7	Sequence 7, Appl
304	9	2	US-08-679-856-15	Sequence 15, Appl	377	9	3	27.3	9	3	US-09-263-975-16	Sequence 16, Appl
305	9	2	US-08-973-559-22	Sequence 22, Appl	378	9	3	27.3	9	3	US-09-171-878-20	Sequence 20, Appl
306	9	2	US-09-070-756-1	Sequence 1, Appl	379	9	3	27.3	9	3	US-08-713-354C-8	Sequence 8, Appl
307	9	2	US-09-070-756-5	Sequence 5, Appl	380	9	3	27.3	9	3	US-09-510-738A-131	Sequence 131, Appl
308	9	2	US-09-076-756-6	Sequence 6, Appl	381	9	3	27.3	9	3	US-09-217-352-203	Sequence 203, Appl
309	9	2	US-08-690-876-16	Sequence 16, Appl	382	9	3	27.3	9	3	US-09-061-388-19	Sequence 19, Appl
310	9	2	US-08-598-873-47	Sequence 47, Appl	383	9	3	27.3	9	3	US-09-133-521-16	Sequence 16, Appl
311	9	2	US-08-993-738A-8	Sequence 8, Appl	384	9	3	27.3	9	3	US-05-166-448-48	Sequence 48, Appl
312	9	2	US-08-595-543A-61	Sequence 41, Appl	385	9	3	27.3	9	3	US-09-502-600-95	Sequence 95, Appl
313	9	2	US-08-350-260A-62	Sequence 60, Appl	386	9	3	27.3	9	3	US-09-502-600-111	Sequence 111, Appl
314	9	2	US-09-076-582-4	Sequence 4, Appl	387	9	3	27.3	9	3	US-09-567-995-7	Sequence 7, Appl
315	9	2	US-08-586-234-71	Sequence 71, Appl	388	9	3	27.3	9	3		
316	9	2	US-08-460-898A-57	Sequence 57, Appl	389	9	3	27.3	9	3		
317	9	3	US-08-880-963-14	Sequence 14, Appl	390	9	3	27.3	9	3		
318	9	3	US-08-596-965-13	Sequence 13, Appl	391	9	3	27.3	9	3		
319	9	3	US-08-597-924A-14	Sequence 14, Appl	392	9	3	27.3	9	3		

594	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	465	3	27.3	10	1	US-08-071-811A-10	Sequence 10, Appl
595	3	27.3	9	4	US-09-440-844-1	Sequence 2, Appl	467	3	27.3	10	1	US-08-457-166-9	Sequence 9, Appl
596	3	27.3	9	4	US-09-452-543-95	Sequence 95, Appl	468	3	27.3	10	1	US-08-240-514-53	Sequence 53, Appl
597	3	27.3	9	4	US-09-241-268-8	Sequence 8, Appl	469	3	27.3	10	1	US-08-349-902B-4	Sequence 4, Appl
598	3	27.3	9	4	US-09-543-543-19	Sequence 19, Appl	470	3	27.3	10	1	US-08-349-902B-5	Sequence 5, Appl
599	3	27.3	9	4	US-08-478-057-1	Sequence 1, Appl	471	3	27.3	10	1	US-08-449-902B-16	Sequence 16, Appl
600	3	27.3	9	4	US-09-412-928-19	Sequence 19, Appl	472	3	27.3	10	1	US-08-349-902B-29	Sequence 29, Appl
601	3	27.3	9	4	US-09-461-083-19	Sequence 19, Appl	473	3	27.3	10	1	US-08-077-797A-22	Sequence 22, Appl
602	3	27.3	9	4	US-09-705-160-24	Sequence 24, Appl	474	3	27.3	10	1	US-09-429-820-25	Sequence 25, Appl
603	3	27.3	9	4	US-09-705-160-49	Sequence 49, Appl	475	3	27.3	10	1	US-08-429-820-198	Sequence 198, Appl
604	3	27.3	9	4	US-09-561-368-1	Sequence 1, Appl	476	3	27.3	10	1	US-08-444-855-8	Sequence 8, Appl
605	3	27.3	9	4	US-09-165-863-4	Sequence 4, Appl	477	3	27.3	10	1	US-08-487-568-21	Sequence 21, Appl
606	3	27.3	9	4	US-08-197-484-6	Sequence 6, Appl	478	3	27.3	10	1	US-08-594-447-22	Sequence 22, Appl
607	3	27.3	9	4	US-08-197-484-86	Sequence 86, Appl	479	3	27.3	10	1	US-08-541-964-21	Sequence 21, Appl
608	3	27.3	9	4	US-08-197-484-147	Sequence 147, Appl	480	3	27.3	10	2	US-08-612-302A-53	Sequence 53, Appl
609	3	27.3	9	4	US-09-479-479-5	Sequence 5, Appl	481	3	27.3	10	2	US-08-406-130-7	Sequence 7, Appl
610	3	27.3	9	4	US-09-479-479-5	Sequence 5, Appl	482	3	27.3	10	2	US-09-448-547-2	Sequence 2, Appl
611	3	27.3	9	4	US-09-444-827A-7	Sequence 7, Appl	483	3	27.3	10	2	US-08-402-461B-28	Sequence 28, Appl
612	3	27.3	9	4	US-09-297-851-4	Sequence 11, Appl	484	3	27.3	10	2	US-08-456-112B-17	Sequence 17, Appl
613	3	27.3	9	4	US-09-697-884-48	Sequence 48, Appl	485	3	27.3	10	2	US-08-479-223-2	Sequence 2, Appl
614	3	27.3	9	4	US-09-495-562-8	Sequence 8, Appl	486	3	27.3	10	2	US-08-623-833B-39	Sequence 39, Appl
615	3	27.3	9	4	US-08-627-820-5	Sequence 5, Appl	487	3	27.3	10	2	US-08-764-640-31	Sequence 31, Appl
616	3	27.3	9	4	US-09-847-185-24	Sequence 24, Appl	488	3	27.3	10	2	US-08-637-759B-283	Sequence 283, Appl
617	3	27.3	9	4	US-09-104-337A-62	Sequence 605, Appl	489	3	27.3	10	2	US-08-556-597-7	Sequence 7, Appl
618	3	27.3	9	4	US-09-496-195-1	Sequence 16, Appl	490	3	27.3	10	2	US-08-556-597-147	Sequence 147, Appl
619	3	27.3	9	4	US-09-129-192-16	Sequence 53, Appl	491	3	27.3	10	2	US-08-556-597-169	Sequence 169, Appl
620	3	27.3	9	4	US-09-430-619-63	Sequence 80, Appl	492	3	27.3	10	2	US-08-928-958-14	Sequence 14, Appl
621	3	27.3	9	4	US-09-430-619-80	Sequence 80, Appl	493	3	27.3	10	2	US-08-928-958-15	Sequence 15, Appl
622	3	27.3	9	4	US-09-449-249-26	Sequence 25, Appl	494	3	27.3	10	2	US-08-973-563A-21	Sequence 21, Appl
623	3	27.3	9	4	US-09-449-249-30	Sequence 30, Appl	495	3	27.3	10	2	US-08-973-559-21	Sequence 21, Appl
624	3	27.3	9	4	US-09-515-514-17	Sequence 17, Appl	496	3	27.3	10	2	US-08-993-738A-9	Sequence 9, Appl
625	3	27.3	9	4	US-09-344-219-7	Sequence 7, Appl	497	3	27.3	10	2	US-08-665-647-36	Sequence 36, Appl
626	3	27.3	9	4	US-09-344-219-11	Sequence 11, Appl	498	3	27.3	10	2	US-08-735-253-3	Sequence 3, Appl
627	3	27.3	9	4	US-09-861-966-151	Sequence 131, Appl	499	3	27.3	10	2	US-08-735-253-9	Sequence 9, Appl
628	3	27.3	9	4	US-09-861-966-152	Sequence 150, Appl	500	3	27.3	10	5	PCT-US95-03236-13	Sequence 13, Appl
629	3	27.3	9	4	US-09-114-176-1	Sequence 1, Appl							
630	3	27.3	9	4	US-09-451-067-4	Sequence 4, Appl							
631	3	27.3	9	4	US-09-520-405B-488	Sequence 488, Appl							
632	3	27.3	9	4	US-09-289-350-4	Sequence 4, Appl							
633	3	27.3	9	4	US-08-773-235-4	Sequence 4, Appl							
634	3	27.3	9	4	US-09-667-481-90	Sequence 90, Appl							
635	3	27.3	9	4	US-09-744-0400-99	Sequence 99, Appl							
636	3	27.3	9	4	US-09-574-749B-4	Sequence 4, Appl							
637	3	27.3	9	4	US-09-594-870A-32	Sequence 42, Appl							
638	3	27.3	9	4	US-09-128-281-9	Sequence 6, Appl							
639	3	27.3	9	4	US-09-178-281-9	Sequence 7, Appl							
640	3	27.3	9	4	US-09-441-782-7	Sequence 7, Appl							
641	3	27.3	9	4	US-09-430-473-25	Sequence 25, Appl							
642	3	27.3	9	4	US-09-235-221-15	Sequence 15, Appl							
643	3	27.3	9	4	US-09-634-267A-488	Sequence 488, Appl							
644	3	27.3	9	5	PCT-US91-07508-44	Sequence 44, Appl							
645	3	27.3	9	5	PCT-US91-05245-9	Sequence 6, Appl							
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647	3	27.3	9	5	PCT-US95-02121-63	Sequence 63, Appl							
648	3	27.3	9	5	PCT-US95-02121-68	Sequence 88, Appl							
649	3	27.3	9	5	PCT-US95-02121-147	Sequence 147, Appl							
650	3	27.3	9	5	PCT-US95-09262-178	Sequence 178, Appl							
651	3	27.3	9	5	PCT-US95-10976A-92	Sequence 92, Appl							
652	3	27.3	9	5	PCT-US95-10976A-92	Sequence 96, Appl							
653	3	27.3	10	1	US-07-329-513-2	Sequence 2, Appl							
654	3	27.3	10	1	US-07-801-812A-21	Sequence 21, Appl							
655	3	27.3	10	1	US-07-965-675-1	Sequence 1, Appl							
656	3	27.3	10	1	US-07-965-675-4	Sequence 6, Appl							
657	3	27.3	10	1	US-07-965-675-7	Sequence 7, Appl							
658	3	27.3	10	1	US-07-965-675-11	Sequence 10, Appl							
659	3	27.3	10	1	US-07-965-675-11	Sequence 11, Appl							
660	3	27.3	10	1	US-08-151-056-1	Sequence 1, Appl							
661	3	27.3	10	1	US-08-479-233-9	Sequence 9, Appl							
662	3	27.3	10	1	US-08-481-888A-21	Sequence 21, Appl							
663	3	27.3	10	1	US-08-294-434-9	Sequence 9, Appl							
664	3	27.3	10	1	US-08-485-276A-25	Sequence 21, Appl							
665	3	27.3	10	1	US-08-697-830E-17	Sequence 17, Appl							

## ALIGNMENT:

RESULT 1  
US-09-325-601-13  
Sequence 13, Application US/09325601;  
Patent No. 6573045  
GENERAL INFORMATION:  
APPLICANT: Kato  
APPLICANT: Prescott  
TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds  
FILE REFERENCE: 4950781245  
CURRENT APPLICATION NUMBER: US/09/325,601  
CURRENT FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.  
OTHER INFORMATION: Q. R-peptide library  
US-09-325-601-13

Query Match 45.5% Score 5; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KRRKG 9  
DB 7 KRRKG 11

RESULT 2  
US-09-325-601-16

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1 Sequence No. Application US/09/425601
2 Patent No. 6574045
3 GENERAL INFORMATION:
4 APPLICANT: Kato
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: 4950/81235
8 CURRENT APPLICATION NUMBER: US/09/425601
9 CURRENT FILING DATE: 1999-06-03
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 1
13 LENGTH: 13
14 TYPE: PRI
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
18 OTHER INFORMATION: Q. R pentapeptide library
19 US-09-425-601-22
20
21 Query Match 45.5% Score 51 DB 41 Length 13
22 Best Local Similarity 100.0% Pctd. No. 20
23 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
24
25 QY 5 KKKKG 9
26 1111
27 7 KKKKG 11
28
29 RESULT 4
30 US-09-425-601-19
31 Sequence 29, Application US/09/425601
32 Patent No. 6574045
33 GENERAL INFORMATION:
34 APPLICANT: Kato
35 APPLICANT: Prescott
36 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
37 FILE REFERENCE: 4950/81235
38 CURRENT APPLICATION NUMBER: US/09/425601
39 CURRENT FILING DATE: 1999-06-03
40 NUMBER OF SEQ ID NOS: 53
41 SOFTWARE: Patent In Ver. 2.1
42 SEQ ID NO 19
43 LENGTH: 13
44 TYPE: PRI
45 ORGANISM: Artificial Sequence
46 FEATURE:
47 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
48 OTHER INFORMATION: Q. R pentapeptide library
49 US-09-425-601-19
50
51 Query Match 45.5% Score 51 DB 41 Length 13
52 Best Local Similarity 100.0% Pctd. No. 20
53 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
54
55 QY 5 KKKKG 9
56 1111
57 7 KKKKG 11
58
59 RESULT 4
60 US-09-425-601-22
61 Sequence 22, Application US/09/425601
62 Patent No. 6574045
63 GENERAL INFORMATION:
64 APPLICANT: Kato
65 APPLICANT: Prescott
66 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
67 FILE REFERENCE: 4950/81235
68 CURRENT APPLICATION NUMBER: US/09/425601
69 CURRENT FILING DATE: 1999-06-03
70 NUMBER OF SEQ ID NOS: 53
71 SOFTWARE: Patent In Ver. 2.1
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1 SEQ ID NO 22
2 LENGTH: 13
3 TYPE: PRI
4 ORGANISM: Artificial Sequence
5 FEATURE:
6 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
7 OTHER INFORMATION: Q. R pentapeptide library
8 US-09-425-601-22
9
10 Query Match 45.5% Score 51 DB 41 Length 13
11 Best Local Similarity 100.0% Pctd. No. 20
12 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
13
14 QY 5 KKKKG 9
15 1111
16 7 KKKKG 11
17
18 RESULT 5
19 US-09-425-601-25
20 Sequence 25, Application US/09/425601
21 Patent No. 6574045
22 GENERAL INFORMATION:
23 APPLICANT: Kato
24 APPLICANT: Prescott
25 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
26 FILE REFERENCE: 4950/81235
27 CURRENT APPLICATION NUMBER: US/09/425601
28 CURRENT FILING DATE: 1999-06-03
29 NUMBER OF SEQ ID NOS: 53
30 SOFTWARE: Patent In Ver. 2.1
31 SEQ ID NO 25
32 LENGTH: 13
33 TYPE: PRI
34 ORGANISM: Artificial Sequence
35 FEATURE:
36 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
37 OTHER INFORMATION: Q. R pentapeptide library
38 US-09-425-601-25
39
40 Query Match 45.5% Score 51 DB 41 Length 13
41 Best Local Similarity 100.0% Pctd. No. 20
42 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
43
44 QY 5 KKKKG 9
45 1111
46 7 KKKKG 11
47
48 RESULT 6
49 US-09-425-601-28
50 Sequence 28, Application US/09/425601
51 Patent No. 6574045
52 GENERAL INFORMATION:
53 APPLICANT: Kato
54 APPLICANT: Prescott
55 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
56 FILE REFERENCE: 4950/81235
57 CURRENT APPLICATION NUMBER: US/09/425601
58 CURRENT FILING DATE: 1999-06-03
59 NUMBER OF SEQ ID NOS: 53
60 SOFTWARE: Patent In Ver. 2.1
61 SEQ ID NO 28
62 LENGTH: 13
63 TYPE: PRI
64 ORGANISM: Artificial Sequence
65 FEATURE:
66 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
67 OTHER INFORMATION: Q. R pentapeptide library
68 US-09-425-601-28
69
70 Query Match 45.5% Score 51 DB 41 Length 13
71 Best Local Similarity 100.0% Pctd. No. 20
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Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

RESULT 7
US 09-425 601-41
Sequence 41, Application US/09-425-01
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Kato
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
FILE REFERENCE: US/09-425-01
CURRENT APPLICATION NUMBER: US/09-425-01
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 39
LENGTH 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
OTHER INFORMATION: Q: R pentapeptide library
US 09-425 601-41

Query Match      45.5%, Score 53, DB 4, Length 13;
Best Local Similarity 100.0%, Ident. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

US 09-425 601-41
Sequence 41, Application US/09-425-01
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Kato
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
FILE REFERENCE: US/09-425-01
CURRENT APPLICATION NUMBER: US/09-425-01
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 41
LENGTH 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
OTHER INFORMATION: Q: R pentapeptide library
US 09-425 601-41

Query Match      45.5%, Score 53, DB 4, Length 13;
Best Local Similarity 100.0%, Ident. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

US 09-425 601-41
Sequence 41, Application US/09-425-01
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Kato
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
FILE REFERENCE: US/09-425-01
CURRENT APPLICATION NUMBER: US/09-425-01
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 44
LENGTH 13

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GENERAL INFORMATION:
APPLICANT: Kato
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
FILE REFERENCE: US/09-425-01
CURRENT APPLICATION NUMBER: US/09-425-01
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 39
LENGTH 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
OTHER INFORMATION: Q: R pentapeptide library
US 09-425 601-41

Query Match      45.5%, Score 53, DB 4, Length 13;
Best Local Similarity 100.0%, Ident. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

US 09-425 601-41
Sequence 41, Application US/09-425-01
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Kato
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
FILE REFERENCE: US/09-425-01
CURRENT APPLICATION NUMBER: US/09-425-01
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 41
LENGTH 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
OTHER INFORMATION: Q: R pentapeptide library
US 09-425 601-41

Query Match      45.5%, Score 53, DB 4, Length 13;
Best Local Similarity 100.0%, Ident. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

US 09-425 601-44
Sequence 44, Application US/09-425-01
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Kato
TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
FILE REFERENCE: US/09-425-01
CURRENT APPLICATION NUMBER: US/09-425-01
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 44
LENGTH 13

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1 TYPE: EST
2 ORGANISM: Artificial Sequence
3 FEATURE:
4 OTHER INFORMATION: Description of Artificial Sequence: Coding Frame K
5 OTHER INFORMATION: Q: R-peptidase inhibitor
6 US 09-425-601-44
7
8 Query Match: 45.5%, Score 51, DP 40, Length 14
9 Best Local Similarity: 100.0%, Pred. No. 20
10 Matches: 0; Conservative 0; Mismatches 0; Gaps 0
11
12 QY 5 KRKG 7
13 11 11
14 7 KRKG 11
15
16 RESULT 12
17 US-09-425-601-47
18 Sequence 47: Application US/09325607
19 Patent No. 6573045
20 GENERAL INFORMATION:
21 APPLICANT: KARI
22 APPLICANT: Pirescott
23 TITLE OF INVENTION: Methods and kits for Discovery of RNA Binding Compounds
24 FILE REFERENCE: 4950/81235
25 CURRENT APPLICATION NUMBER: US/09/425,601
26 CURRENT FILING DATE: 1999-05-05
27 NUMBER OF SEQ ID NOS: 53
28 SOFTWARE: Patent In Ver. 2.1
29 SEQ ID NO 47
30 LENGTH: 14
31 TYPE: EST
32 ORGANISM: Artificial Sequence
33 FEATURE:
34 OTHER INFORMATION: Description of Artificial Sequence: Coding Frame K
35 OTHER INFORMATION: Q: R-peptidase inhibitor
36 US 09-425-601-47
37
38 Query Match: 45.5%, Score 51, DP 40, Length 14
39 Best Local Similarity: 100.0%, Pred. No. 20
40 Matches: 0; Conservative 0; Mismatches 0; Gaps 0
41
42 QY 5 KRKG 7
43 11 11
44 7 KRKG 11
45
46 RESULT 13
47 US-09-425-601-45
48 Sequence 45: Application US/09325744
49 Patent No. 6422641
50 GENERAL INFORMATION:
51 APPLICANT: Boretta, Alberto
52 TITLE OF INVENTION: HIV PROTEIN EPTOPES
53 NUMBER OF SEQUENCES: 90
54 CORRESPONDENCE ADDRESS:
55 ADDRESSEE: Baker & Bots, L.L.P.
56 STREET: 40 Rockefeller Plaza
57 CITY: New York
58 STATE: NY
59 COUNTRY: U.S.A.
60 ZIP: 10112-0228
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Diskette
63 OPERATING SYSTEM: IBM Compatible
64 OPERATING SYSTEM: DOS
65 SOFTWARE: FastSeq Version 1.5
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/345,730
68 FILING DATE: 10-NOV-1994
69 CLASSIFICATION: 435
70 PRIOR APPLICATION DATA:
71 ATTORNEY/AGENT INFORMATION:
72 NAME: MacLeod, Janet M
73 REGISTRATION NUMBER: 35,263
74 REFERENCE/DOCKET NUMBER: A2928-ECT-USA
75 TELECOMMUNICATION INFORMATION:
76 TELEPHONE: 212-408 2500
77 TELEFAX: 212-765 2519
78 TELEX:
79 INFORMATION FOR SEQ ID NO: 44:
80 SEQUENCE CHARACTERISTICS:
81 LENGTH: 8 amino acids
82 TYPE: amino acid
83 STRANDEDNESS:

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1 APPLICATION NUMBER:
2 FILING DATE:
3 ATTORNEY/AGENT INFORMATION:
4 NAME: MacLeod, Janet M
5 REGISTRATION NUMBER: 35,263
6 REFERENCE/DOCKET NUMBER: A2928-ECT-USA
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 212 408 2500
9 TELEFAX: 212 765 2519
10 TELEX:
11 INFORMATION FOR SEQ ID NO: 43:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 8 amino acids
14 TYPE: amino acid
15 STRANDEDNESS:
16 MOLECULE TYPE: peptide
17 HYPOTHEICAL: NO
18 ANTI-SENSE: NO
19 FRAGMENT TYPE: internal
20 ORIGINAL SOURCE:
21 US-08-335-730D-43
22
23 Query Match: 35.4%, Score 4; DP 3; Length 8;
24 Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
25 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
26
27 QY 4 AKRR 7
28 1 1
29 5 AKRR 8
30
31 DB
32
33 RESULT 14
34 US-08-335-730D-44
35 Sequence 44: Application US/08357330
36 Patent No. 6042641
37 GENERAL INFORMATION:
38 APPLICANT: Boretta, Alberto
39 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
40 NUMBER OF SEQUENCES: 90
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: Baker & Bots, L.L.P.
43 STREET: 40 Rockefeller Plaza
44 CITY: New York
45 STATE: NY
46 COUNTRY: U.S.A.
47 ZIP: 10112-0228
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Diskette
50 OPERATING SYSTEM: IBM Compatible
51 OPERATING SYSTEM: DOS
52 SOFTWARE: FastSeq Version 1.5
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/08/335,733D
55 FILING DATE: 10-NOV-1994
56 CLASSIFICATION: 435
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER:
59 FILING DATE:
60 ATTORNEY/AGENT INFORMATION:
61 NAME: MacLeod, Janet M
62 REGISTRATION NUMBER: 35,263
63 REFERENCE/DOCKET NUMBER: A2928-ECT-USA
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: 212-408 2500
66 TELEFAX: 212-765 2519
67 TELEX:
68 INFORMATION FOR SEQ ID NO: 44:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 8 amino acids
71 TYPE: amino acid
72 STRANDEDNESS:

```

1 Topology: linear  
2 MOLECULE TYPE: peptide  
3 HYPOTHETICAL: NO  
4 ANTI SENSE: NO  
5 FRAGMENT TYPE: internal  
6 ORIGINAL SOURCE:  
US 08-335-7330-44

Query Match: 36.4%, Score 41, ID 4, Length 81  
Best Local Similarity 100.0%, Pfam No. 2 5e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

CY 4 AKRR 7

ID 4 AKRR 7

RESULT 15  
US-08-335-7330-45  
1 Sequence 45, Application US/083557330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betotia, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 NUMBER OF SEQUENCES: 90  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: Baker & Botts, L.L.P.  
9 STREET: 30 Rockefeller Plaza  
10 CITY: New York  
11 STATE: NY  
12 COUNTRY: U.S.A.  
13 ZIP: 10112-0228  
14 COMPUTER READABLE FORM:  
15 MEDIUM TYPE: Diskette  
16 OPERATING SYSTEM: DOS  
17 SOFTWARE: FASTSEQ Version 1.5  
18 CURRENT APPLICATION DATA:  
19 APPLICATION NUMBER: US/08/335,7330  
20 FILING DATE: 10-NOV-1994  
21 CLASSIFICATION: 435  
22 PRIOR APPLICATION DATA:  
23 APPLICATION NUMBER:  
24 FILING DATE:  
25 ATTORNEY/AGENT INFORMATION:  
26 NAME: MacLeod, Janet M.  
27 REGISTRATION NUMBER: 35,263  
28 REFERENCE/DOCKET NUMBER: A29928-101 USA  
29 TELECOMMUNICATION INFORMATION:  
30 TELEPHONE: 212-408-2500  
31 TELEFAX: 212-765-2519  
32 TELEX:  
33 INFORMATION FOR SEQ ID NO: 45:  
34 SEQUENCE CHARACTERISTICS:  
35 LENGTH: 8 amino acids  
36 TYPE: amino acid  
37 STRANDEDNESS:  
38 TOPOLOGY: linear  
39 MOLECULE TYPE: peptide  
40 HYPOTHETICAL: NO  
41 ANTI SENSE: N  
42 FRAGMENT TYPE: internal  
43 ORIGINAL SOURCE:  
US 08-335-7330-46

Query Match: 36.4%, Score 41, ID 4, Length 81  
Best Local Similarity 100.0%, Pfam No. 2 5e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

CY 4 AKRR 7

ID 4 AKRR 7

RESULT 16  
US-08-335-7330-46  
1 Sequence 46, Application US/083557330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betotia, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 NUMBER OF SEQUENCES: 90  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: Baker & Botts, L.L.P.  
9 STREET: 30 Rockefeller Plaza  
10 CITY: New York  
11 STATE: NY  
12 COUNTRY: U.S.A.  
13 ZIP: 10112-0228  
14 COMPUTER READABLE FORM:  
15 MEDIUM TYPE: Diskette  
16 OPERATING SYSTEM: DOS  
17 SOFTWARE: FASTSEQ Version 1.5  
18 CURRENT APPLICATION DATA:  
19 APPLICATION NUMBER: US/08/335,7330  
20 FILING DATE: 10-NOV-1994  
21 CLASSIFICATION: 435  
22 PRIOR APPLICATION DATA:  
23 APPLICATION NUMBER:  
24 FILING DATE:  
25 ATTORNEY/AGENT INFORMATION:  
26 NAME: MacLeod, Janet M.  
27 REGISTRATION NUMBER: 35,263  
28 REFERENCE/DOCKET NUMBER: A29928-101 USA  
29 TELECOMMUNICATION INFORMATION:  
30 TELEPHONE: 212-408-2500  
31 TELEFAX: 212-765-2519  
32 TELEX:  
33 INFORMATION FOR SEQ ID NO: 46:  
34 SEQUENCE CHARACTERISTICS:  
35 LENGTH: 8 amino acids  
36 TYPE: amino acid  
37 STRANDEDNESS:  
38 TOPOLOGY: linear  
39 MOLECULE TYPE: peptide  
40 HYPOTHETICAL: NO  
41 ANTI SENSE: N  
42 FRAGMENT TYPE: internal  
43 ORIGINAL SOURCE:  
US 08-335-7330-47

Query Match: 36.4%, Score 41, ID 4, Length 81  
Best Local Similarity 100.0%, Pfam No. 2 5e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

CY 4 AKRR 7

ID 4 AKRR 7

RESULT 17  
US-08-335-7330-47  
1 Sequence 47, Application US/083557330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betotia, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 NUMBER OF SEQUENCES: 90  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: Baker & Botts, L.L.P.  
9 STREET: 30 Rockefeller Plaza  
10 CITY: New York  
11 STATE: NY  
12 COUNTRY: U.S.A.  
13 ZIP: 10112-0228  
14 COMPUTER READABLE FORM:  
15 MEDIUM TYPE: Diskette  
16 OPERATING SYSTEM: DOS  
17 SOFTWARE: FASTSEQ Version 1.5  
18 CURRENT APPLICATION DATA:  
19 APPLICATION NUMBER: US/08/335,7330  
20 FILING DATE: 10-NOV-1994  
21 CLASSIFICATION: 435  
22 PRIOR APPLICATION DATA:  
23 APPLICATION NUMBER:  
24 FILING DATE:  
25 ATTORNEY/AGENT INFORMATION:  
26 NAME: MacLeod, Janet M.  
27 REGISTRATION NUMBER: 35,263  
28 REFERENCE/DOCKET NUMBER: A29928-101 USA  
29 TELECOMMUNICATION INFORMATION:  
30 TELEPHONE: 212-408-2500  
31 TELEFAX: 212-765-2519  
32 TELEX:  
33 INFORMATION FOR SEQ ID NO: 47:  
34 SEQUENCE CHARACTERISTICS:  
35 LENGTH: 8 amino acids  
36 TYPE: amino acid  
37 STRANDEDNESS:  
38 TOPOLOGY: linear  
39 MOLECULE TYPE: peptide  
40 HYPOTHETICAL: NO  
41 ANTI SENSE: N  
42 FRAGMENT TYPE: internal  
43 ORIGINAL SOURCE:  
US 08-335-7330-48

Query Match: 36.4%, Score 41, ID 4, Length 81  
Best Local Similarity 100.0%, Pfam No. 2 5e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

CY 4 AKRR 7

ID 4 AKRR 7

US 08-335-7330-48  
1 Sequence 48, Application US/083557330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betotia, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 NUMBER OF SEQUENCES: 90  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: Baker & Botts, L.L.P.  
9 STREET: 30 Rockefeller Plaza  
10 CITY: New York  
11 STATE: NY  
12 COUNTRY: U.S.A.  
13 ZIP: 10112-0228  
14 COMPUTER READABLE FORM:  
15 MEDIUM TYPE: Diskette  
16 OPERATING SYSTEM: DOS  
17 SOFTWARE: FASTSEQ Version 1.5  
18 CURRENT APPLICATION DATA:  
19 APPLICATION NUMBER: US/08/335,7330  
20 FILING DATE: 10-NOV-1994  
21 CLASSIFICATION: 435  
22 PRIOR APPLICATION DATA:  
23 APPLICATION NUMBER:  
24 FILING DATE:  
25 ATTORNEY/AGENT INFORMATION:  
26 NAME: MacLeod, Janet M.  
27 REGISTRATION NUMBER: 35,263  
28 REFERENCE/DOCKET NUMBER: A29928-101 USA  
29 TELECOMMUNICATION INFORMATION:  
30 TELEPHONE: 212-408-2500  
31 TELEFAX: 212-765-2519  
32 TELEX:  
33 INFORMATION FOR SEQ ID NO: 48:  
34 SEQUENCE CHARACTERISTICS:  
35 LENGTH: 8 amino acids  
36 TYPE: amino acid  
37 STRANDEDNESS:  
38 TOPOLOGY: linear  
39 MOLECULE TYPE: peptide  
40 HYPOTHETICAL: NO  
41 ANTI SENSE: N  
42 FRAGMENT TYPE: internal  
43 ORIGINAL SOURCE:  
US 08-335-7330-49

Query Match: 36.4%, Score 41, ID 4, Length 81  
Best Local Similarity 100.0%, Pfam No. 2 5e+05  
Matches 4: Conservative 0; Mismatches 0; Indels 0;

CY 4 AKRR 7

ID 4 AKRR 7

STATE: NY  
 COUNTRY: U.S.A.  
 ZIPS: 10112-0228  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: diskette  
 COMPUTERS: IBM Compatib.c  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/99/435,743  
 FILING DATE: 10-NOV-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MacLeod, Janet M  
 REGISTRATION NUMBER: 35,263  
 REFERENCE/DOCKET NUMBER: A29724-PCT-USA  
 TELEPHONE: 212-408-2500  
 TELEFAX: 212-765-2519  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 47:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYDROPHATIC NO:  
 ANTI-SENSE NO:  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US 08-435,735-47

Query Match 36.4% Score 4: DB 4: Length 8;  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 4 AKK 7  
 LB 1 1  
 1 AKKK 4

PESH1 LB  
 US-09-485-286-4  
 Sequence 4: Application US/99/485,286  
 Patent No. 6559324  
 GENERAL INFORMATION:  
 APPLICANT: Stahl, Stefan  
 APPLICANT: Jonsson, Per  
 APPLICANT: Nygren, Per-Ake  
 APPLICANT: Ustun, Mathias  
 TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN  
 TITLE OF INVENTION: C-PEPTIDE  
 FILE REFERENCE: 11541-00200  
 CURRENT APPLICATION NUMBER: US/99/485,286  
 PRIOR FILING DATE: 2000-02-07  
 PRIOR APPLICATION NUMBER: PCT/SE98/02180  
 PRIOR FILING DATE: 1998-08-07  
 PRIOR APPLICATION NUMBER: GB 9716390.2  
 PRIOR FILING DATE: 1997-08-07  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 4  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURES:  
 OTHER INFORMATION: Representative linker region  
 US 09-485-286-4

Query Match 36.4% Score 4: DB 4: Length 8;  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 ASQA 4  
 LB 1 1  
 1 ASQA 4

RESULT 14  
 US-08-432-518-2  
 Sequence 2: Application US/08/432,518  
 Patent No. 5803240  
 GENERAL INFORMATION:  
 APPLICANT: TWIST, Michael  
 APPLICANT: SUMNER SMITH, Martin  
 TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foery & Hardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIPS: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/432,518  
 FILING DATE: 31-OCT-1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/139,757  
 FILING DATE: 22-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/872,398  
 FILING DATE: 23-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/779,735  
 FILING DATE: 24-OCT-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/602,953  
 FILING DATE: 24-OCT-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/995,742  
 FILING DATE: 22-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/872,318  
 FILING DATE: 23-APR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 16777/266/ALLE  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-332-518-2

Query Match 36.4% Score 4: DB 1: Length 9;  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 5 KKK b

14. 5 KRK 5

US-08-439-747A-23

Sequence 23, Application US/084 19747A

Patent No. 5757233

GENERAL INFORMATION:

APPLICANT: Zhang, Rongli

APPLICANT: Karamanian, Lela

TITLE OF INVENTION: Soluble, Circulable Substrates of the Hepatitis

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering Corp.

STREET: 2000 Gallopina Hill Road

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033-0530

COMPUTER REARABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5.3

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,747A

FILING DATE: May 12, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Linn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/AGENT NUMBER: J060509

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-298-5361

TELEFAX: 908-298-5368

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: Linear

FEATURE:

NAME/KEY: hydrophobic tail

US-06-439-747A-23

Query Match 36.4% Score 4, DB 1, Length 9:

Best Local Similarity 100.0%, Pred. No. 2,5e+05:

Matches 4, Conservative 0, Mismatches 0, Indels 0

5 KRK 8

4 KRK 7

///

US-08-439-709-4

Sequence 3, Application US/084709

Patent No. 561003

GENERAL INFORMATION:

APPLICANT: Twist, Michael

APPLICANT: Barnett, Richard

APPLICANT: Reid, Lorrie

APPLICANT: Sumner-Smith, Mattie

TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0293

COMPUTER REARABLE FORM:

MEDIUM TYPE: Floppy disk

US-08-432-518-20

Sequence 10, Application US/08432518

Patent No. 5644240

GENERAL INFORMATION:

APPLICANT: Twist, Michael

APPLICANT: Sumner-Smith, Mattie

TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER REARABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Epi-Info Release #1.0, Version #1.00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,518

FILING DATE: 31-OCT-1994

CLASSIFICATION: 514

PSI-R APPLICATION DATA:

APPLICATION NUMBER: US 08/113,757

FILING DATE: 22-OCT-1993

PRELIM APPLICATION DATA:

APPLICATION NUMBER: US 07/872,698

FILING DATE: 23-APR-1992

PRELIM APPLICATION DATA:

APPLICATION NUMBER: US 07/779,175

FILING DATE: 23-OCT-1991

PRELIM APPLICATION DATA:

APPLICATION NUMBER: US 07/632,953

FILING DATE: 24-OCT-1990

PRELIM APPLICATION DATA:

APPLICATION NUMBER: US 07/400,142

FILING DATE: 22-DEC-1992

PSI-R APPLICATION DATA:

APPLICATION NUMBER: US 07/400,142

FILING DATE: 23-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Kent, Stephen A

REGISTRATION NUMBER: 29,768

REFERENCE/AGENT NUMBER: 16717/2002AL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)572-5500

TELEFAX: (202)672-5399

TELEX: 954136

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: Linear

US-08-432-518-10

Query Match 36.4% Score 4, DB 1, Length 9:

Best Local Similarity 100.0%, Pred. No. 2,5e+05:

Matches 4, Conservative 0, Mismatches 0, Indels 0

5 KRK 8

4 KRK 6

///

RESULT 21



```

1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patent In Release #1.0, Virus #1.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/09/378,709
6  FILING DATE:
7  CLASSIFICATION: 530
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 01/872,498
10 FILING DATE: 23-APR-1992
11 APPLICATION NUMBER: US 07/779,740
12 FILING DATE: 23-OCT-1991
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/602,734
15 FILING DATE: 24-OCT-1990
16 ATTORNEY/AGENT INFORMATION:
17 NAME: BENT, Stephen A.
18 REGISTRATION NUMBER: 29,768
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (703)836-9300
21 TELEFAX: (703)663-4109
22 TELEX: 899149
23 INFORMATION FOR SEQ ID NO: 1:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 9 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 US 09 378-709-11
29
30 Query Match: 96.4%; Score 4; DB 2; Length 9;
31 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
32 Mismatches 4; Conservative 0; Indels 0; Gaps 0;
33
34 QY 5 KKKK R
35 1 1 1
36 3 KKKK S
37
38 RESULT 24
39 US-09-440-409B-23
40 Sequence 23, Application US/08440409B
41 Patent No. 5843752
42 GENERAL INFORMATION:
43 APPLICANT: Basmahapatia, Rupal
44 APPLICANT: Murray, Michael
45 APPLICANT: Ramnarayan, Lata
46 APPLICANT: Bakiewicz, Nancy
47 TITLE OF INVENTION: Soluble Active Hepatitis C Virus Protease
48 NUMBER OF SEQUENCES: 14
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Schering Corp.
51 STREET: 2060 Gallop Hill Road
52 CITY: Kenilworth
53 STATE: New Jersey
54 COUNTRY: USA
55 ZIP: 07033-0530
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 COMPUTER: Apple Macintosh
59 OPERATING SYSTEM: Macintosh 7.5.3
60 SOFTWARE: Microsoft Word 5.1a
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/440,409B
63 FILING DATE: May 12, 1995
64 CLASSIFICATION: 435
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Gaud, Paul G.
67 REGISTRATION NUMBER: 42,743
68 REFERENCE/DOCKET NUMBER: JH0494
69 TELECOMMUNICATION INFORMATION:
70 TELEPHONE: 408-298-5001
71 TELEFAX: 408-248-5388
72 INFORMATION FOR SEQ ID NO: 23:
73 SEQUENCE CHARACTERISTICS:
74 LENGTH: 9 amino acids
75 TYPE: amino acid
76 STRANDEDNESS: single
77 TOPOLOGY: linear
78 MOLECULE TYPE: polypeptide
79 FEATURE:
80 NAME/KEY: hydrophobic tail
81 US-08-440-409B-23
82
83 Query Match: 96.4%; Score 4; DB 2; Length 9;
84 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
85 Mismatches 4; Conservative 0; Indels 0; Gaps 0;

```

```

1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patent In Release #1.0, Virus #1.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/09/378,709
6  FILING DATE:
7  CLASSIFICATION: 530
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 01/872,498
10 FILING DATE: 23-APR-1992
11 APPLICATION NUMBER: US 07/779,740
12 FILING DATE: 23-OCT-1991
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/602,734
15 FILING DATE: 24-OCT-1990
16 ATTORNEY/AGENT INFORMATION:
17 NAME: BENT, Stephen A.
18 REGISTRATION NUMBER: 29,768
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (703)836-9300
21 TELEFAX: (703)663-4109
22 TELEX: 899149
23 INFORMATION FOR SEQ ID NO: 1:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 9 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 US 09 378-709-11
29
30 Query Match: 96.4%; Score 4; DB 2; Length 9;
31 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
32 Mismatches 4; Conservative 0; Indels 0; Gaps 0;
33
34 QY 5 KKKK R
35 1 1 1
36 3 KKKK S
37
38 RESULT 24
39 US-08-440-409B-23
40 Sequence 11, Application US/08440409B
41 Patent No. 5843752
42 GENERAL INFORMATION:
43 APPLICANT: Basmahapatia, Rupal
44 APPLICANT: Murray, Michael
45 APPLICANT: Ramnarayan, Lata
46 APPLICANT: Bakiewicz, Nancy
47 TITLE OF INVENTION: Soluble Active Hepatitis C Virus Protease
48 NUMBER OF SEQUENCES: 14
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Schering Corp.
51 STREET: 2060 Gallop Hill Road
52 CITY: Kenilworth
53 STATE: New Jersey
54 COUNTRY: USA
55 ZIP: 07033-0530
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 COMPUTER: Apple Macintosh
59 OPERATING SYSTEM: Macintosh 7.5.3
60 SOFTWARE: Microsoft Word 5.1a
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/440,409B
63 FILING DATE: May 12, 1995
64 CLASSIFICATION: 435
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Gaud, Paul G.
67 REGISTRATION NUMBER: 42,743
68 REFERENCE/DOCKET NUMBER: JH0494
69 TELECOMMUNICATION INFORMATION:
70 TELEPHONE: 408-298-5001
71 TELEFAX: 408-248-5388
72 INFORMATION FOR SEQ ID NO: 23:
73 SEQUENCE CHARACTERISTICS:
74 LENGTH: 9 amino acids
75 TYPE: amino acid
76 STRANDEDNESS: single
77 TOPOLOGY: linear
78 MOLECULE TYPE: polypeptide
79 FEATURE:
80 NAME/KEY: hydrophobic tail
81 US-08-440-409B-23
82
83 Query Match: 96.4%; Score 4; DB 2; Length 9;
84 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
85 Mismatches 4; Conservative 0; Indels 0; Gaps 0;

```

```

CY 1 KKKK #
LD 1 1
4 KKKK /

RESULT 25
US-08-459-765-4
Sequence 4, Application US/08-459-765-4
Patent No. 6092844
GENERAL INFORMATION:
APPLICANT: Borella, Alberto
TITLE OF INVENTION: HIV PROTEIN FOLDING
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE HIV PROTEIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, LLP
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-459-765-4
FILING DATE: 10-NOV-1994
CLASSIFICATION: 445
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Margaret Janet M
REGISTRATION NUMBER: 35,274
REFERENCE/POCKET NUMBER: A476261
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-459-2503
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQUENCE NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
POLARITY: N-Term
MEDIUM TYPE: peptide
EXTENDED NAME: NO
ANALYSES: N
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-445-740-4

Query Match 46.48% Score 4: 39 5 Length 9:
Best Local Similarity 100.0% Pred. No. 2 5e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 4 AKKR 7
LD 1 1
4 AKKR /

RESULT 26
US-08-726-807B-17
Sequence 17, Application US/08-726-807B-17
Patent No. 6092618
GENERAL INFORMATION:
APPLICANT: Parmacek, Michael S.
APPLICANT: Sorway, Julian
TITLE OF INVENTION: PROTEIN EXPRESSION

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NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Drake
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-726-807B
FILING DATE: 07-01-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 63/004,868
FILING DATE: 05-01-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMillan, Raymond R.
REGISTRATION NUMBER: P-43,393
REFERENCE/POCKET NUMBER: ARSB:510
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-4000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQUENCE NO. 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
POLARITY: N-Term
US-08-726-807B-17

Query Match 36.48% Score 4: 08 3 Length 9:
Best Local Similarity 100.0% Pred. No. 2 5e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 5 KKKK 6
LD 1 1
6 KKKK /

RESULT 27
US-08-478-859-1
Sequence 1, Application US/08-478-859-1
Patent No. 628554
GENERAL INFORMATION:
APPLICANT: Gossyp, Andrew R.
APPLICANT: Sapp, Patricia
APPLICANT: van der, Heidek
APPLICANT: Rotzkoek, Stephen
APPLICANT: Wozniak, John R.
APPLICANT: Johnson, Richard A.
APPLICANT: Wood, Patricia J.
APPLICANT: Burton, Steven J.
APPLICANT: Glick, Alan V.
TITLE OF INVENTION: High Purity Albumin
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The BCC Group, Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill, New Providence
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER: US/08/478,659
2  FILING DATE: 26-JAN-1995
3  CLASSIFICATION: 435
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Swope, R Haln
6  REGISTRATION NUMBER: 24,864
7  REFERENCE/DOCKET NUMBER: 92H8501
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: (908) 771 6292
10  TELEFAX: (908) 771 6159
11  INFORMATION FOR SEQ ID NO: 1:
12  SEQUENCE CHARACTERISTICS:
13  LENGTH: 10 amino acids
14  TYPE: amino acid
15  STRANDEDNESS: single
16  TOPOLOGY: linear
17  MOLECULE TYPE: peptide
18  HYPOTHETICAL: NO
19  ANTI-SENSE: NO
20  FRAGMENT TYPE: internal
21  ORGANISM: Peptide fragment of human serum albumin
22  US-08-478-659-1
23
24  Query Match: 36.4%; Score 4; OR 2: Length 10;
25  Best Local Similarity: 100.0%; Pred. No. 1: 0;
26  Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
27
28  QY 1 ASQA 4
29  11 1
30  4 ASQA 7
31
32  RESULT 28
33  US-08-726-66A 6
34  Sequence 6, Application US/08/726-66A
35  Patent No. 5958684
36  GENERAL INFORMATION:
37  APPLICANT: van Leeuwen, Frederic Willem
38  APPLICANT: Boudach, Johannes Peter Heert
39  APPLICANT: Grosveld, Franklin G.
40  TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
41  NUMBER OF SEQUENCES: 189
42  CURRENT INVENTION ADDRESS:
43  ADDRESSEE: Warner & Wolfelt, Ltd.
44  STREET: 1 Financial Center
45  CITY: Boston
46  STATE: MA
47  COUNTRY: US
48  ZIP: 02111
49  COMPUTER READABLE FORM:
50  MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, 800000
51  OPERATING SYSTEM: IBM PC compatible
52  SOFTWARE: WordPerfect 6.1
53  CURRENT APPLICATION DATA:
54  APPLICATION NUMBER: US/08/726,66A
55  FILING DATE: 02 Oct-1996
56  PRIOR APPLICATION DATA:
57  APPLICATION NUMBER: GB 95/20047 4
58  FILING DATE: 02-Oct-1995
59  PRIOR APPLICATION DATA:
60  APPLICATION NUMBER: US 60/059,852
61  FILING DATE: 03-Jan-1996
62  ATTORNEY/AGENT INFORMATION:
63  NAME: Williams, Ph.D., Kathleen M
64  REGISTRATION NUMBER: 34,380
65  REFERENCE/DOCKET NUMBER: 92,045 A (2,577,003-4)
66  TELECOMMUNICATION INFORMATION:
67  TELEPHONE: (617) 345-9100
68  TELEFAX: (617) 345-9111
69  INFORMATION FOR SEQ ID NO: 6:
70  SEQUENCE CHARACTERISTICS:

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1  LENGTH: 10 amino acids
2  TYPE: amino acid
3  STRANDEDNESS: single
4  TOPOLOGY: unknown
5  MOLECULE TYPE: peptide
6  US-08-726-66A-6
7
8  Query Match: 36.4%; Score 4; OR 2: Length 10;
9  Best Local Similarity: 100.0%; Pred. No. 1: 0;
10  Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
11
12  QY 7 RKGP 10
13  111
14  6 RKGP 9
15
16  RESULT 29
17  US-08-970-648-1
18  Sequence 1, Application US/08/970-648
19  Patent No. 6034221
20  GENERAL INFORMATION:
21  APPLICANT: Goodey, Andrew K
22  APPLICANT: Sleep, Darrell
23  APPLICANT: van Dijk, Hendrik
24  APPLICANT: Berezakko, Stephen
25  APPLICANT: Woodrow, John K
26  APPLICANT: Johnson, Richard A
27  APPLICANT: Wood, Patricia C
28  APPLICANT: Butts, Steven J
29  APPLICANT: Quirk, Alan V
30  TITLE OF INVENTION: High Purity Albumin
31  NUMBER OF SEQUENCES: 4
32  CORRESPONDENCE ADDRESS:
33  ADDRESSEE: The BOC Group, Inc
34  STREET: 100 Mountain Avenue
35  CITY: Murray Hill, New Providence
36  STATE: New Jersey
37  COUNTRY: United States of America
38  ZIP: 07974
39  COMPUTER READABLE FORM:
40  MEDIUM TYPE: Floppy Disk
41  OPERATING SYSTEM: IBM PC compatible
42  SOFTWARE: Patent Release #1.0, Version #1.25
43  CURRENT APPLICATION DATA:
44  APPLICATION NUMBER: US/08/970,648
45  FILING DATE:
46  CLASSIFICATION: 530
47  PRIOR APPLICATION DATA:
48  APPLICATION NUMBER: US 06/578,659
49  FILING DATE: 26-JAN-1995
50  ATTORNEY/AGENT INFORMATION:
51  NAME: Swope, R Haln
52  REGISTRATION NUMBER: 24,864
53  REFERENCE/DOCKET NUMBER: 92H8501
54  TELECOMMUNICATION INFORMATION:
55  TELEPHONE: (908) 771 6292
56  TELEFAX: (908) 771 6159
57  INFORMATION FOR SEQ ID NO: 1:
58  SEQUENCE CHARACTERISTICS:
59  LENGTH: 10 amino acids
60  TYPE: amino acid
61  STRANDEDNESS: single
62  TOPOLOGY: linear
63  MOLECULE TYPE: peptide
64  HYPOTHETICAL: NO
65  ANTI-SENSE: NO
66  FRAGMENT TYPE: internal
67  ORGANISM: Peptide fragment of human serum albumin
68  US-08-970-648-1
69
70  Query Match: 36.4%; Score 4; OR 3: Length 10;

```

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Best Local Similarity 100.0%; Pred. No. 3 Best 2;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

CY 1 ASQA 4
DB 4 ASQA 7

RESULT 40
US 09-159-139A-746
: Sequence 746; Application US/09159-746
: Patent No. 6495135
: GENERAL INFORMATION:
: APPLICANT: KUGO, Ralph J.
: APPLICANT: Grey, Howard M.
: APPLICANT: Sette, Alessandro
: APPLICANT: Sette, Esoban
: TITLE OF INVENTION: HLA Binding peptides and their
: NUMBER OF SEQUENCES: 1254
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3644
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/159-746
: FILING DATE: 29-NOV-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/926,460
: FILING DATE: 07-AUG-1992
: APPLICATION NUMBER: US 08/127,746
: FILING DATE: 05-MAR-1995
: APPLICATION NUMBER: US 08/158,500
: FILING DATE: 06-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Weber, Ellen Leaver
: REGISTRATION NUMBER: 32,762
: REFERENCE/DOCKET NUMBER: 3180-23-00000-02
: PUBLICATION INFORMATION:
: TELEPHONE: (415) 575-0209
: TELEFAX: (415) 576-0000
: INDEX
: INFORMATION FOR SEQ ID NO: 746:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRAND: single
: LOCATION: linear
: MOLECULE TYPE: peptide
US-09-159-139A-746

Query Match: 96.4%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1 Best 2;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

CY # KQPR 11
DB 7 KQPR 10

RESULT 41
US-09-434-476A-4
: Sequence 4; Application US/09434-76A
: Patent No. 6495138
: GENERAL INFORMATION:
: APPLICANT: van Nieuwstadt, Antonie
: APPLICANT: Janszweid, Jan
: APPLICANT: Meulenbergh, Janneke
: TITLE OF INVENTION: PRRSV Antigenic Sites Identifying Peptide Sequences of PRRS
: FILE REFERENCE: 2193-421718
: CURRENT APPLICATION NUMBER: US/09/434-476A
: PRIOR FILING DATE: 1999-11-05
: PRIOR APPLICATION NUMBER: EP 97231443.2
: PRIOR FILING DATE: 1997-05-16
: PRIOR APPLICATION NUMBER: PCT/NL98/00251
: PRIOR FILING DATE: 1998-05-05
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patent In version 3.0
: SEQ ID NO: 4
: LENGTH: 10
: TYPE: PEPT
: ORGANISM: Porcine reproductive and respiratory syndrome virus
US-09-434-476A-4

Query Match: 96.4%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1 Best 2;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

CY 5 QARK 6
DB 5 QARK 8

RESULT 42
US 09-129-192C-56
: Sequence 56; Application US/99129-192C
: Patent No. 6495664
: GENERAL INFORMATION:
: APPLICANT: Aurora Biosciences Corporation
: APPLICANT: Cubitt, Andrew B.
: TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modification
: FILE REFERENCE: AUR02270 (08366/031001)
: CURRENT APPLICATION NUMBER: US/09/129-192C
: CURRENT FILING DATE: 1998-07-24
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: Patent In version 3.0
: SEQ ID NO: 56
: LENGTH: 10
: TYPE: PEPT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Phosphorylation motif
US 9-129-192C-56

Query Match: 96.4%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1 Best 2;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

CY 6 RRG 9
DB 4 RRG 7

RESULT 43
US-09-129-192C-57
: Sequence 57; Application US/99129-192C
: Patent No. 6495664
: GENERAL INFORMATION:
: APPLICANT: Aurora Biosciences Corporation
: APPLICANT: Cubitt, Andrew B.
: TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modification
: FILE REFERENCE: AUR02270 (08366/031001)
: CURRENT APPLICATION NUMBER: US/09/129-192C
: CURRENT FILING DATE: 1998-07-24
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: Patent In version 3.0

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: SEQ ID NO: 57
: LENGTH: 10
: TYPE: PPT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Phosphorylation Ser4,1
US 09 129 1920 57

Query Match
: Sequence 1, Application US/0637859
: Best Local Similarity 100.0%, Pctd. No. 26-02,
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 AKKG 7
LB 4 AKKG 7

RESULT 35
US-08-664-721 17
: Sequence 17, Application US/08669721
: Patent No. 5814236
: GENERAL INFORMATION:
: APPLICANT: Jacob et al., Christopher J.
: TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
: TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/669,721
: FILING DATE: 27-JUN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ellison, Eldora L.
: REGISTRATION NUMBER: 19,967
: REFERENCE/PACKET NUMBER: 07251/014001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US 08-669 721 17

Query Match
: Sequence 1, Application US/08540389
: Best Local Similarity 100.0%, Pctd. No. 26-02,
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7
LB 2 AKKR 5

RESULT 36
US-08-540 388 1
: Sequence 1, Application US/08540389
: Patent No. 5858964
: GENERAL INFORMATION:
: APPLICANT: ARARONI, Rana
: APPLICANT: ARNON, Ruth
: APPLICANT: CHAO, Nelson J.
: APPLICANT: SCHLEGEL, Paul G.
: APPLICANT: SELA, Michael
: APPLICANT: TEITELBAUM, David
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
: TITLE OF INVENTION: SYNTHETIC PEPTIDE COPOLYMER FOR PREVENTION OF GVHD
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street N.W., Ste. 300

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: SEQ ID NO: 57
: LENGTH: 10
: TYPE: PPT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Phosphorylation Ser4,1
US 09 129 1920 57

Query Match
: Sequence 4, Application US/0637859
: Best Local Similarity 100.0%, Pctd. No. 26-02,
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 AKKG 7
LB 4 AKKG 7

RESULT 35
US-08-664-721 17
: Sequence 17, Application US/08669721
: Patent No. 5814236
: GENERAL INFORMATION:
: APPLICANT: Jacob et al., Christopher J.
: TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
: TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/669,721
: FILING DATE: 27-JUN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ellison, Eldora L.
: REGISTRATION NUMBER: 19,967
: REFERENCE/PACKET NUMBER: 07251/014001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US 08-669 721 17

Query Match
: Sequence 1, Application US/08540389
: Best Local Similarity 100.0%, Pctd. No. 26-02,
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7
LB 2 AKKR 5

RESULT 36
US-08-540 388 1
: Sequence 1, Application US/08540389
: Patent No. 5858964
: GENERAL INFORMATION:
: APPLICANT: ARARONI, Rana
: APPLICANT: ARNON, Ruth
: APPLICANT: CHAO, Nelson J.
: APPLICANT: SCHLEGEL, Paul G.
: APPLICANT: SELA, Michael
: APPLICANT: TEITELBAUM, David
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
: TITLE OF INVENTION: SYNTHETIC PEPTIDE COPOLYMER FOR PREVENTION OF GVHD
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street N.W., Ste. 300

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1 CITY: Washington
2 STATE: D.C.
3 COUNTRY: United States of America
4 ZIP: 20004
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/09/540,443
12 FILING DATE:
13 CLASSIFICATION: 514
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/421,412
16 FILING DATE: 14-APR-1995
17 ATTORNEY/AGENT INFORMATION:
18 NAME: BROWDY, Roger L.
19 REGISTRATION NUMBER: 25,618
20 REFERENCE/DCKET NUMBER: AHARONI, A.
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (202) 528-5197
23 TELEFAX: (202) 737-3528
24 TELEX: 248643
25 INFORMATION FOR SEQ ID NO: 1:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 11 amino acids
28 TYPE: amino acid
29 STRANDEDNESS: single
30 TOPOLOGY: linear
31 Molecule type: peptide
32 FEATURE:
33 OTHER INFORMATION: The diagram at position 1 is not a free
34 US 08 540-443
35
36 Query Match: 46.4%, Score 4, DB 2, Length 11
37 Best Local Similarity: 100.0%, Fred. No. 20022
38 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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1 REFERENCE/DCKET NUMBER: 600-1-097CIP1
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: 201-487-5800
4 TELEFAX: 201-343-1484
5 INFORMATION FOR SEQ ID NO: 1:
6 SEQUENCE CHARACTERISTICS:
7 LENGTH: 11 amino acids
8 TYPE: amino acid
9 STRANDEDNESS: single
10 TOPOLOGY: linear
11 Molecule type: peptide
12 US 08 448 3543
13
14 Query Match: 46.4%, Score 4, DB 2, Length 11
15 Best Local Similarity: 100.0%, Fred. No. 20022
16 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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1  LENGTH: 11 amino acids
2  TYPE: amino acid
3  STRANDEDNESS: single
4  TAGGAGE: linear
5  MOLECULE TYPE: peptide
6  US-08-415-965-3
7
8  Query Match          36.4%, Score 4; DB 3; Length 11;
9  Best Local Similarity 100.0%; Pred. No. 2e-02;
10 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;
11
12 QY 3 QAKR 6
13 DL 4 QAKR 7
14
15 RESULT 40
16 US-08-970-648-4
17 1 Sequence 4; Application: US/08970648
18 2 Patent No.: 6584241
19 3 GENERAL INFORMATION:
20 4 APPLICANT: Goosky, Andrew R
21 5 APPLICANT: Sleep, Darrell
22 6 APPLICANT: van Elk, Brenda
23 7 APPLICANT: Berzenkov, Stephen
24 8 APPLICANT: Woodrow, John W
25 9 APPLICANT: Johnson, Richard A
26 10 APPLICANT: Wood, Patricia C
27 11 APPLICANT: Burton, Steven C
28 12 APPLICANT: Quirk, Alan V
29 13 TITLE OF INVENTION: High Purity Albumin
30 14 NUMBER OF SEQUENCES: 4
31 15 CORRESPONDENCE ADDRESS:
32 16 ADDRESSEE: 120 BOC Group, Inc
33 17 STREET: 100 Mainland Avenue
34 18 CITY: Murray Hill, New Providence
35 19 STATE: New Jersey
36 20 COUNTRY: United States of America
37 21 ZIP: 07974
38 22 COMPUTER READABLE FORM:
39 23 MEDIUM TYPE: Floppy disk
40 24 COMPUTER: IBM PC compatible
41 25 OPERATING SYSTEM: PC-DOS/MS-DOS
42 26 SOFTWARE: Patent Release #1.0, Version #1.25
43 27 CURRENT APPLICATION DATA:
44 28 APPLICATION NUMBER: US/08/415,965
45 29 FILING DATE: 06-JUN-1995
46 30 CLASSIFICATION: 424
47 31 PRIOR APPLICATION DATA:
48 32 APPLICATION NUMBER: 06/448,454
49 33 FILING DATE: 30 NOV-1994
50 34 CLASSIFICATION: 424
51 35 PRIOR APPLICATION DATA:
52 36 APPLICATION NUMBER: 08/243,674
53 37 FILING DATE: 23-MAY-1994
54 38 CLASSIFICATION: 424
55 39 PRIOR APPLICATION DATA:
56 40 APPLICATION NUMBER: 07/295,614
57 41 FILING DATE: 03-MAY-1991
58 42 CLASSIFICATION: 424
59 43 AID PNEY/AGENT INFORMATION:
60 44 NAME: Jackson, David
61 45 REGISTRATION NUMBER: 26,742
62 46 REFERENCE/BOOKET NUMBER: 602,100,016-119.
63 47 TELECOMMUNICATION INFORMATION:
64 48 TELEPHONE: 201-487-5800
65 49 TELEFAX: 201-343-1684
66 50 INFORMATION FOR SEQ ID NO: 3:
67 51 SEQUENCE CHARACTERISTICS:
68 52 LENGTH: 11 amino acids
69 53 TYPE: amino acid
70 54 STRANDEDNESS: single
71 55 TAGGAGE: linear
72 56 MOLECULE TYPE: peptide
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82 RESULT 40
83 US-08-970-648-4
84 1 Sequence 4; Application: US/08970648
85 2 Patent No.: 6584241
86 3 GENERAL INFORMATION:
87 4 APPLICANT: Goosky, Andrew R
88 5 APPLICANT: Sleep, Darrell
89 6 APPLICANT: van Elk, Brenda
90 7 APPLICANT: Berzenkov, Stephen
91 8 APPLICANT: Woodrow, John W
92 9 APPLICANT: Johnson, Richard A
93 10 APPLICANT: Wood, Patricia C
94 11 APPLICANT: Burton, Steven C
95 12 APPLICANT: Quirk, Alan V
96 13 TITLE OF INVENTION: High Purity Albumin
97 14 NUMBER OF SEQUENCES: 4
98 15 CORRESPONDENCE ADDRESS:
99 16 ADDRESSEE: 120 BOC Group, Inc
100 17 STREET: 100 Mainland Avenue
101 18 CITY: Murray Hill, New Providence
102 19 STATE: New Jersey
103 20 COUNTRY: United States of America
104 21 ZIP: 07974
105 22 COMPUTER READABLE FORM:
106 23 MEDIUM TYPE: Floppy disk
107 24 COMPUTER: IBM PC compatible
108 25 OPERATING SYSTEM: PC-DOS/MS-DOS
109 26 SOFTWARE: Patent Release #1.0, Version #1.25
110 27 CURRENT APPLICATION DATA:
111 28 APPLICATION NUMBER: US/08/415,965
112 29 FILING DATE: 06-JUN-1995
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114 31 PRIOR APPLICATION DATA:
115 32 APPLICATION NUMBER: 06/448,454
116 33 FILING DATE: 30 NOV-1994
117 34 CLASSIFICATION: 424
118 35 PRIOR APPLICATION DATA:
119 36 APPLICATION NUMBER: 08/243,674
120 37 FILING DATE: 23-MAY-1994
121 38 CLASSIFICATION: 424
122 39 PRIOR APPLICATION DATA:
123 40 APPLICATION NUMBER: 07/295,614
124 41 FILING DATE: 03-MAY-1991
125 42 CLASSIFICATION: 424
126 43 AID PNEY/AGENT INFORMATION:
127 44 NAME: Jackson, David
128 45 REGISTRATION NUMBER: 26,742
129 46 REFERENCE/BOOKET NUMBER: 602,100,016-119.
130 47 TELECOMMUNICATION INFORMATION:
131 48 TELEPHONE: 201-487-5800
132 49 TELEFAX: 201-343-1684
133 50 INFORMATION FOR SEQ ID NO: 3:
134 51 SEQUENCE CHARACTERISTICS:
135 52 LENGTH: 11 amino acids
136 53 TYPE: amino acid
137 54 STRANDEDNESS: single
138 55 TAGGAGE: linear
139 56 MOLECULE TYPE: peptide
140 57 US-08-415-965-3

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1  PRIOR APPLICATION NUMBER: US 08/669,721
2  PRIOR FILING DATE: 1998-06-27
3  NUMBER OF SEQ ID NOS: 28
4  SOFTWARE: FASTSEQ for Windows Version 4.0
5  SEQ ID NO 20
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11 Query Match: 36.4% Score 41 DB 4 Length 11
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OTHER INFORMATION: /note "Added carboxy-terminal  
OTHER INFORMATION: Glycine residue"  
PCT US92 10068 7

Query Match 36.4% Score 4: DB 1 Length 11  
Best Local Similarity 100.0% Pred. No. 200 2  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ASQA 6  
DB 111  
4 ASQA 7

## RESULT 44

PCT US95 11127-16  
Sequence 16: Application PCT/US9511127  
GENERAL INFORMATION:  
APPLICANT: ROBERT WEHNER  
TITLE OF INVENTION: DOPAMINE RECEPTOR PEPTIDES AND  
ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIELEN, PETERSON & LANGE  
STREET: 1790 N. CALIFORNIA BOULEVARD, SUITE 720  
CITY: WALNUT CREEK  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94596

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE 5.25 INCH, 1.2 MB FLOPPY  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11127  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: NONE  
FILING DATE: NONE

ATTORNEY/AGENT INFORMATION:  
NAME: THEODORE J. BIELEN, JR.  
REGISTRATION NUMBER: 27,420  
REFERENCE/DOCKET NUMBER: 1206#  
TELEPHONE: (510) 937-1515  
TELEFAX: (510) 937-1529  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11  
TYPE: AMINO ACID  
STRANDEDNESS: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURES:  
NAME/KEY: D3 RECEPTOR (22-42)  
IDENTIFICATION METHOD: AMINO ACID ANALYSIS

OTHER INFORMATION: DOPAMINE D3 RECEPTOR PEPTIDE  
PCT US95 11127-16  
Query Match 36.4% Score 4: DB 1 Length 11  
Best Local Similarity 100.0% Pred. No. 200 2  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ASQA 4  
DB 2 ASQA 5

## RESULT 45

US CR 012-846-20  
Sequence 20: Application US/08012846  
Patent No. 5662596

GENERAL INFORMATION:  
APPLICANT: Barbet, Jack R.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Respass, James G.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
TITLE OF INVENTION: CANCER IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Betty  
STREET: 6000 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104 7072  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: PUBLIIC Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,846  
FILING DATE:  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMASTER, David D.  
REGISTRATION NUMBER: 34,963  
REFERENCE/DOCKET NUMBER: 930049.40R  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 522-4903  
TELEFAX: (206) 682-6631  
TELEX: 4723636  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: peptide  
HYDROTHERMAL: NO  
FRAGMENT TYPE: N-terminal  
US-08-032-846-20

Query Match 46.4% Score 4: DB 1: Length 12:  
Best Local Similarity 100.0% Pred. No. 2.1e-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ASQA 4  
DB 4 ASQA 7

## RESULT 46

US-08-330-599-5  
Sequence 5: Application US/08340599  
Patent No. 5731409

GENERAL INFORMATION:  
APPLICANT: Furcht, Leo I.  
APPLICANT: McCarthy, James B.  
APPLICANT: Fields, Gregg B.  
TITLE OF INVENTION: Polypeptides with Type 1 Collagen  
TITLE OF INVENTION: Activity  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 5731409west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:

QY 1 ASQA 4  
DB 2 ASQA 5

1 MEDIUM TYPE: Floppy disk  
 2 COMPUTER: IBM PC compatible  
 3 OPERATING SYSTEM: PC-DOS/MS-DOS  
 4 SOFTWARE: Patent in Release #112, Version #1.2  
 5 CURRENT APPLICATION DATA:  
 6 APPLICATION NUMBER: US/09/300,500  
 7 FILING DATE: 28-OCT-1994  
 8 CLASSIFICATION: 530  
 9 ATTORNEY/AGENT INFORMATION:  
 10 NAME: CARTOT, Charles G.  
 11 REGISTRATION NUMBER: 45,054  
 12 REFERENCE/DOCKET NUMBER: 600,265,881  
 13 TELECOMMUNICATION INFORMATION:  
 14 TELEPHONE: 612-332-5300  
 15 TELEFAX: 612-332-9081  
 16 INFORMATION FOR SEQ ID NO: 5:  
 17 SEQUENCE CHARACTERISTICS:  
 18 LENGTH: 12 amino acids  
 19 TYPE: amino acid  
 20 TOPOLOGY: linear  
 21 MOLECULE TYPE: peptide  
 22 US 09-300,500-5

Query Match 36.4% Score 4: DB 1: Length 12:  
 Best Local Similarity 100.0% Pred. No. 2, 1e+02:  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 KKKP 11

DB 5 KKKP 9

RESULT 47

1 US-09-478-709 41  
 2 Sequence 31, Application US/09/478,709  
 3 Patent No. 5958684  
 4 GENERAL INFORMATION:  
 5 APPLICANT: TWIST, Michael  
 6 APPLICANT: HARNETT, Richard  
 7 APPLICANT: REID, Lorne  
 8 APPLICANT: SUMNER-SMITH, Martin  
 9 TITLE OF INVENTION: TREATMENT OF HEADS VIBES EXPLOSION  
 10 NUMBER OF SEQUENCES: 33  
 11 CROSS-REFERENCE ADDRESS:  
 12 ADDRESSEE: Foley & Lardner  
 13 STREET: 2500 Diagonal Road, Suite 500  
 14 CITY: Alexandria  
 15 STATE: VA  
 16 COUNTRY: USA  
 17 ZIP: 22304-2299  
 18 COMPUTER READABLE FORM:  
 19 MEDIUM TYPE: Floppy disk  
 20 COMPUTER: IBM PC compatible  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 SOFTWARE: Patent in Release #112, Version #1.2  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: US/09/478,709  
 25 FILING DATE:  
 26 CLASSIFICATION: 530  
 27 PRIOR APPLICATION DATA:  
 28 APPLICATION NUMBER: US 07/872,348  
 29 FILING DATE: 23-APR-1992  
 30 APPLICATION NUMBER: US 07/736,746  
 31 FILING DATE: 23-OCT-1991  
 32 PRIOR APPLICATION DATA:  
 33 APPLICATION NUMBER: US 07/602,954  
 34 FILING DATE: 24-OCT-1990  
 35 ATTORNEY/AGENT INFORMATION:  
 36 NAME: BENT, Stephen A.  
 37 REGISTRATION NUMBER: 29,748  
 38 REFERENCE/DOCKET NUMBER: 16711/176 AL...  
 39 TELECOMMUNICATION INFORMATION:  
 40 TELEPHONE: (703)836-9300

1 TELEFAX: (703)836-4109  
 2 TELEX: 899149  
 3 INFORMATION FOR SEQ ID NO: 31:  
 4 SEQUENCE CHARACTERISTICS:  
 5 LENGTH: 12 amino acids  
 6 TYPE: amino acid  
 7 TOPOLOGY: linear  
 8 US 09-478-709-41  
 9 Query Match 36.4% Score 4: DB 2: Length 12:  
 10 Best Local Similarity 100.0% Pred. No. 2, 1e+02:  
 11 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 5 KKKP 8

DB 5 KKKP 8

RESULT 48

1 US-08-726-306A 140  
 2 Sequence 140, Application US/08/726,306A  
 3 Patent No. 5958684  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Van Leeuwen, Frederik Willem  
 6 APPLICANT: Burdach, Johannes Peter Henri  
 7 APPLICANT: Graspeld, Franklig G.  
 8 TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
 9 NUMBER OF SEQUENCES: 189  
 10 CORRESPONDENCE ADDRESS:  
 11 ADDRESSEE: Banner & Witcoff, Ltd.  
 12 STREET: 1 Financial Center  
 13 CITY: Boston  
 14 STATE: MA  
 15 COUNTRY: US  
 16 ZIP: 02111

17 COMPUTER READABLE FORM:  
 18 MEDIUM TYPE: Diskette, 4.50 inch, 1.44 Mb storage  
 19 COMPUTER: IBM PC compatible  
 20 OPERATING SYSTEM: PC-DOS/MS-DOS  
 21 SOFTWARE: WordPerfect 6.1  
 22 CURRENT APPLICATION DATA:  
 23 APPLICATION NUMBER: US/08/726,306A  
 24 FILING DATE: 02-OCT-1996  
 25 PRIOR APPLICATION DATA:  
 26 APPLICATION NUMBER: GB 95/26080.4  
 27 FILING DATE: 02-OCT-1995  
 28 PRIOR APPLICATION DATA:  
 29 APPLICATION NUMBER: US 60/009,832  
 30 FILING DATE: 01-Jan-1996  
 31 ATTORNEY/AGENT INFORMATION:  
 32 NAME: Williams, Ph.D., Kathleen M.  
 33 REGISTRATION NUMBER: 34,380  
 34 REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
 35 TELECOMMUNICATION INFORMATION:  
 36 TELEPHONE: (617) 345 9100  
 37 TELEFAX: (617) 345 9111  
 38 INFORMATION FOR SEQ ID NO: 140:  
 39 SEQUENCE CHARACTERISTICS:  
 40 LENGTH: 12 amino acids  
 41 TYPE: amino acid  
 42 STRANDEDNESS: single  
 43 TOPOLOGY: unknown  
 44 MOLECULE TYPE: peptide  
 45 US 08-726-306A-140

Query Match 36.4% Score 4: DB 2: Length 12:  
 Best Local Similarity 100.0% Pred. No. 2, 1e+02:  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 7 KKKP 10

DB 8 KKKP 11

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RESULT 49
US-09-188-529-51
1 Sequence 51: Application US/091495748
2 Patent No. 6,109,410
3 GENERAL INFORMATION:
4 APPLICANT: Shonano, Stewart
5 TITLE OF INVENTION: Pharmacological interaction of RNA cap format
6 FILE REFERENCE: 06185
7 CURRENT APPLICATION NUMBER: US/09/188,529
8 PRIOR FILING DATE: 1998-11-09
9 NUMBER OF SEQ ID NOS: 114
10 SEQ ID NO 51
11 LENGTH: 12
12 TYPE: PRG
13 ORGANISM: Crithidia fasciculata
14 FEATURE:
15 OTHER INFORMATION: Note: Title of RNA query is: 100188529
US-09-188-529-51

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Query Match: 36.4% Score 40.10 C Length 12
Best Local Similarity 100.0% Prior No. 2 (0.02)
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

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US-09-188-529-51
1 Sequence 51: Application US/091495748
2 Patent No. 6,109,410
3 GENERAL INFORMATION:
4 APPLICANT: Shonano, Stewart
5 TITLE OF INVENTION: Pharmacological interaction of RNA cap format
6 FILE REFERENCE: 06185
7 CURRENT APPLICATION NUMBER: US/09/188,529
8 PRIOR FILING DATE: 1998-11-09
9 NUMBER OF SEQ ID NOS: 116
10 SEQ ID NO 51
11 LENGTH: 12
12 TYPE: PRG
13 ORGANISM: Crithidia fasciculata
14 FEATURE:
15 OTHER INFORMATION: Note: Title of RNA query is: 100188529
US-09-188-529-51

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Query Match: 36.4% Score 40.10 C Length 12
Best Local Similarity 100.0% Prior No. 2 (0.02)
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

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Searched: September 30, 2003, 11:06:55  
 Job Time: 14.9187 secs



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91	2	18.2	8	8	Q8Q240	Q8Q240	mesarea tuon	164	2	18.2	9	12	Q67605	O67605	squash leaf
92	2	18.2	8	8	Q79956	Q79956	qossysprum a	165	2	18.2	9	12	Q69349	O69349	herpes simp
93	2	18.2	8	8	Q8Q9K4	Q8Q9K4	bacter topia	166	2	18.2	9	12	Q71069	O71069	canine dist
94	2	18.2	8	8	Q8Q9J9	Q8Q9J9	bacter topia	167	2	18.2	9	12	Q92766	O92766	canine dist
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97	2	18.2	8	8	Q8Q9J4	Q8Q9J4	bacter topia	170	2	18.2	9	13	Q8JAI4	O8JAI4	gallus gall
98	2	18.2	8	8	Q8Q9J3	Q8Q9J3	bacter topia	171	2	18.2	9	13	Q8JFA7	O8JFA7	tiredula al
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101	2	18.2	8	8	Q8Q9J0	Q8Q9J0	bacter topia	174	2	18.2	10	2	Q47651	O47651	eschlerichia
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103	2	18.2	8	8	Q8Q9J3	Q8Q9J3	bacter topia	176	2	18.2	10	2	Q9X534	O9X534	eschlerichia
104	2	18.2	8	8	Q8Q9J2	Q8Q9J2	bacter topia	177	2	18.2	10	2	Q8VN85	O8VN85	helicobacte
105	2	18.2	8	8	Q8Q9J6	Q8Q9J6	bacter topia	178	2	18.2	10	2	Q931X4	O931X4	vibrio chol
106	2	18.2	8	8	Q8Q9J5	Q8Q9J5	bacter topia	179	2	18.2	10	2	Q9X3M2	O9X3M2	prochloroco
107	2	18.2	8	8	Q8Q9J4	Q8Q9J4	bacter topia	180	2	18.2	10	2	Q9X3J6	O9X3J6	eschlerichia
108	2	18.2	8	8	Q42507	Q42507	trichium ac	181	2	18.2	10	2	Q930J2	O930J2	eschlerichia
109	2	18.2	8	8	Q8Q9J5	Q8Q9J5	typhosico	182	2	18.2	10	2	Q9R7J6	O9R7J6	helicobacte
110	2	18.2	8	8	Q9R4D2	Q9R4D2	mus musculi	183	2	18.2	10	2	Q44693	O44693	bacillus am
111	2	18.2	8	8	Q9R4D2	Q9R4D2	mus musculi	184	2	18.2	10	2	Q931J5	O931J5	acinetobact
112	2	18.2	8	8	Q9R4D2	Q9R4D2	mus musculi	185	2	18.2	10	2	Q931J5	O931J5	strepococ
113	2	18.2	8	8	Q62528	Q62528	mus musculi	186	2	18.2	10	2	Q8R1J1	O8R1J1	anaplasma p
114	2	18.2	8	8	Q84271	Q84271	human papil	187	2	18.2	10	2	Q9AE19	O9AE19	strepococ
115	2	18.2	8	8	Q84271	Q84271	human papil	188	2	18.2	10	2	Q9R7J9	O9R7J9	helicobacte
116	2	18.2	8	8	Q84271	Q84271	human papil	189	2	18.2	10	2	Q83066	O83066	bacillus ce
117	2	18.2	8	8	Q84271	Q84271	human papil	190	2	18.2	10	2	Q83160	O83160	anabaena sp
118	2	18.2	8	8	Q84271	Q84271	human papil	191	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
119	2	18.2	8	8	Q84271	Q84271	human papil	192	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
120	2	18.2	8	8	Q84271	Q84271	human papil	193	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
121	2	18.2	8	8	Q84271	Q84271	human papil	194	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
122	2	18.2	8	8	Q84271	Q84271	human papil	195	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
123	2	18.2	8	8	Q84271	Q84271	human papil	196	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
124	2	18.2	8	8	Q84271	Q84271	human papil	197	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
125	2	18.2	8	8	Q84271	Q84271	human papil	198	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
126	2	18.2	8	8	Q84271	Q84271	human papil	199	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
127	2	18.2	8	8	Q84271	Q84271	human papil	200	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
128	2	18.2	8	8	Q84271	Q84271	human papil	201	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
129	2	18.2	8	8	Q84271	Q84271	human papil	202	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
130	2	18.2	8	8	Q84271	Q84271	human papil	203	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
131	2	18.2	8	8	Q84271	Q84271	human papil	204	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
132	2	18.2	8	8	Q84271	Q84271	human papil	205	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
133	2	18.2	8	8	Q84271	Q84271	human papil	206	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
134	2	18.2	8	8	Q84271	Q84271	human papil	207	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
135	2	18.2	8	8	Q84271	Q84271	human papil	208	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
136	2	18.2	8	8	Q84271	Q84271	human papil	209	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
137	2	18.2	8	8	Q84271	Q84271	human papil	210	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
138	2	18.2	8	8	Q84271	Q84271	human papil	211	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
139	2	18.2	8	8	Q84271	Q84271	human papil	212	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
140	2	18.2	8	8	Q84271	Q84271	human papil	213	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
141	2	18.2	8	8	Q84271	Q84271	human papil	214	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
142	2	18.2	8	8	Q84271	Q84271	human papil	215	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
143	2	18.2	8	8	Q84271	Q84271	human papil	216	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
144	2	18.2	8	8	Q84271	Q84271	human papil	217	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
145	2	18.2	8	8	Q84271	Q84271	human papil	218	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
146	2	18.2	8	8	Q84271	Q84271	human papil	219	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
147	2	18.2	8	8	Q84271	Q84271	human papil	220	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
148	2	18.2	8	8	Q84271	Q84271	human papil	221	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
149	2	18.2	8	8	Q84271	Q84271	human papil	222	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
150	2	18.2	8	8	Q84271	Q84271	human papil	223	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
151	2	18.2	8	8	Q84271	Q84271	human papil	224	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
152	2	18.2	8	8	Q84271	Q84271	human papil	225	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
153	2	18.2	8	8	Q84271	Q84271	human papil	226	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
154	2	18.2	8	8	Q84271	Q84271	human papil	227	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
155	2	18.2	8	8	Q84271	Q84271	human papil	228	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
156	2	18.2	8	8	Q84271	Q84271	human papil	229	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
157	2	18.2	8	8	Q84271	Q84271	human papil	230	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
158	2	18.2	8	8	Q84271	Q84271	human papil	231	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
159	2	18.2	8	8	Q84271	Q84271	human papil	232	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
160	2	18.2	8	8	Q84271	Q84271	human papil	233	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
161	2	18.2	8	8	Q84271	Q84271	human papil	234	2	18.2	10	4	Q8NERC	O8NERC	homo sapien
162	2	18.2	8	8	Q84271	Q84271	human papil	235	2	18.2	10	4	Q8NERC	O8NERC	homo sapien



482	2	18.2	12	6	Q8MJ76	Q8MJ76: genome, la py
483	2	18.2	12	6	Q8J1R8	Q8J1R8: los laurus
484	2	18.2	12	6	Q8MJ83	Q8MJ83: salmuni sci
485	2	18.2	12	6	Q8MJ82	Q8MJ82: atelles fuse
486	2	18.2	12	6	Q8MJ82	Q8MJ82: cebus apelli
487	2	18.2	12	6	Q8N270	Q8N270: papio troglody
488	2	18.2	12	6	Q8J589	Q8J589: equus caball
489	2	18.2	12	6	Q8MJ84	Q8MJ84: vitus ovinus
490	2	18.2	12	6	Q8MJ84	Q8MJ84: canis familiar
491	2	18.2	12	6	Q8J1R7	Q8J1R7: bos laurus
492	2	18.2	12	6	Q8J1R7	Q8J1R7: bos indicus
493	2	18.2	12	7	Q8J1R6	Q8J1R6: bos indicus
494	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
495	2	18.2	12	8	Q8MJ86	Q8MJ86: vitus ovinus
496	2	18.2	12	8	Q8MJ86	Q8MJ86: vitus ovinus
497	2	18.2	12	8	Q8J1R5	Q8J1R5: bos laurus
498	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
499	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
500	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
501	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
502	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
503	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
504	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
505	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
506	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
507	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
508	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
509	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
510	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
511	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
512	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
513	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
514	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
515	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
516	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
517	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
518	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
519	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
520	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
521	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
522	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
523	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
524	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
525	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
526	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
527	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
528	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
529	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
530	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
531	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
532	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
533	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
534	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
535	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
536	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
537	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
538	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
539	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
540	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
541	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
542	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
543	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
544	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
545	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
546	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
547	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
548	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
549	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus
550	2	18.2	12	8	Q8MJ84	Q8MJ84: vitus ovinus

## ALIGNMENTS

RES011_1	Q9FXC5	PRELIMINARY:	PIR:	15 AA.
AC	Q9FXC5			
DE	Q1-MAY-2000 (11EMBLrel. 15, Created)			
DE	Q1-MAY-2000 (11EMBLrel. 13, Last sequence update)			
DE	Q1-MAY-2000 (11EMBLrel. 13, Last annotation update)			
DE	Small nuclear inclusion polyprotein cleavage product.			
OS	Tobacco etch virus (TEV)			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;			
OC	Polyvirus			
OX	NTBL:TaxID=12227;			
OX	(1)			
RP	SEQUENCE:			
RX	MEDLINE: Q106428; PubMed:1854555;			
RA	Dougherty W.G., Parks T.D.;			
RT	"Post-translational processing: identification of an internal cleavage			
RT	nuclear inclusion polyprotein; VPg and proteinase domains.";			
RI	site and determination of VPg and proteinase domains.";			
PL	Viridgory 16:4449-4456(1991).			
SQ	SEQUENCE 15 AA: 227-4646100P28C CRC64;			







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RN      SEQUENCE FROM N.A.
RP      SPECIES: Y enterocolitica; STRAIN: Various strains;
RX      MEDLINE: 95274477; PubMed: 7753910;
PA      Osbourne S.E.V., Turner A.K., Grimes J.,
R1      "Nucleotide sequence within Jn926 confirms this as a Y. enterocolitica
R2      transposable element and provides evidence for the origin of the hcr
R3      operon carried by plasmid pK1H20."
RL      Plasmid J3:55-65(1995).
RN      14
RN      SEQUENCE FROM N.A.
RP      SPECIES: mercury resistant bacterium 96 S000;
RA      Bell R.J., Bruce K.D., Strike P.;
R1      "Conservation of transposon structures in S. flexneri."
R2      FEMS Microbiol. Ecol. 0:0-9(1999).
RN      15
RN      SEQUENCE FROM N.A.
RP      SPECIES: A. calcoaceticus; STRAIN: KHM19; PLASMID: pK1H20;
RA      Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
R1      Nikiforov V.G.;
R2      "pK1H2-like aberrant transposons and possible mechanisms of their
R3      dissemination."
R4      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases
RL      EMBL: AF213017; AAA19685.1;
DR      EMBL: Y28992; CAA70180.1;
DR      EMBL: Y28993; CAA70193.1;
DR      EMBL: Y05025; CAA70234.1;
DR      EMBL: Y10102; CAA71186.1;
DR      EMBL: X78959; CAA54979.1;
DR      EMBL: AF134211; AAD34400.1;
DR      EMBL: AJ251597; CAC80877.1;
KW      Plasmid.
R1      NCN_TER 12 12
SQ      SEQUENCE 12 AA: 1219 MW: 04B99D4E821DC776 CRC64;

Query Match 27.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 ASQ 3
DB      11
4 ASQ 5

RESULT 10
QUERY 1
ID  Q8GMV1 PRELIMINARY: PRT; 12 AA.
AC  Q8GMV1
DI  01-MAR-2003 (TrEMBLrel. 23; Created)
DT  01-MAR-2003 (TrEMBLrel. 23; Last sequence update)
DE  01-MAR-2003 (TrEMBLrel. 23; Last annotation update)
GE  01-2X protein.
GN  01P-2X
OS  Acinetobacter sp. H22-05.
OG  Plasmid pK1H20.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OQ  Moraxellaceae; Acinetobacter.
OX  NCBI_TaxID:109250;
RN  11
RP      SEQUENCE FROM N.A.
RA      Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
R1      Nikiforov V.G.;
R2      "pK1H2-like aberrant transposons and possible mechanisms of their
R3      dissemination."
R4      Submitted (NOV 1999) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AJ250245; CAC80792.1;
KW      Plasmid.
SQ      SEQUENCE 12 AA: 1219 MW: 04B99D4E821DC776 CRC64;

Query Match 27.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 ASQ 3
DB      11
4 ASQ 5

RESULT 12
QUERY 2
ID  Q8GMV2 PRELIMINARY: PRT; 12 AA.
AC  Q8GMV2
DI  01-MAR-2003 (TrEMBLrel. 23; Created)
DT  01-MAR-2003 (TrEMBLrel. 23; Last sequence update)
DE  01-MAR-2003 (TrEMBLrel. 23; Last annotation update)
GE  01-2X protein.
GN  01P-2X
OS  Acinetobacter sp. H22-05.
OG  Plasmid pK1H20.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OQ  Moraxellaceae; Acinetobacter.
OX  NCBI_TaxID:109250;
RN  11
RP      SEQUENCE FROM N.A.
RA      Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
R1      Nikiforov V.G.;
R2      "pK1H2-like aberrant transposons and possible mechanisms of their
R3      dissemination."
R4      Submitted (NOV 1999) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AJ251274; CAC80895.1;
KW      Plasmid.
SQ      SEQUENCE 12 AA: 1219 MW: 04B99D3E821DC776 CRC64;

Query Match 27.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 ASQ 3
DB      11
4 ASQ 5

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20          1 ASQ 5
RESULT 13
Q8J1G2          PRELIMINARY:      PRT:      13 AA
ID Q8J1G2
AC Q8J1G2
DT 01-MAR-2003 (TRENBERG: 23, Created)
DI 01-MAR-2003 (TRENBERG: 23, Last sequence update)
DE 12 kDa cell wall protein (Fragment).
OS Nicotiana glauca (Solanaceae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteroideae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID:45977
RN 1
RP SEQUENCE
RC STRAIN: CV, PEFF HAVANA.
RA Blec K.A., Bohner V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Woloszewicz P., Bo. wall 3.P.
RI "Proteomic study of secondary cell wall proteins from transgenic
RI tobacco culture."
PL Planta 010 6(2003).
OC 1- SUBCELLULAR LOCATION: CELL WALL.
CC 1- TISSUE SPECIFICITY: XYLEM
KW Cell wall.
FT NON-TER
SQ SEQUENCE 13 AA: 150 MW: D5022297D8697DC6 CRC64:
Query Match 27.48; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pctid. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AKR 6
DB 5 AKR 7
RESULT 14
Q8J1G2          PRELIMINARY:      PRT:      14 AA
ID Q8J1G2
AC Q8J1G2
DT 01-MAR-2003 (TRENBERG: 23, Created)
DI 01-MAR-2003 (TRENBERG: 23, Last sequence update)
DE YPL156 (Fragment).
OS Ashbya gossypii (Deinotectum gossypii).
OC Eukaryota; Fungi; Ascomycota; Sacccharomycotina; Sacccharomycetes;
OC Sacccharomycetales; Sacccharomycetaceae; Ashbya.
OX NCBI_TaxID:341692
RN 1
RP SEQUENCE FROM K.A.
RA Alberti-Seefeld C., Dupertuis F., Philippson P.
RI "Identification of kinases related proteins in the filamentous fungus
RI Ashbya gossypii."
RC Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL AF478570; AAN4739.1;
FT NON-TER
SQ SEQUENCE 14 AA: 1646 MW: BC3A12E8808H1D15 CRC64:
Query Match 27.48; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pctid. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PKG 9
DB 8 AKG 10
RESULT 17
G15998          PRELIMINARY:      PRT:      14 AA
ID G15998
AC G15998
DT 01-NOV-1996 (TRENBERG: 01, Created)
DI 01-NOV-1996 (TRENBERG: 01, Last sequence update)
DE 01-DEC-2001 (TRENBERG: 19, Last annotation update)
DE Neurothrombolysis type 1 gene protein (Fragment).

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20          1 ASQ 5
RESULT 13
Q8J1G2          PRELIMINARY:      PRT:      13 AA
ID Q8J1G2
AC Q8J1G2
DT 01-MAR-2003 (TRENBERG: 23, Created)
DI 01-MAR-2003 (TRENBERG: 23, Last sequence update)
DE 12 kDa cell wall protein (Fragment).
OS Nicotiana glauca (Solanaceae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteroideae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID:45977
RN 1
RP SEQUENCE
RC STRAIN: CV, PEFF HAVANA.
RA Blec K.A., Bohner V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Woloszewicz P., Bo. wall 3.P.
RI "Proteomic study of secondary cell wall proteins from transgenic
RI tobacco culture."
PL Planta 010 6(2003).
OC 1- SUBCELLULAR LOCATION: CELL WALL.
CC 1- TISSUE SPECIFICITY: XYLEM
KW Cell wall.
FT NON-TER
SQ SEQUENCE 13 AA: 150 MW: D5022297D8697DC6 CRC64:
Query Match 27.48; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pctid. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AKR 6
DB 5 AKR 7
RESULT 14
Q8J1G2          PRELIMINARY:      PRT:      14 AA
ID Q8J1G2
AC Q8J1G2
DT 01-MAR-2003 (TRENBERG: 23, Created)
DI 01-MAR-2003 (TRENBERG: 23, Last sequence update)
DE YPL156 (Fragment).
OS Ashbya gossypii (Deinotectum gossypii).
OC Eukaryota; Fungi; Ascomycota; Sacccharomycotina; Sacccharomycetes;
OC Sacccharomycetales; Sacccharomycetaceae; Ashbya.
OX NCBI_TaxID:341692
RN 1
RP SEQUENCE FROM K.A.
RA Alberti-Seefeld C., Dupertuis F., Philippson P.
RI "Identification of kinases related proteins in the filamentous fungus
RI Ashbya gossypii."
RC Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL AF478570; AAN4739.1;
FT NON-TER
SQ SEQUENCE 14 AA: 1646 MW: BC3A12E8808H1D15 CRC64:
Query Match 27.48; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pctid. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PKG 9
DB 8 AKG 10
RESULT 17
G15998          PRELIMINARY:      PRT:      14 AA
ID G15998
AC G15998
DT 01-NOV-1996 (TRENBERG: 01, Created)
DI 01-NOV-1996 (TRENBERG: 01, Last sequence update)
DE 01-DEC-2001 (TRENBERG: 19, Last annotation update)
DE Neurothrombolysis type 1 gene protein (Fragment).

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OS Brca sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A
RX MEDLINE 93216281; PubMed 8465367;
SA Answorth P.J., Rodenhiser D.L., Gusto R.L.;
R "Identification and characterization of sporadic and inherited
R1 mutations in exon 31 of the breast tumour suppressor gene (BRCA1);
R2 Hum. Genet. 91:151-156(1993);
DR EMBL: S07966; A01389(1);
FT NON-TER 1
SQ SEQUENCE 14 AA; 1660 MW; 667B9EBA7675276527
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKK 5
DB 1
PB 2 AKK 4

RESULT 19
PB2452
ID PB2452 PRELIMINARY; PRI; 14 AA.
DT 01-MAR-2002 (TRENBLREL, 14, Last sequence update)
DT 01-MAR-2002 (TRENBLREL, 14, Last sequence update)
DE Unknown protein from 2D page of: thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fatales; Fabaceae; Papilionoideae; Viciaeae; Pisum;
OX NCBI_TaxID=3838;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE 20181728; PubMed-10715320;
RA Peltier J.-H., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON-TER 14
SQ SEQUENCE 14 AA; 1505 MW; 2EAEAF980F3D7D7 CRC64;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QAK 5
DB 1
PB 2 QAK 4

RESULT 19
PB2452
ID PB2452 PRELIMINARY; PRI; 14 AA.
DT 01-JUN-2000 (TRENBLREL, 14, Created)
DT 01-JUN-2000 (TRENBLREL, 14, Last sequence update)
DE 60S ribosomal protein L26 (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Gamopetalaceae; Spinacia;
OX NCBI_TaxID=3562;

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RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALWARD; TISSUE=LEAF;
SA Yamauchi K., Subramanian A.R.;
R "N-terminal sequence of spinach cytosolic 60S ribosomal protein L26.";
R1 Submitted (APR 2000) to the SWISS-PROT data bank.
CC -|- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
DR INTERPRO: IPR005825; RIBOSOMA_L24_26.
DR PROSITE: PS01187; RIBOSOMA_L24; PARTIAL.
KW Ribosomal protein.
FT NON-TER 14
SQ SEQUENCE 14 AA; 1723 MW; 187C68AC21AD9CA2 CRC64;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RAK 6
DB 1
PB 11 RAK 14

RESULT 20
PB2340
ID PB2340 PRELIMINARY; PRI; 14 AA.
DT 01-JUN-2000 (TRENBLREL, 14, Created)
DT 01-JUN-2000 (TRENBLREL, 14, Last sequence update)
DT 01-OCT-2000 (TRENBLREL, 15, Last annotation update)
DE Unknown protein from 2D page of: thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fatales; Fabaceae; Papilionoideae; Viciaeae; Pisum;
OX NCBI_TaxID=3838;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE 20181728; PubMed-10715320;
RA Peltier J.-H., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON-TER 14
SQ SEQUENCE 14 AA; 1505 MW; 2EAEAF980F3D7D7 CRC64;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKG 5
DB 1
PB 11 RKG 14

RESULT 21
Q9EPX6
ID Q9EPX6 PRELIMINARY; PRI; 14 AA.
DT 01-MAR-2001 (TRENBLREL, 16, Created)
DT 01-MAR-2001 (TRENBLREL, 16, Last sequence update)
DT 01-MAR-2001 (TRENBLREL, 16, Last annotation update)
DE ITSN (Fragment).
GN ITSN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN [1]

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IN ARCT.
AC Physarum polycephalum (Slime mold)
AC E. Karyotax: Mycetozoa: Myxogastria: Myxosporidia: Physaridae
AC Physarum.
CX NCBI_TaxID:5741;
RN (1);
RP SEQUENCE FROM N.A.
RX MEDLINE:9618211; PubMed:862276;
SA Record M.A. Campbell, C. Poirier to be published;
RT *Mutated and replicated within the presence of two
RT polyphosphate;
RI Nature 4:9433-38(2003)
RL Mol. Cell. Biol. 23:968-70(2003)
RE EMBL: M7459; AAC03766.1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 878 MW: 14622.600kDa: 100.0%
Query Match: 16.2% Score 21.0 DB 6; Length 8;
Best Local Similarity: 100.0%; Pred. No. B.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GA 4
LE 1 1
2 GA 5

RESULT 4:
ID P22686 PRELIMINARY: PRI: 8 AA.
AC Q939H4;
DI 01-MAR-2001 (TrEMBLrel. 16, created)
DI 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE K12n 2 (PDB K 2);
US Escherichia americana (American e. coli);
AC Eukaryota: Metazoa: Artthropoda: hexapoda: Insecta: coleoptera:
AC Mephila: Mephilidae: Mephilinae: Mephilini: Mephilini:
AC Mephilini: Mephilini:
CX NCBI_TaxID:5778;
RN (1);
RP SEQUENCE FROM N.A.
RX MEDLINE:9618211; PubMed:862276;
SA Record M.A. Campbell, C. Poirier to be published;
RT *Mutated and replicated within the presence of two
RT polyphosphate;
RI Nature 4:9433-38(2003)
RL Mol. Cell. Biol. 23:968-70(2003)
RE EMBL: M7459; AAC03766.1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 878 MW: 14622.600kDa: 100.0%
Query Match: 16.2% Score 21.0 DB 6; Length 8;
Best Local Similarity: 100.0%; Pred. No. B.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
LE 1 1
2 AS 3

RESULT 4:
ID Q939H4 PRELIMINARY: PRI: 8 AA.
AC Q939H4;
DI 01-JUN-2001 (TrEMBLrel. 17, created)
DI 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE CAMP responsive element mediated (fragment)
UN CRR9

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US Metapleura gonodactylae (Humpback whale);
AC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
AC Mammalia: Cetartiodactyla: Cetacea: Mysticeti:
AC Balenopteridae: Megaptera
CX NCBI_TaxID:9774;
RN (1);
RP SEQUENCE FROM N.A.
RX MEDLINE:2108202; PubMed:1121419;
SA Murphy W.D., Estroff B., Johnson W.E., Zhang Y.P., Wyder O.A.,
SA Chertov, S.;
RI *Molecular phylogenetics and the origins of placental mammals.
RI Nature 4:9433-38(2003)
RL EMBL: AY01167; AAC12800.1;
FI N-N TER 1
SQ SEQUENCE 8 AA: 125 MW: 16245.240kDa: 100.0%
Query Match: 16.2% Score 21.0 DB 6; Length 8;
Best Local Similarity: 100.0%; Pred. No. B.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KK 8
LE 1 1
5 KK 5

RESULT 5:
ID Q939H4 PRELIMINARY: PRI: 8 AA.
AC Q939H4;
DI 01-MAR-2001 (TrEMBLrel. 16, created)
DI 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE Art 15 (fragment);
US Lagenorhynchus obscurus (bushy dolphin);
AC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
AC Mammalia: Cetartiodactyla: Cetacea: Odontoceti: Delphinidae;
AC Lagenorhynchus
CX NCBI_TaxID:27611;
RN (1);
RP SEQUENCE FROM N.A.
RX MEDLINE:9618211; PubMed:862276;
SA Record M.A. Campbell, C. Poirier to be published;
RT *Slow Evolution of Genetic Morphology in Dolphins: Implications for
RT Speciation, Systematics and Conservation.
RX Submitted (Apr 1999) to the EMBL/GenBank/DBS databases
DE EMBL: AF140943; AAC9866.1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 962 MW: 58018.177kDa: 100.0%
Query Match: 16.2% Score 21.0 DB 6; Length 8;
Best Local Similarity: 100.0%; Pred. No. B.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PR 11
LE 1 1
5 PR 6

Search completed: September 01, 2003, 10:17:31
Core time: 35.6697 secs

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Genome version 5.1.6  
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of protein - protein search, using sw model

Run date: September 30, 2003, 11:06:56, 24 seconds  
(without databases)  
52,967 Multiple COIL files/ses

File: us-09-787-443-15

Percent score: 13

Sequence: 1 ASQAKKKCPK 11

Search: 127864 seqs, 4702765 residues

Word size: 6

Total number of hits satisfying chosen parameters: 707

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: Listing first 50 summaries

Database: SwissProt\_41\*

Prod. No. is the number of results predicted by above to have a

score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

Summary

Score Match Length DB ID Description

1 4 46.4 8 1 RS7\_MCT1 14444 cytochrome c

2 4 27.3 9 1 PAS2\_ASNS1 14471 aspartate aminotransferase

3 4 27.3 9 1 PAS2\_ASNS1 14472 aspartate aminotransferase

4 4 27.3 9 1 PAS2\_ASNS1 14473 aspartate aminotransferase

5 4 27.3 14 1 PAS2\_ASNS1 14474 aspartate aminotransferase

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40 4 27.3 15 1 PAS2\_ASNS1 14509 aspartate aminotransferase

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46	2	18.2	9	1	HCTU_KLEAB
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51	2	18.2	9	1	PRK1_PERAM
52	2	18.2	9	1	RT33_PCVIN
53	2	18.2	9	1	TKL1_LOCM1
54	2	18.2	9	1	ULAK_MGUSE
55	2	18.2	9	1	YMER_AZONI
56	2	18.2	9	1	ABC_PROSE
57	2	18.2	9	1	BPZ2_PCTJA
58	2	18.2	9	1	BRV_VIPAS
59	2	18.2	9	1	BRK2_ONCMY
60	2	18.2	9	1	COXA_ONCMY
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62	2	18.2	9	1	COX2_THUGB
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76	2	18.2	9	1	URC5_RAT
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80	2	18.2	9	1	XYNB_DICB4
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83	2	18.2	9	1	YHPS_POTIN
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P41861	calliphora
P83350	sarcophaga
P12381	klebsiella
P41489	locusta mig
P34966	cavia porce
P04277	homo sapien
P23879	cyprinus ca
P82641	periplaneta
P82926	bos taurus
P16223	locusta mig
P49031	mus muscula
P25825	azotobacter
P29261	pronus sero
P01022	bothrops ja
P31351	vipeira aspi
P9przi	oncothynchu
P80328	oncothynchu
P80432	rattus norv
P80982	thomomys obe
P80337	ovis aries
P41488	locusta mig
P81135	mycobacteri
P83382	locusta mig
P80466	comamonas t
P81084	pinus pinas
P29221	acholeptasm
P30249	locusta mig
P80608	scyllorhinu
P22690	rana catesb
P40751	urechis uni
P81739	leucophaea
P81740	leucophaea
P56573	rattus norv
P32080	homo sapien
P38003	chlamydia t
P99012	saccharomyc
P80717	dictyodromo
P30423	bothrops in
P30424	bothrops in
P01021	adkistodon
P04562	adkistodon
P12797	megascollia
P59072	pseudonaja
P82684	carausius m
P41837	periplaneta
P80464	comamonas t
P42341	cnepholis
P82651	hoplobatrach
P82026	uperoleia i
P86616	uperoleia r
P19850	gallus gall
P28498	gallus morhu
P28499	oncothynchu
P41333	scyllorhinu
P08615	physalaemus
P99013	saccharomyc
P50983	conus impe
P83322	penaeus mon
P40754	rana rugosa
P83176	carcinus ma
Q10584	megathura c
P22395	locusta mig
P47733	locusta mig
P54713	canis fami
P82619	periplaneta
P82690	periplaneta
P81555	periplaneta
P58805	conus spuri
P36207	ginkgo bilo
Q46490	clover yell
Q47881	elm yellows
P82006	white spot
P17776	escherichia

127	13	2	18.2	13	1	AP4_PULSE	P24262 prunus serot	180	2	18.2	15	1	POKH_PHYPA	P80659 physcomitre
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129	13	2	18.2	13	1	BP17_LEUMA	P81754 leucophaea	182	2	18.2	15	1	PSAO_CUCSA	P42052 cumis sat
130	13	2	18.2	13	1	BRK_PARIJA	P21020 bothriops ja	183	2	18.2	15	1	RKGG_CACR	P21568 bacillus car
131	13	2	18.2	13	1	BRK_PARIJA	P42717 parapiolybia	184	2	18.2	15	1	RS10_BACST	P59683 bacillus st
132	13	2	18.2	13	1	CERG_CANEA	P42618 canis latit	185	2	18.2	15	1	RS20_BACST	P59682 bacillus st
133	13	2	18.2	13	1	CERG_PARIO	P42718 parapiolybia	186	2	18.2	15	1	RS5_BACST	P59681 bacillus st
134	13	2	18.2	13	1	CRBL_CANSI	P12247 canis sp	187	2	18.2	15	1	RT32_BOVIN	P82927 bos taurus
135	13	2	18.2	13	1	CRBL_VESAN	P12248 vespa crabi	188	2	18.2	15	1	TAL_TREBR	P34070 tremella br
136	13	2	18.2	13	1	CRBL_VESER	P12249 vespa crabi	189	2	18.2	15	1	TERM_BPM2	P19897 bacterioph
137	13	2	18.2	13	1	CRBL_VESER	P12250 vespa crabi	190	2	18.2	15	1	THL_CLOPA	P81347 clostridium
138	13	2	18.2	13	1	CRBL_VESNA	P12251 vespa crabi	191	2	18.2	15	1	UCUG_MAIZE	P80612 zea mays (m
139	13	2	18.2	13	1	EL65_HUMAN	P42761 el65 sapien	192	2	18.2	15	1	UC19_MAIZE	P80625 zea mays (m
140	13	2	18.2	13	1	EL65_HUMAN	P42762 el65 sapien	193	2	18.2	15	1	UC28_MAIZE	P80634 zea mays (m
141	13	2	18.2	13	1	EL65_HUMAN	P42763 el65 sapien	194	2	18.2	15	1	UP02_METAN	P83439 metathizium
142	13	2	18.2	13	1	EL65_HUMAN	P42764 el65 sapien	195	2	18.2	15	1	URE1_MORMO	P71337 morganella
143	13	2	18.2	13	1	EL65_HUMAN	P42765 el65 sapien	196	2	18.2	15	1	VORA_METIM	P80907 methanobact
144	13	2	18.2	13	1	EL65_HUMAN	P42766 el65 sapien	197	2	18.2	15	1	ACT_THUAL	P18691 thunnus alb
145	13	2	18.2	13	1	EL65_HUMAN	P42767 el65 sapien	198	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
146	13	2	18.2	13	1	EL65_HUMAN	P42768 el65 sapien	199	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
147	13	2	18.2	13	1	EL65_HUMAN	P42769 el65 sapien	200	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
148	13	2	18.2	13	1	EL65_HUMAN	P42770 el65 sapien	201	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
149	13	2	18.2	13	1	EL65_HUMAN	P42771 el65 sapien	202	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
150	13	2	18.2	13	1	EL65_HUMAN	P42772 el65 sapien	203	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
151	13	2	18.2	13	1	EL65_HUMAN	P42773 el65 sapien	204	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
152	13	2	18.2	13	1	EL65_HUMAN	P42774 el65 sapien	205	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
153	13	2	18.2	13	1	EL65_HUMAN	P42775 el65 sapien	206	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
154	13	2	18.2	13	1	EL65_HUMAN	P42776 el65 sapien	207	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
155	13	2	18.2	13	1	EL65_HUMAN	P42777 el65 sapien	208	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
156	13	2	18.2	13	1	EL65_HUMAN	P42778 el65 sapien	209	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
157	13	2	18.2	13	1	EL65_HUMAN	P42779 el65 sapien	210	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
158	13	2	18.2	13	1	EL65_HUMAN	P42780 el65 sapien	211	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
159	13	2	18.2	13	1	EL65_HUMAN	P42781 el65 sapien	212	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
160	13	2	18.2	13	1	EL65_HUMAN	P42782 el65 sapien	213	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
161	13	2	18.2	13	1	EL65_HUMAN	P42783 el65 sapien	214	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
162	13	2	18.2	13	1	EL65_HUMAN	P42784 el65 sapien	215	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
163	13	2	18.2	13	1	EL65_HUMAN	P42785 el65 sapien	216	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
164	13	2	18.2	13	1	EL65_HUMAN	P42786 el65 sapien	217	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
165	13	2	18.2	13	1	EL65_HUMAN	P42787 el65 sapien	218	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
166	13	2	18.2	13	1	EL65_HUMAN	P42788 el65 sapien	219	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
167	13	2	18.2	13	1	EL65_HUMAN	P42789 el65 sapien	220	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
168	13	2	18.2	13	1	EL65_HUMAN	P42790 el65 sapien	221	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
169	13	2	18.2	13	1	EL65_HUMAN	P42791 el65 sapien	222	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
170	13	2	18.2	13	1	EL65_HUMAN	P42792 el65 sapien	223	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
171	13	2	18.2	13	1	EL65_HUMAN	P42793 el65 sapien	224	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
172	13	2	18.2	13	1	EL65_HUMAN	P42794 el65 sapien	225	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
173	13	2	18.2	13	1	EL65_HUMAN	P42795 el65 sapien	226	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
174	13	2	18.2	13	1	EL65_HUMAN	P42796 el65 sapien	227	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
175	13	2	18.2	13	1	EL65_HUMAN	P42797 el65 sapien	228	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
176	13	2	18.2	13	1	EL65_HUMAN	P42798 el65 sapien	229	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
177	13	2	18.2	13	1	EL65_HUMAN	P42799 el65 sapien	230	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
178	13	2	18.2	13	1	EL65_HUMAN	P42800 el65 sapien	231	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
179	13	2	18.2	13	1	EL65_HUMAN	P42801 el65 sapien	232	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
180	13	2	18.2	13	1	EL65_HUMAN	P42802 el65 sapien	233	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
181	13	2	18.2	13	1	EL65_HUMAN	P42803 el65 sapien	234	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
182	13	2	18.2	13	1	EL65_HUMAN	P42804 el65 sapien	235	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
183	13	2	18.2	13	1	EL65_HUMAN	P42805 el65 sapien	236	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
184	13	2	18.2	13	1	EL65_HUMAN	P42806 el65 sapien	237	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
185	13	2	18.2	13	1	EL65_HUMAN	P42807 el65 sapien	238	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
186	13	2	18.2	13	1	EL65_HUMAN	P42808 el65 sapien	239	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
187	13	2	18.2	13	1	EL65_HUMAN	P42809 el65 sapien	240	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
188	13	2	18.2	13	1	EL65_HUMAN	P42810 el65 sapien	241	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
189	13	2	18.2	13	1	EL65_HUMAN	P42811 el65 sapien	242	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
190	13	2	18.2	13	1	EL65_HUMAN	P42812 el65 sapien	243	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
191	13	2	18.2	13	1	EL65_HUMAN	P42813 el65 sapien	244	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
192	13	2	18.2	13	1	EL65_HUMAN	P42814 el65 sapien	245	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
193	13	2	18.2	13	1	EL65_HUMAN	P42815 el65 sapien	246	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
194	13	2	18.2	13	1	EL65_HUMAN	P42816 el65 sapien	247	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
195	13	2	18.2	13	1	EL65_HUMAN	P42817 el65 sapien	248	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
196	13	2	18.2	13	1	EL65_HUMAN	P42818 el65 sapien	249	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
197	13	2	18.2	13	1	EL65_HUMAN	P42819 el65 sapien	250	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
198	13	2	18.2	13	1	EL65_HUMAN	P42820 el65 sapien	251	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
199	13	2	18.2	13	1	EL65_HUMAN	P42821 el65 sapien	252	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
200	13	2	18.2	13	1	EL65_HUMAN	P42822 el65 sapien	253	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
201	13	2	18.2	13	1	EL65_HUMAN	P42823 el65 sapien	254	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
202	13	2	18.2	13	1	EL65_HUMAN	P42824 el65 sapien	255	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
203	13	2	18.2	13	1	EL65_HUMAN	P42825 el65 sapien	256	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
204	13	2	18.2	13	1	EL65_HUMAN	P42826 el65 sapien	257	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
205	13	2	18.2	13	1	EL65_HUMAN	P42827 el65 sapien	258	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
206	13	2	18.2	13	1	EL65_HUMAN	P42828 el65 sapien	259	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
207	13	2	18.2	13	1	EL65_HUMAN	P42829 el65 sapien	260	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
208	13	2	18.2	13	1	EL65_HUMAN	P42830 el65 sapien	261	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
209	13	2	18.2	13	1	EL65_HUMAN	P42831 el65 sapien	262	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
210	13	2	18.2	13	1	EL65_HUMAN	P42832 el65 sapien	263	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
211	13	2	18.2	13	1	EL65_HUMAN	P42833 el65 sapien	264	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
212	13	2	18.2	13	1	EL65_HUMAN	P42834 el65 sapien	265	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
213	13	2	18.2	13	1	EL65_HUMAN	P42835 el65 sapien	266	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
214	13	2	18.2	13	1	EL65_HUMAN	P42836 el65 sapien	267	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
215	13	2	18.2	13	1	EL65_HUMAN	P42837 el65 sapien	268	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
216	13	2	18.2	13	1	EL65_HUMAN	P42838 el65 sapien	269	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
217	13	2	18.2	13	1	EL65_HUMAN	P42839 el65 sapien	270	2	18.2	15	1	AKHG_GRYBI	P14086 gryllus blm
218	13	2	18.2	13	1	EL65_HUMAN	P42840 el65 sapien	271						

254	1	9.1	9	1	FAR1_CALVO	P41876 caliphora	326	1	9.1	10	1	CAER_LITXA	P56264 litoria xan
255	1	9.1	9	1	FAR2_PANRE	P41875 pandrellus	327	1	9.1	10	1	CATR_SHEEP	P83205 ovitis aries
256	1	9.1	9	1	FAR3_MACRS	P42766 macrobrachi	328	1	9.1	10	1	COXH_ONCMY	P80331 oncorhynchu
257	1	9.1	9	1	FAR4_PENMG	P4338 penaeus mon	329	1	9.1	10	1	COXK_ONCMY	P80332 oncorhynchu
258	1	9.1	9	1	FAR5_CALVO	P41859 caliphora	330	1	9.1	10	1	COXK_RAT	P80431 rattus norv
259	1	9.1	9	1	FAR6_ASTRG	P43170 ascaris suu	331	1	9.1	10	1	COXO_RABIT	P80336 onycholaquus
260	1	9.1	9	1	FAR7_CALVO	P41600 caliphora	332	1	9.1	10	1	CU10_LOCM1	P11745 locusta miq
261	1	9.1	9	1	FAR8_PANRE	P42601 pandrellus	333	1	9.1	10	1	EST_LACCA	P81758 lactobacilli
262	1	9.1	9	1	FAR9_PENMG	P43420 penaeus mon	334	1	9.1	10	1	ESTA_SCHGA	P81012 schizaphis
263	1	9.1	9	1	FAR10_PANRE	P42767 macrobrachi	335	1	9.1	10	1	FAR2_PENMG	P83377 penaeus mon
264	1	9.1	9	1	FAR11_CALVO	P41662 caliphora	336	1	9.1	10	1	FAR5_MACRS	P83278 macrobrachi
265	1	9.1	9	1	FAR12_PANRE	P42481 macrobrachi	337	1	9.1	10	1	FAR6_PANRE	P82660 pandrellus
266	1	9.1	9	1	FAR13_CALVO	P41365 caliphora	338	1	9.1	10	1	FAR7_MACRS	P83260 macrobrachi
267	1	9.1	9	1	FAR14_PANRE	P42482 caliphora	339	1	9.1	10	1	FAR8_CALVO	P41867 caliphora
268	1	9.1	9	1	FAR15_CALVO	P42475 caliphora	340	1	9.1	10	1	FAR9_LOCM1	P38553 locusta miq
269	1	9.1	9	1	FAR16_CALVO	P42446 caliphora	341	1	9.1	10	1	FAR10_LOCM1	P41852 locusta miq
270	1	9.1	9	1	FAR17_CALVO	P42445 caliphora	342	1	9.1	10	1	FAR11_MANSE	P42563 manduca sex
271	1	9.1	9	1	FAR18_PANRE	P42444 caliphora	343	1	9.1	10	1	FAR12_MANSE	P42560 mytilus edu
272	1	9.1	9	1	FAR19_PANRE	P42443 caliphora	344	1	9.1	10	1	FAR13_CERS1	P41537 ceratotheri
273	1	9.1	9	1	FAR20_PANRE	P42442 caliphora	345	1	9.1	10	1	FAR14_HUMAN	P01358 homo sapien
274	1	9.1	9	1	FAR21_PANRE	P42441 caliphora	346	1	9.1	10	1	FAR15_HUMAN	P02128 homo sapien
275	1	9.1	9	1	FAR22_PANRE	P42440 caliphora	347	1	9.1	10	1	FAR16_HUMAN	P37041 alligator m
276	1	9.1	9	1	FAR23_PANRE	P42439 caliphora	348	1	9.1	10	1	GONI_ALGMI	P80677 chelyosoma
277	1	9.1	9	1	FAR24_PANRE	P42438 caliphora	349	1	9.1	10	1	GONI_CHEPR	P81749 clupea pall
278	1	9.1	9	1	FAR25_PANRE	P42437 caliphora	350	1	9.1	10	1	GONI_CLOPA	P81749 clupea pall
279	1	9.1	9	1	FAR26_PANRE	P42436 caliphora	351	1	9.1	10	1	GONI_PETMA	P04378 petromyzon
280	1	9.1	9	1	FAR27_PANRE	P42435 caliphora	352	1	9.1	10	1	GONI_CHEPR	P80678 chelyosoma
281	1	9.1	9	1	FAR28_PANRE	P42434 caliphora	353	1	9.1	10	1	GONI_CHEPR	P37043 gallus gall
282	1	9.1	9	1	FAR29_PANRE	P42433 caliphora	354	1	9.1	10	1	GONI_CHEPR	P20367 oncorhynchu
283	1	9.1	9	1	FAR30_PANRE	P42432 caliphora	355	1	9.1	10	1	GONI_PETMA	P30948 petromyzon
284	1	9.1	9	1	FAR31_PANRE	P42431 caliphora	356	1	9.1	10	1	GONI_PETMA	P27429 squalus aca
285	1	9.1	9	1	FAR32_PANRE	P42430 caliphora	357	1	9.1	10	1	GRP_RANRI	P23260 rana ridibu
286	1	9.1	9	1	FAR33_PANRE	P42429 caliphora	358	1	9.1	10	1	GRP_RANRI	P80343 bacillus su
287	1	9.1	9	1	FAR34_PANRE	P42428 caliphora	359	1	9.1	10	1	GRP_RANRI	P18110 romalea mic
288	1	9.1	9	1	FAR35_PANRE	P42427 caliphora	360	1	9.1	10	1	GRP_RANRI	P11385 carausius m
289	1	9.1	9	1	FAR36_PANRE	P42426 caliphora	361	1	9.1	10	1	GRP_RANRI	P16353 heliothis z
290	1	9.1	9	1	FAR37_PANRE	P42425 caliphora	362	1	9.1	10	1	GRP_RANRI	P10939 nauphocta c
291	1	9.1	9	1	FAR38_PANRE	P42424 caliphora	363	1	9.1	10	1	GRP_RANRI	P14596 tabanus atr
292	1	9.1	9	1	FAR39_PANRE	P42423 caliphora	364	1	9.1	10	1	GRP_RANRI	P13370 jatropha mu
293	1	9.1	9	1	FAR40_PANRE	P42422 caliphora	365	1	9.1	10	1	GRP_RANRI	P21144 leucophaea
294	1	9.1	9	1	FAR41_PANRE	P42421 caliphora	366	1	9.1	10	1	GRP_RANRI	P09039 leucophaea
295	1	9.1	9	1	FAR42_PANRE	P42420 caliphora	367	1	9.1	10	1	GRP_RANRI	Q05564 klebsiella
296	1	9.1	9	1	FAR43_PANRE	P42419 caliphora	368	1	9.1	10	1	GRP_RANRI	P19662 clypeaster
297	1	9.1	9	1	FAR44_PANRE	P42418 caliphora	369	1	9.1	10	1	GRP_RANRI	P81533 microplitis
298	1	9.1	9	1	FAR45_PANRE	P42417 caliphora	370	1	9.1	10	1	GRP_RANRI	P55962 nicotiana t
299	1	9.1	9	1	FAR46_PANRE	P42416 caliphora	371	1	9.1	10	1	GRP_RANRI	P11180 bos taurus
300	1	9.1	9	1	FAR47_PANRE	P42415 caliphora	372	1	9.1	10	1	GRP_RANRI	P81863 pardachirus
301	1	9.1	9	1	FAR48_PANRE	P42414 caliphora	373	1	9.1	10	1	GRP_RANRI	P22103 homo sapien
302	1	9.1	9	1	FAR49_PANRE	P42413 caliphora	374	1	9.1	10	1	GRP_RANRI	P22196 rattus norv
303	1	9.1	9	1	FAR50_PANRE	P42412 caliphora	375	1	9.1	10	1	GRP_RANRI	P80901 methanobact
304	1	9.1	9	1	FAR51_PANRE	P42411 caliphora	376	1	9.1	10	1	GRP_RANRI	P80525 fasciola he
305	1	9.1	9	1	FAR52_PANRE	P42410 caliphora	377	1	9.1	10	1	GRP_RANRI	Q03367 capsicum an
306	1	9.1	9	1	FAR53_PANRE	P42409 caliphora	378	1	9.1	10	1	GRP_RANRI	P80465 comamonas t
307	1	9.1	9	1	FAR54_PANRE	P42408 caliphora	379	1	9.1	10	1	GRP_RANRI	P35946 phocine dis
308	1	9.1	9	1	FAR55_PANRE	P42407 caliphora	380	1	9.1	10	1	GRP_RANRI	P82923 bos taurus
309	1	9.1	9	1	FAR56_PANRE	P42406 caliphora	381	1	9.1	10	1	GRP_RANRI	P49325 bacillus th
310	1	9.1	9	1	FAR57_PANRE	P42405 caliphora	382	1	9.1	10	1	GRP_RANRI	P81545 dictyosteli
311	1	9.1	9	1	FAR58_PANRE	P42404 caliphora	383	1	9.1	10	1	GRP_RANRI	Q10997 halocynthia
312	1	9.1	9	1	FAR59_PANRE	P42403 caliphora	384	1	9.1	10	1	GRP_RANRI	Q46464 campylobact
313	1	9.1	9	1	FAR60_PANRE	P42402 caliphora	385	1	9.1	10	1	GRP_RANRI	P56923 rana tempor
314	1	9.1	9	1	FAR61_PANRE	P42401 caliphora	386	1	9.1	10	1	GRP_RANRI	P16224 locusta miq
315	1	9.1	9	1	FAR62_PANRE	P42400 caliphora	387	1	9.1	10	1	GRP_RANRI	P30250 locusta miq
316	1	9.1	9	1	FAR63_PANRE	P42399 caliphora	388	1	9.1	10	1	GRP_RANRI	P19851 gallus gall
317	1	9.1	9	1	FAR64_PANRE	P42398 caliphora	389	1	9.1	10	1	GRP_RANRI	P28500 oncorhynchu
318	1	9.1	9	1	FAR65_PANRE	P42397 caliphora	390	1	9.1	10	1	GRP_RANRI	P22689 rana catesb
319	1	9.1	9	1	FAR66_PANRE	P42396 caliphora	391	1	9.1	10	1	GRP_RANRI	P22935 rana ridibu
320	1	9.1	9	1	FAR67_PANRE	P42395 caliphora	392	1	9.1	10	1	GRP_RANRI	P01292 sus scrofa
321	1	9.1	9	1	FAR68_PANRE	P42394 caliphora	393	1	9.1	10	1	GRP_RANRI	P08610 phyllomedus
322	1	9.1	9	1	FAR69_PANRE	P42393 caliphora	394	1	9.1	10	1	GRP_RANRI	P42634 aedes aegypt
323	1	9.1	9	1	FAR70_PANRE	P42392 caliphora	395	1	9.1	10	1	GRP_RANRI	P40752 urechis uni
324	1	9.1	9	1	FAR71_PANRE	P42391 caliphora	396	1	9.1	10	1	GRP_RANRI	P19425 aedes aegypt
325	1	9.1	9	1	FAR72_PANRE	P42390 caliphora	397	1	9.1	10	1	GRP_RANRI	P19118 nicotiana p
	1	9.1	9	1	FAR73_PANRE	P42389 caliphora	398	1	9.1	10	1	GRP_RANRI	P81737 leucophaea
	1	9.1	9	1	FAR74_PANRE	P42388 caliphora	399	1	9.1	10	1	GRP_RANRI	P81738 leucophaea
	1	9.1	9	1	FAR75_PANRE	P42387 caliphora	400	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR76_PANRE	P42386 caliphora	401	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR77_PANRE	P42385 caliphora	402	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR78_PANRE	P42384 caliphora	403	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR79_PANRE	P42383 caliphora	404	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR80_PANRE	P42382 caliphora	405	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR81_PANRE	P42381 caliphora	406	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR82_PANRE	P42380 caliphora	407	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR83_PANRE	P42379 caliphora	408	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR84_PANRE	P42378 caliphora	409	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR85_PANRE	P42377 caliphora	410	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR86_PANRE	P42376 caliphora	411	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR87_PANRE	P42375 caliphora	412	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR88_PANRE	P42374 caliphora	413	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR89_PANRE	P42373 caliphora	414	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR90_PANRE	P42372 caliphora	415	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR91_PANRE	P42371 caliphora	416	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR92_PANRE	P42370 caliphora	417	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR93_PANRE	P42369 caliphora	418	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR94_PANRE	P42368 caliphora	419	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR95_PANRE	P42367 caliphora	420	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR96_PANRE	P42366 caliphora	421	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR97_PANRE	P42365 caliphora	422	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR98_PANRE	P42364 caliphora	423	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR99_PANRE	P42363 caliphora	424	1	9.1	10	1	GRP_RANRI	
	1	9.1	9	1	FAR100_PANRE	P42362 caliphora	425	1	9.1	10	1	GRP_RANRI	











Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 KR 6  
DB 5 KR 6

RESULT 15  
ID LKKA DEUMA STANDARD: PRT: 8 AA  
AC 621143  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 18, Last annotation update)  
DE Leucokinin IV (I-IV)  
OS Leucokinaea maderae (Mammalia: Cnidaria)  
OC Eukaryota; Metazoa; Anthozoda; Hexapoda; Insecta; Pterygota;  
NC Neoptera; Orthoptera; Blattellidae; Blattaria; Blattelloidea;  
NCB TaxID: 988  
KN [1]  
RP SEQUENCE AND SYNTHESIS  
RC TISSUE-Head  
RA Holman G.M.; Cook R.J.; Nachman R.J.;  
RT "Primary structure and synthesis of two additional neuropeptides  
RT from Leucokinaea maderae: members of a new family of  
RT Cephalomyotopins."  
RL Comp. Biochem. Physiol. 84C:271-276(1986).  
CC -1- FUNCTION: THIS CEPHALOMYOTOPIC PEPTIDE STIMULATES CONTRACTILE  
CC -1- ACTIVITY OF COELODACH PROTEIN (HINDGUT).  
KW Neuropeptide; Amidation  
FT MOD.RES 5 8 AMIDATION  
SQ SEQUENCE 8 AA: 906 MW: 106365b1e9d5b0da CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1; Seq. 0;  
Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 AS 2  
DB 2 AS 4

RESULT 16  
ID LKKA DEUMA STANDARD: PRT: 8 AA  
AC 621143  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locustamyotropin 2 (COM MT 2)  
OS Locusta migratoria (Migratory locust)  
OC Eukaryota; Metazoa; Anthozoda; Hexapoda; Insecta; Pterygota;  
NC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;  
NCB TaxID: 7004  
KN [1]  
RP SEQUENCE  
RC TISSUE-Heart; Cardiac  
RA Schorff L.; Holman G.M.; Hayes I.K.; Nachman R.J.; de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin II, an  
RT additional neuropeptide of Locusta migratoria. Member of the  
RT cephalomyotopins peptide family."  
RL Insect Biochem. 20:479-484(1990).  
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC -1- (MYOTROPIC ACTIVITY).  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DE InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS-0539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin  
FT MOD.RES 8 8 AMIDATION  
SQ SEQUENCE 8 AA: 934 MW: 26341771a9caa87b CRC64:

Query Match 16.2% Score 2; DB 1; Length 8;

Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 KR 6  
DB 5 KR 6

RESULT 14  
ID LKKA DEUMA STANDARD: PRT: 8 AA  
AC 621143  
DT 01-MAY-1991 (Rel. 19, Created)  
DT 01-MAY-1991 (Rel. 19, Last sequence update)  
DT 01-MAY-1991 (Rel. 19, Last annotation update)  
DE Locustamyotropin 2 (COM MT 2)  
OS Locusta migratoria (Migratory locust)  
OC Eukaryota; Metazoa; Anthozoda; Hexapoda; Insecta; Pterygota;  
NC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;  
NCB TaxID: 7004  
KN [1]  
RP SEQUENCE  
RC TISSUE-Heart; Cardiac  
RA Schorff L.; Holman G.M.; Hayes I.K.; Nachman R.J.; de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin II, an  
RT additional neuropeptide of Locusta migratoria. Member of the  
RT cephalomyotopins peptide family."  
RL Insect Biochem. 20:479-484(1990).  
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC -1- (MYOTROPIC ACTIVITY).  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DE InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS-0539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin  
FT MOD.RES 8 8 AMIDATION  
SQ SEQUENCE 8 AA: 934 MW: 26341771a9caa87b CRC64:

Query Match 16.2% Score 2; DB 1; Length 8;







RJ "Invertebrate vasopressin/oxytocin homologs: Characterization of  
 peptides from conus geographies and conus striatus venom."

JA Biol Chem. 262:15821-15824(1987)

24

REVIEW.

XX MEDLINE 89-24586; PubMed 3052280;

XX Gray W.R., Olivera B.M., 1987, 1988

XX "Peptide toxins from venomous cone snails."

XX Ann Rev Biochem. 57:685-701(1988)

XX 1- SUBCELLULAR LOCATION: Secreted.

XX 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

XX PIR: A28495; A28495.

XX Characterization: (P000981; Neurhyp\_1 form

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

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XX PIR: A28495; A28495; A28495.

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XX PIR: A28495; A28495; A28495.

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XX PIR: A28495; A28495; A28495.

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XX PIR: A28495; A28495; A28495.

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XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

UY 10 PR 11

11

7 PR 8

RESULT 24

DNFL LocMI

10 DNFL LocMI

STANDARD

PR: 9 AA

AC 01559;

BT 01 AUG 1998 (Ref. 15; Created)

BT 01 AUG 1998 (Ref. 15; Last sequence update)

BT 15-SEP-1998 (Ref. 17; Last annotation update)

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

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BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

BT Locupressin (Genetic peptide, F1/F2).

Query Match 18.2% Score 21 DB 11 Length 9;

Best Local Similarity 100.0% Pred. No. 13e+05;

Matches 21 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 10 PR 11

11

7 PR 8

RESULT 30

DNFL LocMI

10 DNFL LocMI

STANDARD

PR: 9 AA

AC 01559;

BT 21 AUG 1998 (Ref. 21; Created)

BT 21 AUG 1998 (Ref. 21; Last sequence update)

BT 16-OCT-2001 (Ref. 46; Last annotation update)

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

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BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

BT Delta sleep-inducing peptide (DSIP).

Query Match 18.2% Score 21 DB 11 Length 9;

Best Local Similarity 100.0% Pred. No. 13e+05;

Matches 21 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 10 PR 11

11

7 PR 8

RESULT 30

DNFL LocMI

10 DNFL LocMI

STANDARD

PR: 9 AA

AC 01559;

RJ "Invertebrate vasopressin/oxytocin homologs: Characterization of  
 peptides from conus geographies and conus striatus venom."

JA Biol Chem. 262:15821-15824(1987)

24

REVIEW.

XX MEDLINE 89-24586; PubMed 3052280;

XX Gray W.R., Olivera B.M., 1987, 1988

XX "Peptide toxins from venomous cone snails."

XX Ann Rev Biochem. 57:685-701(1988)

XX 1- SUBCELLULAR LOCATION: Secreted.

XX 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

XX PIR: A28495; A28495.

XX Characterization: (P000981; Neurhyp\_1 form

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

XX PIR: A28495; A28495; A28495.

RA Schenckeburger G.A., Maier P.F., Fisher H.J., Wilson K., Mangieri V.  
 K "The delta EEG (sleep)-inducing peptide (DSIP): XI. Amino acid  
 E analysis, sequence, synthesis and activity of the nonapeptide."  
 E J Neurosci Arch. 376:119-129(1973).  
 EN 31  
 RP REV.FW.  
 RA MEDLINE: 87125129; PubMed: 4550726.  
 RX Gray R.V., Kastin A.J.:  
 RL "Delta-sleep-inducing peptide (DSIP): an isolation."  
 RL Peptides 7:1165-1187(1986).  
 CC -1- FUNCTION: WHEN INFUSED INTO THE MESS LIEN RHALIS VENTRICLE 4  
 CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND  
 CC REDUCED MOTOR ACTIVITIES.  
 CC -1- MISCELLANEOUS: THIS PEPTIDE WAS ISOLATED FROM RHALIS 4  
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KID, ASSES BY ELECTRO-  
 CC STIMULATION OF THE THALAMUS.  
 CC -1- LATABASE: NAME-PROTEIN Spotlight  
 CC NIDH Issue 8 of March 2001.  
 CC WWW:"http://www.expasy.org/spotlight/articles/spotlight.html".  
 EX PIR: A01422; Q00B. 849 MW; 250365R06A087670 (2004).  
 SQ SEQUENCE 9 AA: 1128 MW; 250365R06A087670 (2004).

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DE 6 AS 7

RESULT 31

FAR2\_CALVO  
 ID FAR2\_CALVO STANDARD; PRT; 9 AA.  
 AC P41857;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliophora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestridae;  
 CC Calliphoridae; Calliphora.  
 CC NCBI\_TaxID=27454;  
 EN 111  
 RP SEQUENCE  
 RX TISSUE: Thoracic ganglion;  
 RX MEDLINE: 92195111; PubMed 1549595;  
 RA Duvé H., Johnson A.R., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.:  
 RT "Isolation, structure, and activity of Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphrinamides) from the blowfly  
 RT Calliphora vomitoria".  
 CC Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
 CC SALIVARY GLAND OF CALLIPHORA.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 EX PIR: G41978; G41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA: 1128 MW; 250365R06A087670 (2004).

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3

DE 3 SQ 4

RESULT 32

FAR3\_CALVO  
 ID FAR3\_CALVO STANDARD; PRT; 9 AA.  
 AC P41858;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliophora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestridae;  
 CC Calliphoridae; Calliphora.  
 CC NCBI\_TaxID=27454;  
 EN 111  
 RP SEQUENCE  
 RX TISSUE: Thoracic ganglion;  
 RX MEDLINE: 92195111; PubMed 1549595;  
 RA Duvé H., Johnson A.R., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.:  
 RT "Isolation, structure, and activity of Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphrinamides) from the blowfly  
 RT Calliphora vomitoria".  
 CC Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
 CC SALIVARY GLAND OF CALLIPHORA.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 EX PIR: G41978; G41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA: 1128 MW; 250365R06A087670 (2004).

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FAR3\_CALVO  
 ID FAR3\_CALVO STANDARD; PRT; 9 AA.  
 AC P41858;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliophora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestridae;  
 CC Calliphoridae; Calliphora.  
 CC NCBI\_TaxID=27454;  
 EN 111  
 RP SEQUENCE  
 RX TISSUE: Thoracic ganglion;  
 RX MEDLINE: 92195111; PubMed 1549595;  
 RA Duvé H., Johnson A.R., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.:  
 RT "Isolation, structure, and activity of Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphrinamides) from the blowfly  
 RT Calliphora vomitoria".  
 CC Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
 CC SALIVARY GLAND OF CALLIPHORA.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 EX PIR: G41978; G41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA: 1114 MW; 250365R06A087670 (2004).

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3

DE 3 SQ 4









80 PEPs (cell. 261-397.401(1999))  
 81 1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION + THE  
 82 CONTRACT AND FOREGUT  
 83 1- SUBCELLULAR LOCATION: Secreted.  
 84 1- SIMILARITY: SOME SIMILARITY TO CATHYKININS  
 85 LYSKININS; Neuropeptide: Activation  
 86 MATCHES 9 AA: 439 MW: 2486.406940542 Da  
 87 SEQUENCE 9 AA: 439 MW: 2486.406940542 Da  
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 89 Query Match 18.2% Score 21 DB 1 Length 9  
 90 Best Local Similarity 100.0% Pred. No. 1.1e+05  
 91 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
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Bothrops jararaca (Jararaca);  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Lepidosauria; Squamata; Serpentes; Ophidia; Viperidae;  
 Crotalinae; Bothrops;  
 NCBI\_TaxID:8724;  
 [1]  
 SEQUENCE;  
 TISSUE:Venom;  
 MEDLINE:7218596; PubMed:4344 2;  
 Ondetti M.A.; Williams N.J.; Saba R.E.; Presser J.; Weaver R.R.;  
 Kury O.;  
 "Angiotensin converting enzyme inhibitors from the venom of Bothrops  
 jararaca. Isolation, elucidation of structure and synthesis."  
 Biochemistry 10:4033-4039(1971).  
 -1 FUNCTION: This peptide both inhibits the activity of the  
 angiotensin-converting enzyme and enhances the activity of the  
 bradykinin by inhibiting the kinases that inactivate it.  
 It acts as an indirect hypotensive agent.  
 DR PIR: A0225; XAV148;  
 KW Hypotensive agent; Pyrrolidone carboxylic acid;  
 FC MCFES 1 1 PYRROLIDONE CARBOXYLIC ACID;  
 SQ SEQUENCE 10 AA: 1342 MW: 30053546774.774 CRC64;

Query Match: 18.2% Score 21 DB 1; Length 10;  
 Best local Similarity 100.0% Pred. No. 1.1e+04;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PR 11

DB 4 PR 5

RESULT 48

REP\_VIPAS

AC REP\_VIPAS STANDARD: PRT: 10 AA;  
 A0243511

BT 01-OCT-1994 (Rel. 26, (reated)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DI 28-FEB-2003 (Rel. 43, Last annotation update)  
 DE Bradykinin potentiating peptide (Angiotensin-converting  
 enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Serpentes; Ophidia; Viperidae;  
 OC Viperidae; Viperinae; Vipera;  
 CX NCBI\_TaxID:8706;  
 RN [1]  
 RP SEQUENCE

RX MEDLINE:9032676; PubMed:210091  
 RA Kozlowski J.; Sotgiu G.;  
 R1 "Characterization of a new inhibitor of the angiotensin  
 converting enzyme from the venom of Vipera aspis and  
 Vipera berus."  
 Int J Biochem 22:767-77.(1990)  
 CC -1 FUNCTION: This peptide both inhibits the activity of the  
 angiotensin-converting enzyme and enhances the activity of the  
 bradykinin by inhibiting the kinases that inactivate it.  
 It acts as an indirect hypotensive agent.

DR PIR: A0572; XASNP;  
 KW Hypotensive agent; Pyrrolidone carboxylic acid;  
 FC MCFES 1 1 PYRROLIDONE CARBOXYLIC ACID;  
 SQ SEQUENCE 10 AA: 1062 MW: 30053546774.774 CRC64;

Query Match: 18.2% Score 21 DB 1; Length 10;  
 Best local Similarity 100.0% Pred. No. 1.1e+04;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GP 10

DB 5 GP 6

RESULT 49

REP\_VIPAS

AC REP\_VIPAS STANDARD: PRT: 10 AA;  
 A0243511

BT 01-OCT-1994 (Rel. 26, (reated)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DI 28-FEB-2003 (Rel. 43, Last annotation update)  
 DE Bradykinin potentiating peptide (Angiotensin-converting  
 enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Serpentes; Ophidia; Viperidae;  
 OC Viperidae; Viperinae; Vipera;  
 CX NCBI\_TaxID:8706;  
 RN [1]  
 RP SEQUENCE

RX MEDLINE:9032676; PubMed:210091  
 RA Kozlowski J.; Sotgiu G.;  
 R1 "Characterization of a new inhibitor of the angiotensin  
 converting enzyme from the venom of Vipera aspis and  
 Vipera berus."  
 Int J Biochem 22:767-77.(1990)  
 CC -1 FUNCTION: This peptide both inhibits the activity of the  
 angiotensin-converting enzyme and enhances the activity of the  
 bradykinin by inhibiting the kinases that inactivate it.  
 It acts as an indirect hypotensive agent.

BT 01-OCT-2001 (Rel. 40, (reated)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DI 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus;  
 CX NCBI\_TaxID:8022;  
 RN [1]  
 RP SEQUENCE

RX MEDLINE:9409617; PubMed:624242;  
 RA Conlon J.M.; Wilson K.R.;  
 R1 "Purification of a vasoactive peptide related to lysyl-bradykinin from  
 trout plasma."  
 FEBS Lett. 334:75-78(1993).  
 CC -1 FUNCTION: SMOOTH MUSCLE CONTRACTION PROBABLY PLAYS A ROLE FOR  
 THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 TISSUE SPECIFICITY: Plasma.  
 CC -1 SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

DR PIR: S49030; S49030;  
 KW Bradykinin; Vasodilator;  
 SQ SEQUENCE 10 AA: 1193 MW: 3305907931786777 CRC64;

Query Match: 18.2% Score 21 DB 1; Length 10;  
 Best local Similarity 100.0% Pred. No. 1.1e+04;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KR 6

DB 11

DB 1 KR 2

RESULT 50

REP\_VIPAS

AC REP\_VIPAS STANDARD: PRT: 10 AA;  
 A0243511

BT 01-OCT-1994 (Rel. 30, (reated)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DI 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus;  
 CX NCBI\_TaxID:8022;  
 RN [1]  
 RP SEQUENCE

RX MEDLINE:9427150; PubMed:8161469;  
 RA Friedberg R.; Kadonaga R.;  
 R1 "Identification of tissue specific isoforms for subunits Vb and Vlla  
 of cytochrome c oxidase isolated from rainbow trout."  
 Eur J Biochem 221:1111-1116(1994).  
 CC -1 FUNCTION: THIS IS THE HEME A CONTAINING CHAIN OF CYTOCHROME C  
 OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

CC -1 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2O).  
 CC -1 SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -1 SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 DR PIR: S4625; S4625;  
 KW Cytochrome c oxidase; Heme; Mitochondrion; Inner membrane;  
 FC MCFES 1 10  
 SQ SEQUENCE 10 AA: 1144 MW: C535C5B1AB02C33D CRC64;

Query Match: 18.2% Score 21 DB 1; Length 10;  
 Best local Similarity 100.0% Pred. No. 1.1e+04;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 4 AK 5  
14 11  
14 3 AK 4

Source: compressed: September 30, 2003, 10:26:00  
Sub time : 7.25 sec



153	2	18.2	9	2	356974	collagen alpha 1(I)	176	2	18.2	10	2	PH0944	T-cell receptor be
154	2	18.2	9	2	356975	collagen alpha 2(I)	177	2	18.2	10	2	PH0933	T-cell receptor be
155	2	18.2	9	2	326508	collagen alpha 2(V)	178	2	18.2	10	2	PH0894	T-cell receptor be
156	2	18.2	9	2	357915	spectrin synhes	179	2	18.2	10	2	PH0946	T-cell receptor be
157	2	18.2	9	2	357916	spectrin alpha chain	180	2	18.2	10	2	PH0925	T-cell receptor be
158	2	18.2	9	2	357917	T-cell receptor be	181	2	18.2	10	2	PH0926	T-cell receptor be
159	2	18.2	9	2	357918	T-cell receptor be	182	2	18.2	10	2	PH0916	T-cell receptor be
160	2	18.2	9	2	357919	T-cell receptor be	183	2	18.2	10	2	PH0923	T-cell receptor be
161	2	18.2	9	2	357920	bone gla protein	184	2	18.2	10	2	PH0895	T-cell receptor be
162	2	18.2	9	2	357921	T-cell receptor be	185	2	18.2	10	2	PH0948	T-cell receptor be
163	2	18.2	9	2	357922	T-cell receptor be	186	2	18.2	10	2	152645	gene B-59 protein
164	2	18.2	9	2	357923	T-cell receptor be	187	2	18.2	10	2	152646	monohydroascorba
165	2	18.2	9	2	357924	T-cell receptor be	188	2	18.2	10	2	152647	NADH2 dehydrogenas
166	2	18.2	9	2	357925	T-cell receptor be	189	2	18.2	10	2	152648	NADH2 dehydrogenas
167	2	18.2	9	2	357926	T-cell receptor be	190	2	18.2	10	2	152649	bradykinin potenti
168	2	18.2	9	2	357927	T-cell receptor be	191	2	18.2	10	2	152650	bradykinin potenti
169	2	18.2	9	2	357928	T-cell receptor be	192	2	18.2	10	2	152651	dihydroorotase (EC
170	2	18.2	9	2	357929	T-cell receptor be	193	2	18.2	10	2	152652	substance P - chic
171	2	18.2	9	2	357930	T-cell receptor be	194	2	18.2	10	2	152653	ribosomal protein
172	2	18.2	9	2	357931	T-cell receptor be	195	2	18.2	10	2	152654	rhodopsin homolog
173	2	18.2	9	2	357932	T-cell receptor be	196	2	18.2	10	2	152655	ermg leader peptid
174	2	18.2	9	2	357933	T-cell receptor be	197	2	18.2	10	2	152656	megastrolakinin -
175	2	18.2	9	2	357934	T-cell receptor be	198	2	18.2	10	2	152657	substance P - rain
176	2	18.2	9	2	357935	T-cell receptor be	199	2	18.2	10	2	152658	substance P - Atla
177	2	18.2	9	2	357936	T-cell receptor be	200	2	18.2	10	2	152659	physalaemin - frog
178	2	18.2	9	2	357937	T-cell receptor be	201	2	18.2	10	2	152660	43.5K blue stone p
179	2	18.2	9	2	357938	T-cell receptor be	202	2	18.2	10	2	152661	hypothetical prote
180	2	18.2	9	2	357939	T-cell receptor be	203	2	18.2	10	2	152662	quinoline 2-oxidor
181	2	18.2	9	2	357940	T-cell receptor be	204	2	18.2	10	2	152663	cell protein - Fsc
182	2	18.2	9	2	357941	T-cell receptor be	205	2	18.2	10	2	152664	hypothetical prote
183	2	18.2	9	2	357942	T-cell receptor be	206	2	18.2	10	2	152665	glycylisome 9K 1
184	2	18.2	9	2	357943	T-cell receptor be	207	2	18.2	10	2	152666	58K heat shock pro
185	2	18.2	9	2	357944	T-cell receptor be	208	2	18.2	10	2	152667	probable antigen 5
186	2	18.2	9	2	357945	T-cell receptor be	209	2	18.2	10	2	152668	pyruvate synthase
187	2	18.2	9	2	357946	T-cell receptor be	210	2	18.2	10	2	152669	napin small chain
188	2	18.2	9	2	357947	T-cell receptor be	211	2	18.2	10	2	152670	seed protein ws-23
189	2	18.2	9	2	357948	T-cell receptor be	212	2	18.2	10	2	152671	pyruvate synthase
190	2	18.2	9	2	357949	T-cell receptor be	213	2	18.2	10	2	152672	seed protein ws-23
191	2	18.2	9	2	357950	T-cell receptor be	214	2	18.2	10	2	152673	pyruvate synthase
192	2	18.2	9	2	357951	T-cell receptor be	215	2	18.2	10	2	152674	seed protein ws-23
193	2	18.2	9	2	357952	T-cell receptor be	216	2	18.2	10	2	152675	pyruvate synthase
194	2	18.2	9	2	357953	T-cell receptor be	217	2	18.2	10	2	152676	seed protein ws-23
195	2	18.2	9	2	357954	T-cell receptor be	218	2	18.2	10	2	152677	pyruvate synthase
196	2	18.2	9	2	357955	T-cell receptor be	219	2	18.2	10	2	152678	seed protein ws-23
197	2	18.2	9	2	357956	T-cell receptor be	220	2	18.2	10	2	152679	pyruvate synthase
198	2	18.2	9	2	357957	T-cell receptor be	221	2	18.2	10	2	152680	seed protein ws-23
199	2	18.2	9	2	357958	T-cell receptor be	222	2	18.2	10	2	152681	pyruvate synthase
200	2	18.2	9	2	357959	T-cell receptor be	223	2	18.2	10	2	152682	seed protein ws-23
201	2	18.2	9	2	357960	T-cell receptor be	224	2	18.2	10	2	152683	pyruvate synthase
202	2	18.2	9	2	357961	T-cell receptor be	225	2	18.2	10	2	152684	seed protein ws-23
203	2	18.2	9	2	357962	T-cell receptor be	226	2	18.2	10	2	152685	pyruvate synthase
204	2	18.2	9	2	357963	T-cell receptor be	227	2	18.2	10	2	152686	seed protein ws-23
205	2	18.2	9	2	357964	T-cell receptor be	228	2	18.2	10	2	152687	pyruvate synthase
206	2	18.2	9	2	357965	T-cell receptor be	229	2	18.2	10	2	152688	seed protein ws-23
207	2	18.2	9	2	357966	T-cell receptor be	230	2	18.2	10	2	152689	pyruvate synthase
208	2	18.2	9	2	357967	T-cell receptor be	231	2	18.2	10	2	152690	seed protein ws-23
209	2	18.2	9	2	357968	T-cell receptor be	232	2	18.2	10	2	152691	pyruvate synthase
210	2	18.2	9	2	357969	T-cell receptor be	233	2	18.2	10	2	152692	seed protein ws-23
211	2	18.2	9	2	357970	T-cell receptor be	234	2	18.2	10	2	152693	pyruvate synthase
212	2	18.2	9	2	357971	T-cell receptor be	235	2	18.2	10	2	152694	seed protein ws-23
213	2	18.2	9	2	357972	T-cell receptor be	236	2	18.2	10	2	152695	pyruvate synthase
214	2	18.2	9	2	357973	T-cell receptor be	237	2	18.2	10	2	152696	seed protein ws-23
215	2	18.2	9	2	357974	T-cell receptor be	238	2	18.2	10	2	152697	pyruvate synthase
216	2	18.2	9	2	357975	T-cell receptor be	239	2	18.2	10	2	152698	seed protein ws-23
217	2	18.2	9	2	357976	T-cell receptor be	240	2	18.2	10	2	152699	pyruvate synthase
218	2	18.2	9	2	357977	T-cell receptor be	241	2	18.2	10	2	152700	seed protein ws-23
219	2	18.2	9	2	357978	T-cell receptor be	242	2	18.2	10	2	152701	pyruvate synthase
220	2	18.2	9	2	357979	T-cell receptor be	243	2	18.2	10	2	152702	seed protein ws-23
221	2	18.2	9	2	357980	T-cell receptor be	244	2	18.2	10	2	152703	pyruvate synthase
222	2	18.2	9	2	357981	T-cell receptor be	245	2	18.2	10	2	152704	seed protein ws-23
223	2	18.2	9	2	357982	T-cell receptor be	246	2	18.2	10	2	152705	pyruvate synthase
224	2	18.2	9	2	357983	T-cell receptor be	247	2	18.2	10	2	152706	seed protein ws-23
225	2	18.2	9	2	357984	T-cell receptor be	248	2	18.2	10	2	152707	pyruvate synthase
226	2	18.2	9	2	357985	T-cell receptor be	249	2	18.2	10	2	152708	seed protein ws-23
227	2	18.2	9	2	357986	T-cell receptor be	250	2	18.2	10	2	152709	pyruvate synthase
228	2	18.2	9	2	357987	T-cell receptor be	251	2	18.2	10	2	152710	seed protein ws-23
229	2	18.2	9	2	357988	T-cell receptor be	252	2	18.2	10	2	152711	pyruvate synthase
230	2	18.2	9	2	357989	T-cell receptor be	253	2	18.2	10	2	152712	seed protein ws-23
231	2	18.2	9	2	357990	T-cell receptor be	254	2	18.2	10	2	152713	pyruvate synthase
232	2	18.2	9	2	357991	T-cell receptor be	255	2	18.2	10	2	152714	seed protein ws-23
233	2	18.2	9	2	357992	T-cell receptor be	256	2	18.2	10	2	152715	pyruvate synthase
234	2	18.2	9	2	357993	T-cell receptor be	257	2	18.2	10	2	152716	seed protein ws-23
235	2	18.2	9	2	357994	T-cell receptor be	258	2	18.2	10	2	152717	pyruvate synthase
236	2	18.2	9	2	357995	T-cell receptor be	259	2	18.2	10	2	152718	seed protein ws-23
237	2	18.2	9	2	357996	T-cell receptor be	260	2	18.2	10	2	152719	pyruvate synthase
238	2	18.2	9	2	357997	T-cell receptor be	261	2	18.2	10	2	152720	seed protein ws-23
239	2	18.2	9	2	357998	T-cell receptor be	262	2	18.2	10	2	152721	pyruvate synthase
240	2	18.2	9	2	357999	T-cell receptor be	263	2	18.2	10	2	152722	seed protein ws-23
241	2	18.2	9	2	358000	T-cell receptor be	264	2	18.2	10	2	152723	pyruvate synthase
242	2	18.2	9	2	358001	T-cell receptor be	265	2	18.2	10	2	152724	seed protein ws-23
243	2	18.2	9	2	358002	T-cell receptor be	266	2	18.2	10	2	152725	pyruvate synthase
244	2	18.2	9	2	358003	T-cell receptor be	267	2	18.2	10	2	152726	seed protein ws-23
245	2	18.2	9	2	358004	T-cell receptor be	268	2	18.2	10	2	152727	pyruvate synthase
246	2	18.2	9	2	358005	T-cell receptor be	269	2	18.2	10	2	152728	seed protein ws-23
247	2	18.2	9	2	358006	T-cell receptor be	270	2	18.2	10	2	152729	pyruvate synthase
248	2	18.2	9	2	358007	T-cell receptor be	271	2	18.2	10	2	152730	seed protein ws-23
249	2	18.2	9	2	358008	T-cell receptor be	272	2	18.2	10	2	152731	pyruvate synthase
250	2	18.2	9	2	358009	T-cell receptor be	273	2	18.2	10	2	152732	seed protein ws-23
251	2	18.2	9	2	358010	T-cell receptor be	274	2	18.2	10	2	152733	pyruvate synthase
252	2	18.2	9	2	358011	T-cell receptor be	275	2	18.2	10	2	152734	seed protein ws-23
253	2	18.2	9	2	358012	T-cell receptor be	276	2	18.2	10	2	152735	pyruvate synthase
254	2	18.2	9	2	358013	T-cell receptor be	277	2	18.2	10	2	152736	seed protein ws-23
255	2	18.2	9	2	358014	T-cell receptor be	278	2	18.2	10	2	152737	pyruvate synthase
256	2	18.2	9	2	358015	T-cell receptor be	279	2	18.2	10	2	152738	seed protein ws-23
257	2	18.2	9	2	358016	T-cell receptor be	280	2	18.2	10	2		



245	2	18.2	12	2	PH0514	T-cell receptor be	322	2	18.2	12	2	PH1185	T-cell receptor al
246	2	18.2	11	2	PH0922	T-cell receptor be	323	2	18.2	12	2	PH1180	T-cell receptor al
247	2	18.2	12	2	PH0506	T-cell receptor be	324	2	18.2	12	2	PH1183	T-cell receptor al
248	2	18.2	11	2	S63294	tobulin 2 beta-1 c	325	2	18.2	12	2	PH1188	T-cell receptor al
249	2	18.2	11	4	S19015	hypothetical prote	326	2	18.2	12	2	PH1172	T-cell receptor al
250	2	18.2	11	4	S54081	retinoic acid rece	327	2	18.2	12	2	PH1171	T-cell receptor al
251	2	18.2	12	1	A43975	leucostammin tropin	328	2	18.2	12	2	PH1175	T-cell receptor al
252	2	18.2	12	1	A53769	alpha-conotoxin -m	329	2	18.2	12	2	PH1174	T-cell receptor al
253	2	18.2	12	1	FEF79E	pyr leader pepate	330	2	18.2	12	2	PH1179	T-cell receptor al
254	2	18.2	12	2	PH0577	tyrosine 4-monooxy	331	2	18.2	12	2	PH1181	T-cell receptor al
255	2	18.2	12	2	PH0578	tyrosine 4-monooxy	332	2	18.2	12	2	S51737	T-cell receptor be
256	2	18.2	12	2	PH0583	tyrosine 4-monooxy	333	2	18.2	12	2	A50528	insulin-like growt
257	2	18.2	12	2	PH0581	tyrosine 4-monooxy	334	2	18.2	12	2	S74196	3-hydroxy-3-methyl
258	2	18.2	12	2	PH0576	tyrosine 4-monooxy	335	2	18.2	12	2	S74196	gene Bata protein
259	2	18.2	12	2	A29119	phosphatidase A2 (	336	2	18.2	12	2	S68402	NAD(-)-glycohydrol
260	2	18.2	12	2	A29119	phosphatidase A2 (	337	2	18.2	12	2	PH0663	dystrophin-associa
261	2	18.2	12	2	A29119	phosphatidase A2 (	338	2	18.2	12	2	S20507	14 kappa-1 chain J
262	2	18.2	12	2	A29119	phosphatidase A2 (	339	2	18.2	12	2	S20507	14 kappa-2 chain J
263	2	18.2	12	2	A29119	phosphatidase A2 (	340	2	18.2	12	2	S20507	14 gamma-2 chain J
264	2	18.2	12	2	A29119	phosphatidase A2 (	341	2	18.2	12	2	PH1605	14 gamma-2 chain J
265	2	18.2	12	2	A29119	phosphatidase A2 (	342	2	18.2	12	2	A33520	inhibitory diffus
266	2	18.2	12	2	A29119	phosphatidase A2 (	343	2	18.2	12	2	PH0746	T-cell receptor be
267	2	18.2	12	2	A29119	phosphatidase A2 (	344	2	18.2	12	2	PH1467	T-cell receptor be
268	2	18.2	12	2	A29119	phosphatidase A2 (	345	2	18.2	12	2	PH1458	T-cell receptor be
269	2	18.2	12	2	A29119	phosphatidase A2 (	346	2	18.2	12	2	PH1463	T-cell receptor be
270	2	18.2	12	2	A29119	phosphatidase A2 (	347	2	18.2	12	2	PH1462	T-cell receptor be
271	2	18.2	12	2	A29119	phosphatidase A2 (	348	2	18.2	12	2	PH1470	T-cell receptor be
272	2	18.2	12	2	A29119	phosphatidase A2 (	349	2	18.2	12	2	PH1454	T-cell receptor be
273	2	18.2	12	2	A29119	phosphatidase A2 (	350	2	18.2	12	2	PH1456	T-cell receptor be
274	2	18.2	12	2	A29119	phosphatidase A2 (	351	2	18.2	12	2	PH1461	T-cell receptor be
275	2	18.2	12	2	A29119	phosphatidase A2 (	352	2	18.2	12	2	PH1459	T-cell receptor be
276	2	18.2	12	2	A29119	phosphatidase A2 (	353	2	18.2	12	2	PH1457	T-cell receptor be
277	2	18.2	12	2	A29119	phosphatidase A2 (	354	2	18.2	12	2	PH1459	T-cell receptor be
278	2	18.2	12	2	A29119	phosphatidase A2 (	355	2	18.2	12	2	PH0771	T-cell receptor be
279	2	18.2	12	2	A29119	phosphatidase A2 (	356	2	18.2	12	2	PH1468	T-cell receptor be
280	2	18.2	12	2	A29119	phosphatidase A2 (	357	2	18.2	12	2	S20216	T-cell receptor be
281	2	18.2	12	2	A29119	phosphatidase A2 (	358	2	18.2	12	2	S41946	T-cell receptor be
282	2	18.2	12	2	A29119	phosphatidase A2 (	359	2	18.2	12	2	S42521	hexokinase (EC 2.7
283	2	18.2	12	2	A29119	phosphatidase A2 (	360	2	18.2	12	2	S39690	neural cell adhesi
284	2	18.2	12	2	A29119	phosphatidase A2 (	361	2	18.2	12	2	PH0930	T-cell receptor be
285	2	18.2	12	2	A29119	phosphatidase A2 (	362	2	18.2	12	2	PH0931	T-cell receptor be
286	2	18.2	12	2	A29119	phosphatidase A2 (	363	2	18.2	12	2	PH0936	T-cell receptor be
287	2	18.2	12	2	A29119	phosphatidase A2 (	364	2	18.2	12	2	PH0920	T-cell receptor be
288	2	18.2	12	2	A29119	phosphatidase A2 (	365	2	18.2	12	2	S56049	urinary tract ston
289	2	18.2	12	2	A29119	phosphatidase A2 (	366	2	18.2	12	2	S27024	Na+/K+-exchanging
290	2	18.2	12	2	A29119	phosphatidase A2 (	367	2	18.2	12	2	S27023	Na+/K+-exchanging
291	2	18.2	12	2	A29119	phosphatidase A2 (	368	2	18.2	12	2	S27023	glutamine-L-lysine lig
292	2	18.2	12	2	A29119	phosphatidase A2 (	369	2	18.2	12	2	S27023	angiotensin-conver
293	2	18.2	12	2	A29119	phosphatidase A2 (	370	2	18.2	12	2	S27023	neurotensin - bovi
294	2	18.2	12	2	A29119	phosphatidase A2 (	371	2	18.2	12	2	S27023	neurotensin - brus
295	2	18.2	12	2	A29119	phosphatidase A2 (	372	2	18.2	12	2	S27023	cytochrome P450 CM
296	2	18.2	12	2	A29119	phosphatidase A2 (	373	2	18.2	12	2	S27023	glutathione peroxi
297	2	18.2	12	2	A29119	phosphatidase A2 (	374	2	18.2	12	2	S27023	neurotensin - quin
298	2	18.2	12	2	A29119	phosphatidase A2 (	375	2	18.2	12	2	S27023	neurotensin [valid
299	2	18.2	12	2	A29119	phosphatidase A2 (	376	2	18.2	12	2	S27023	neurotensin - comm
300	2	18.2	12	2	A29119	phosphatidase A2 (	377	2	18.2	12	2	S27023	enkephalin precurs
301	2	18.2	12	2	A29119	phosphatidase A2 (	378	2	18.2	12	2	S27023	alpha-conotoxin SI
302	2	18.2	12	2	A29119	phosphatidase A2 (	379	2	18.2	12	2	S27023	histone H1.c - mou
303	2	18.2	12	2	A29119	phosphatidase A2 (	380	2	18.2	12	2	S27023	histone H1a - mous
304	2	18.2	12	2	A29119	phosphatidase A2 (	381	2	18.2	12	2	S27023	ribosomal protein
305	2	18.2	12	2	A29119	phosphatidase A2 (	382	2	18.2	12	2	S27023	tubulin beta chain
306	2	18.2	12	2	A29119	phosphatidase A2 (	383	2	18.2	12	2	S27023	outer membrane pro
307	2	18.2	12	2	A29119	phosphatidase A2 (	384	2	18.2	12	2	S27023	traA protein - Esc
308	2	18.2	12	2	A29119	phosphatidase A2 (	385	2	18.2	12	2	S27023	OLL protein - vacc
309	2	18.2	12	2	A29119	phosphatidase A2 (	386	2	18.2	12	2	S27023	alpha-2 collagen -
310	2	18.2	12	2	A29119	phosphatidase A2 (	387	2	18.2	12	2	S27023	crabroline - Europe
311	2	18.2	12	2	A29119	phosphatidase A2 (	388	2	18.2	12	2	S27023	bombesin-like pept
312	2	18.2	12	2	A29119	phosphatidase A2 (	389	2	18.2	12	2	S27023	corticostate pept
313	2	18.2	12	2	A29119	phosphatidase A2 (	390	2	18.2	12	2	S27023	protocatachuate 3,
314	2	18.2	12	2	A29119	phosphatidase A2 (	391	2	18.2	12	2	S27023	hypothetical prote
315	2	18.2	12	2	A29119	phosphatidase A2 (	392	2	18.2	12	2	S27023	hypothetical prote
316	2	18.2	12	2	A29119	phosphatidase A2 (	393	2	18.2	12	2	S27023	oxfX protein - Esc
317	2	18.2	12	2	A29119	phosphatidase A2 (	394	2	18.2	12	2	S27023	arqA protein - Sal

395	2	18.2	13	2	A46443	prolactin-binding domain
396	2	18.2	13	2	A62369	glucocorticoid 8K F
397	2	18.2	13	2	A62369	spore protease-like 3
398	2	18.2	13	2	A62369	ribosomal protein
399	2	18.2	13	2	A62369	ribosomal protein
400	2	18.2	13	2	A62369	ribosomal protein
401	2	18.2	13	2	A62369	ribosomal protein
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407	2	18.2	13	2	A62369	ribosomal protein
408	2	18.2	13	2	A62369	ribosomal protein
409	2	18.2	13	2	A62369	ribosomal protein
410	2	18.2	13	2	A62369	ribosomal protein
411	2	18.2	13	2	A62369	ribosomal protein
412	2	18.2	13	2	A62369	ribosomal protein
413	2	18.2	13	2	A62369	ribosomal protein
414	2	18.2	13	2	A62369	ribosomal protein
415	2	18.2	13	2	A62369	ribosomal protein
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417	2	18.2	13	2	A62369	ribosomal protein
418	2	18.2	13	2	A62369	ribosomal protein
419	2	18.2	13	2	A62369	ribosomal protein
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421	2	18.2	13	2	A62369	ribosomal protein
422	2	18.2	13	2	A62369	ribosomal protein
423	2	18.2	13	2	A62369	ribosomal protein
424	2	18.2	13	2	A62369	ribosomal protein
425	2	18.2	13	2	A62369	ribosomal protein
426	2	18.2	13	2	A62369	ribosomal protein
427	2	18.2	13	2	A62369	ribosomal protein
428	2	18.2	13	2	A62369	ribosomal protein
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430	2	18.2	13	2	A62369	ribosomal protein
431	2	18.2	13	2	A62369	ribosomal protein
432	2	18.2	13	2	A62369	ribosomal protein
433	2	18.2	13	2	A62369	ribosomal protein
434	2	18.2	13	2	A62369	ribosomal protein
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438	2	18.2	13	2	A62369	ribosomal protein
439	2	18.2	13	2	A62369	ribosomal protein
440	2	18.2	13	2	A62369	ribosomal protein
441	2	18.2	13	2	A62369	ribosomal protein
442	2	18.2	13	2	A62369	ribosomal protein
443	2	18.2	13	2	A62369	ribosomal protein
444	2	18.2	13	2	A62369	ribosomal protein
445	2	18.2	13	2	A62369	ribosomal protein
446	2	18.2	13	2	A62369	ribosomal protein
447	2	18.2	13	2	A62369	ribosomal protein
448	2	18.2	13	2	A62369	ribosomal protein
449	2	18.2	13	2	A62369	ribosomal protein
450	2	18.2	13	2	A62369	ribosomal protein
451	2	18.2	13	2	A62369	ribosomal protein
452	2	18.2	13	2	A62369	ribosomal protein
453	2	18.2	13	2	A62369	ribosomal protein
454	2	18.2	13	2	A62369	ribosomal protein
455	2	18.2	13	2	A62369	ribosomal protein
456	2	18.2	13	2	A62369	ribosomal protein
457	2	18.2	13	2	A62369	ribosomal protein
458	2	18.2	13	2	A62369	ribosomal protein
459	2	18.2	13	2	A62369	ribosomal protein
460	2	18.2	13	2	A62369	ribosomal protein
461	2	18.2	13	2	A62369	ribosomal protein
462	2	18.2	13	2	A62369	ribosomal protein
463	2	18.2	13	2	A62369	ribosomal protein
464	2	18.2	13	2	A62369	ribosomal protein
465	2	18.2	13	2	A62369	ribosomal protein
466	2	18.2	13	2	A62369	ribosomal protein
467	2	18.2	13	2	A62369	ribosomal protein

## ALIGNMENTS

## RESULT 1

S35538  
 ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
 C:Species: Mycobacterium intracellulare  
 C:Date: 09-Dec-1993 #sequence\_revision: 14-Nov-1997 #text\_change 13-Aug-1999  
 C:Accession: S35538  
 R:Naik, J., Koush, G., Morris, S.  
 Nucleic Acids Res. 21, 1039, 1993  
 A:Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium int  
 A:Reference number: S35537; M01D:93/97130; PMID:8451173  
 A:Accession: S35538  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 359, 5NA's  
 A:Cross-references: EMBL:00471; NID:0149994; PIDN:AAA25376.1; PID:9551901  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 199  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match: 36.4%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0;

7 RKG 10

3 RKG 6

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Accession: 264, 333-341, 1993  
 A:Title: Molecular cloning and quantitation of mRNA and protein encoding P21+ kinase  
 A:Reference number: 151892  
 A:Accession: 264842

A>Status: preliminary; translated from cDNA/EMBL/GenBank

A:Molecule type: mRNA

A:Accession: 18-SEP-99

A:Accession: 18-SEP-99 #sequence\_revision 17-SEP-1999

A:Accession: 18-SEP-99

A:Accession: 18-SEP-99

A:Accession: 18-SEP-99

A:Accession: 18-SEP-99

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Query Match: 27.4% Score 3; DB 2; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 2; Re-05;  
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;

QY 6 RPK 8  
 DB 2 RPK 4

RESULT 5  
 S66456

Species: Rhizobium meliloti (Strain 102)

C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S66456

C:Accession: S66456

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Query Match: 27.4% Score 3; DB 2; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 2; Re-05;  
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;

QY 6 RPK 8  
 DB 2 RPK 4

RESULT 5  
 S66456

Species: Rhizobium meliloti (Strain 102)

C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S66456

C:Accession: S66456

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Query Match: 27.4% Score 3; DB 2; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 2; Re-03;  
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;

QY 1 ASQ 3  
 DB 6 ASQ 6

RESULT 6  
 A40693

Species: Ovis orientalis aries, ovis ammon aries (domestic sheep)

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997

C:Accession: A40693

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Address  
 Protease B, blacktail rattlesnake (fragment)  
 C-Species: Naja molossus molossus (blacktail rattlesnake)  
 C-Date: 2-Jul-1990 #sequence\_revision 2-Jul-1990 #text\_change 1-Jul-1990  
 C-Accession: A34858  
 R-Ramirez, G.A.; Fletcher, C.V.; P.J.; Possanti, L.B.  
 J. Exp. Med. 276: 295-297, 1992  
 A-Title: Characterization of the venom from *Crotalus molossus molossus* (black tail rattlesnake)  
 A-Reference number: A34858; M01D:90260871; PMID:1140654  
 A-Accession: A34858  
 A-Status: preliminary  
 A-Molecule type: protein  
 A-Residues: 1-12 <VAR>  
 C-Keywords: LNA binding; translocation  
 Query Match 27.8% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0% Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 AKR 6  
 IB 11  
 2 AKR 4  
 RESULT 14  
 S71383  
 T-cell receptor beta chain - Vipera labellina  
 C-Species: Vipera labellina  
 C-Date: 11 Mar 1998 #sequence\_revision 12 Apr 1998 #text\_change 19 Mar 1999  
 C-Accession: S71383  
 R-Bathiche, R.; Marrakchi, N.; Mansueti, P.; Krifa, M.; Fournier, H.; B.  
 PERS Lett. 492: 6-10, 1996  
 A-Title: Novel anti-platelet aggregation polypeptides from Vipera labellina venom: isolation  
 A-Reference number: S71383; M01D:96354866; PMID:8769304  
 A-Accession: S71383  
 A-Molecule type: protein  
 A-Residues: 1-12 <VAR>  
 A-Experimental source: venom  
 C-Keywords: anti-coagulant; venom  
 Query Match 27.8% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0% Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 AKR 19  
 IB 7 AKR 9  
 RESULT 15  
 E42762  
 Lactose phosphotransferase system subunit 1 - Bos taurus (fragment)  
 C-Species: Bos taurus lactis  
 C-Date: 14 Sep 1992 #sequence\_revision 14 Sep 1992 #text\_change 11 Jun 2003  
 C-Accession: E42762  
 R-Ramirez, G.A.; van Schaik, S.; de Vries, W.P.  
 J. Biol. Chem. 267: 7176-7181, 1991  
 A-Title: Molecular cloning, characterization, and purification of the subunit 1 of the lactose  
 A-Reference number: A35778; M01D:9120135; PMID:1140654  
 A-Accession: E42762  
 A-Status: preliminary  
 A-Molecule type: DNA  
 A-Residues: 1-13 <VAR>  
 A-Accession: E42762  
 A-Status: preliminary  
 C-Keywords: regulatory protein; quP  
 Query Match 27.8% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0% Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KKR 7  
 IB 10 KKR 12

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RESULT 16  
 PH1479  
 T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)  
 C-Species: Mus musculus (house mouse)  
 C-Date: 10 Mar 1994 #sequence\_revision 10 Mar 1994 #text\_change 11-Apr-1995  
 C-Accession: PH1479  
 R-Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.  
 J. Exp. Med. 177: 811-826, 1993  
 A-Title: T cell receptor selection by and recognition of two class I major histocomp  
 A-Reference number: PH1479; M01D:91171821; PMID:8436911  
 A-Accession: PH1479  
 A-Molecule type: mRNA  
 A-Residues: 1-13 <VAR>  
 A-Experimental source: cytoytic T-lymphocyte  
 C-Superfamily: immunoglobulin hemology  
 C-Keywords: receptor; T-cell  
 Query Match 27.8% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0% Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SCA 4  
 IB 4 SCA 4  
 RESULT 18  
 E42762  
 Proteasome endopeptidase complex (B014.4.25.1) subunit 13 - bovine (fragment)  
 C-Species: Bos primigenius taurus (cattle)  
 C-Date: 04-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 17 Feb-2003  
 C-Accession: E42762  
 R-Dick, D.K.; Moraw, C.B.; Gramanik, B.C.; DeMartino, G.N.; Slaughter, G.A.  
 Biochemistry 31: 7347-7355, 1992  
 A-Title: Identification and localization of a cysteinyl residue critical for the try  
 A-Reference number: A42762; M01D:92378961; PMID:1510924  
 A-Accession: E42762  
 A-Status: preliminary  
 A-Molecule type: protein  
 A-Residues: 1-13 <VAR>  
 A-Experimental source: extracted from N.B. backbone (NCBIP:112180)  
 C-Keywords: hydrolase  
 Query Match 27.8% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0% Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KKR 7  
 IB 10 KKR 12



QY 7 RK3 9  
DB 6 RK3 10

RESULT 26  
S21411  
Combination protein: neda - Rhizobium cell (fragment)  
C:Species: Rhizobium loti  
C:Date: 22 Nov-1999 #sequence\_revision 12 May 1999 #text\_change 08-Jun-1999  
C:Accession: S21411  
K:Schell, D.B.; Yeard, C.A.; Collins-Eaton, J.M.; Torzith, E.A.; Wickham, E.S.; Lewis, submitted to the EMBL data library, April 1992  
A:Description: Mutational and structural analysis of *nod* gene both nodulation genes.  
A:Reference number: S21410  
A:Accession: S21411  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <ORF>  
A:Cross-references: EMBL:X65623; NIKI:04624; F03N:CAA4574; F03N:CAA4574; F03N:CAA4574  
A:Genetic: neda

Query Match 27.4% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 RK3 9  
DB 10 RK3 12

RESULT 26  
A60156  
Cellulase (EC 3.2.1.4) - Gluspiridium (human (fragment))  
N:Alternative names: endo 1,4-beta-glucanase  
C:Species: Gluspiridium joshi  
C:Date: 22 Jan-1978 #sequence\_revision 22-Jan-1999 #text\_change 22-Nov-1999  
C:Accession: A60156  
K:Fujino, T.; Suzuki, T.; Ohmura, K.; Shimizu, S.; Appl. Environ. Microbiol. 56, 1175-1178, 1992  
A:Title: Purification and properties of an endo 1,4-beta-glucanase translated from a *Cl*  
A:Reference number: A60156; M01D:90283156; PMID:214240  
A:Accession: A60156  
A:Molecule type: protein  
A:Residues: 1-15 <FUJ>  
A:Function: cellulose  
A:Description: hydrolysis of 1,4 beta-D-glucosidic linkages in beta-1,4-glucans such as cel  
A:Pathway: cellulose degradation  
C:Keywords: glycosylase; hydrolase; polysaccharide degradation

Query Match 27.4% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 QAK 5  
DB 12 QAK 14

RESULT 27  
S36891  
ribosomal protein - Mycobacterium bovis (fragment)  
C:Species: Mycobacterium bovis  
C:Date: 10-Jan-1995 #sequence\_revision 13-Feb-1995 #text\_change 13-Feb-1995  
C:Accession: S36891  
K:Shah, N.; Kimura, M.; Higashi, Y.; Yamada, I.  
EMBL Lett. 331, 9-14, 1993  
A:Title: Isolation and amino acid sequence of the 6S ribosomal protein S19 from *Mycobac*  
A:Reference number: S36887; M01D:94996587; PMID:8407418  
A:Accession: S36891  
A>Status: preliminary  
A:Molecule type: protein

A:Residues: 1-15 <HHA>

Query Match 27.4% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 RKK 8  
DB 10 RKK 12

RESULT 26  
PA0057  
adenylate isopentenyl transferase (EC 2.5.1.27) - fungus (Fusarium sporotrichoides)  
C:Species: Fusarium sporotrichoides  
C:Date: 20-Feb-1997 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0057  
K:Chow, L.P.; Fukaya, N.; Sudhara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A. submitted to JPIB, October 1994  
A:Description: two dimensional polyacrylamide gel electrophoresis of *Fusarium sporot*  
A:Reference number: PA0051  
A:Accession: PA0057  
A:Molecule type: protein  
A:Residues: 1-15 <ORF>  
C:Keywords: transferase

Query Match 27.4% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AKR 6  
DB 11 AKR 14

RESULT 29  
PH1342  
Ig heavy chain D2 region (clone C507 95) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1342  
K:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor B  
A:Reference number: PH1302; M01D:93094761; PMID:1460419  
A:Accession: PH1342  
A:Molecule type: DNA  
A:Residues: 1-15 <WAS>  
C:Keywords: heteroduplex; immunoglobulin

Query Match 27.4% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 9 GPR 11  
DB 11 GPR 14

RESULT 30  
LFSAME  
probable msra leader peptide - Staphylococcus epidermidis  
C:Species: Staphylococcus epidermidis  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C:Accession: S11157  
K:Ross, J.I.; Bady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumberg, S.; Wootton, J.C. Mol. Microbiol. 4, 1207-1214, 1990  
A:Title: Inducible erythromycin resistance in *Staphylococcus* is encoded by a member o  
A:Reference number: S11157; M01D:91041730; PMID:2233255  
A:Accession: S11157  
A:Molecule type: DNA  
A:Residues: 1-8 <ROS>  
A:Cross-references: EMBL:X52085; NID:q47000; F10N:CAA36304.1; PID:q5h1653

CysSuperfamily1: probable msrA leader peptide

Query Matrix	18.28%	Score 27	16.67%	16.67%	d.
Best Local Similarity	100.00%	100.00%	100.00%	100.00%	
Matrices	27	Conservative	0	Mismatches	0
	1	AS 2			
	1				
	3	AS 4			

RESULT 4:  
 S4372  
 Tumor associated antigen M12 (Pouso-  
 1) Species: Mus musculus (house mouse)  
 Cited: 20 Oct 1994 sequence retrieval: 22 Nov 1995 = tax: Mus musculus  
 Accession: S4372  
 Reference: 1: Barker, G., Fritsch, M., Feldman, M., Henshaw, M., Eisenbach, L.  
 Nature 366, 67-71, 1994  
 A title: TPL induction by a tumor associated antigen and an epoxide derived from a mutagen  
 A reference number: S4371; M12: 94-178.1; 95-208.6-712  
 A accession: S4372  
 A status: preliminary  
 A feature type: protein  
 A residues: 1-6 (MAN)  
 A superfamily: mass tagged animal peptides

Query Match.	16.28.	Score 2:	16.28. Result 2:
Best model Similarity	100.00	Pred No. 2	100.00
Errors	2:	conservative	0: Misclassifications
			0: In-folds
			0: Gaps
Q2	3.24	4	
Q3	7.05	8	

[illegible]

UV	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
UV	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

RESULT: 4  
 PC414  
 Hypothetical protein: 8 [imported] (SwissProt) (Fragment)  
 CysPeptid: Pseudomonas aeruginosa  
 Date: 26 Apr 2000 #sequence revision 26 Apr 2000 change 26 Apr 2000  
 CAccession: PC4141  
 R:Kawasaki, S.; Araki, H.; Igarashi, Y.; Kodama, T.  
 Gene 167, 87-91, 1995  
 A full sequence and characterisation of the downstream region of the genes encoding

Y for breastneoplasms of female dj.  
A:Reference number: J04552; PMID:8566817  
A:Accession: PC4131  
A:Status: preliminary  
A:Molecule type: INA  
A:Residues: 138 KAW  
A:Cross-references: PubMed:1217594  
A:Note: This gene is not annotated in Genbank entry PSEN1NC, release 13.0

Query Match	18 283	Score 21	DB 21	Length 81
Best Local	Similarity	100.0%	Fred. No. 2	RG+G
Matches	21	Conservative	G	Mismatches
			G	Indels
				Status

RESULT 14  
 S57141  
 rpsA protein - Erwinia chrysanthemi  
 O:Species: Erwinia chrysanthemi  
 C:Date: 06-Jan-1995 #sequence, revision 05 Jan-1995 #text\_change 08-Oct-1999  
 C:Accession: S57141  
 R:Reboullet, A.; Toussaint, A.; Faelen, M.  
 submitted to the EMBL Data Library, August 1993  
 A:Description: Identification of the integration host factor genes of E. chrysanthemi  
 A:Reference number: S57139  
 A:Accession: S57141  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 (long)  
 A:Cross-references: EMBL:X74750; NID:q394669; PIDN:CAA52769.1; PID:q581108

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Query Match      18.2% Score 2: DB 2: Length 87
Best local Similarity 100.0% Pred. No. 2 He+05
Matches          2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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RESULT 45  
 S70727  
 IpaQF protein, *Shigella flexneri* (fragment)  
 O:Species: *Shigella flexneri*  
 O:Date: 15-Feb-1997 #sequence:revisions: 13-Mar-1997 #text\_change: 08-Oct-1999  
 O:Accession: S70727  
 O:Accession: A: Saussoletti, P. J.; McNaard, K.; Barzu, S.; Mullier, J.; Phalipon, A.; P  
 Mol. Microbiol. 17, 461-476, 1995  
 A:Title: MxiG, a membrane protein required for secretion of *Shigella* spp. Ipa invasi  
 A:Reference: Embase: S70727; MIMD:96100445; PMID:8559065  
 A:Accession: S70727  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Restrictions: 18 XbaI  
 A:Cross-references: EMBL:244957; NID:4929860; PIDN:CAA88821.1; PID:4929881  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995  
 O:Genetics:  
 O:Gene: ipaQF

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Query Match      18 20 Score 2 DB 2 Length 87
Best local      100.0%
Sim.arity       100.0%   Pred. No. 2.8e+05
Matches         0: Mismatches 0: Indels 0: Gaps 0:
Conservative    0: Mismatches 0: Indels 0: Gaps 0:

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REF.SUL.1 46  
S63493



desulfatase, sulfate reductase, gamma chain, membrane bound and soluble - Desulfatase  
 C-Species: Desulfotribio desulfatase (P-04-1997 #text\_change 17-Mar-1999  
 C-Date: 28-Feb-1996 #sequence\_revision 17-Mar-1997 #text\_change 17-Mar-1999  
 C-Accession: S63493; S63494

E-Sequence: 3:1 Attendson, A.F.; Hagedorn, W.K.; Kierck, F.M.H.  
 Eur. J. Biochem. 255: 873-879, 1999  
 A-Title: Molecular properties of the desulfatase and its membrane bound and soluble  
 A-Reference number: S63489; S63490; S63491; S63492; S63493; S63494

A-Accession: S63493  
 A-Status: preliminary  
 A-Molecule type: protein  
 A-Residues: 18 (STE)  
 A-Accession: S63494  
 A-Status: preliminary  
 A-Molecule type: protein  
 A-Residues: 18 (STE)

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KG 9  
 II  
 BB 6 KG 7

RESULT 47  
 607745  
 endo-1,4-beta-D-glucanase (EC 3.2.1.2); 1: Rhodococcus sp. (Frag-041)  
 C-Species: Rhodococcus sp.  
 C-Date: 13-Feb-1994 #sequence\_revision 10-Jun-1994 #text\_change 17-Mar-1999  
 C-Accession: B43745

P-Title: Molecular cloning, characterization, and expression of the endo-1,4-beta-D-glucanase gene from the thermophilic bacterium Rhodococcus sp. (Frag-041)  
 J. Biol. Chem. 269: 7419-7425, 1994  
 A-Title: Activation of proteins for glycosylation and for glycolysis by endo-1,4-beta-D-glucanase  
 Biochem. Biophys. Res. Commun. 199: 104-107, 1994  
 A-Reference number: A45745; M01991; P01992; P01993; P01994  
 A-Accession: B43745

A-Status: preliminary  
 A-Molecule type: protein  
 A-Residues: 18 (STE)  
 C-Keywords: glycosylase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1:1P 11  
 II  
 BB 6 KG 7

RESULT 48  
 S21266  
 lectin, potato (fragment)  
 C-Species: Solanum tuberosum (potato)  
 C-Date: 29-Mar-1997 #sequence\_revision 01-Jun-1997 #text\_change 17-Mar-1999

C-Accession: S21268  
 R-Title: Purification and characterization of a potato lectin (Solanum tuberosum L.)  
 Biochem. Biophys. Res. Commun. 283: 414-421, 1992  
 A-Title: Lectin binding proteins of potato (Solanum tuberosum L.) - Lectin characterization

A-Reference number: S21268; M01992; P01993; P01994  
 A-Accession: S21268  
 A-Molecule type: protein  
 A-Residues: 18 (STE)  
 A-Status: preliminary  
 A-Export data: source: var. Foster Superior  
 C-Keywords: may be involved in defense mechanism of the plant

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1:1P 11  
 II  
 BB 6 KG 7

QY 1 AS 2  
 II  
 BB 2 AS 1

RESULT 49  
 A23967  
 leucopyrckinin, Madagascariensis  
 C-Species: Leucopyrckinin (Madagascariensis)  
 C-Date: 11-Mar-1998 #sequence\_revision 26-May-1994 #text\_change 11-Jul-1997  
 C-Accession: A23967  
 R-Title: Isolation, purification, and characterization of the insect neuroleptic leucopyrckinin from the Madagascar chrysalis  
 R-Accession: A23967  
 A-Reference number: A23967; M01997; M01998; M01999; M02000; M02001; M02002; M02003; M02004; M02005; M02006; M02007; M02008; M02009; M02010; M02011; M02012; M02013; M02014; M02015; M02016; M02017; M02018; M02019; M02020; M02021; M02022; M02023; M02024; M02025; M02026; M02027; M02028; M02029; M02030; M02031; M02032; M02033; M02034; M02035; M02036; M02037; M02038; M02039; M02040; M02041; M02042; M02043; M02044; M02045; M02046; M02047; M02048; M02049; M02050; M02051; M02052; M02053; M02054; M02055; M02056; M02057; M02058; M02059; M02060; M02061; M02062; M02063; M02064; M02065; M02066; M02067; M02068; M02069; M02070; M02071; M02072; M02073; M02074; M02075; M02076; M02077; M02078; M02079; M02080; M02081; M02082; M02083; M02084; M02085; M02086; M02087; M02088; M02089; M02090; M02091; M02092; M02093; M02094; M02095; M02096; M02097; M02098; M02099; M02100; M02101; M02102; M02103; M02104; M02105; M02106; M02107; M02108; M02109; M02110; M02111; M02112; M02113; M02114; M02115; M02116; M02117; M02118; 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A:Reference number: A28719; M01D:88425920; PM:14261994  
 A:Accession: A28719  
 A:Molecule type: protein  
 A:Residues: 18<BR>

Query Match 18.2%; Score 21; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 9 KP 10  
 lb 4 KP 5

## RESULT 48

148934

apelin-like protein A II - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision: 02 Jul 1996 #ext\_change: 06-Nov-1999

C:Accession: 148934

Riku, M., S. Wang, X. J. Hertog, J. H. H. Bui, M. D. Lakshish, K. Marzaki, Y. Kadeau, J. H.

Mamm Genome 5: 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones in the mouse genome by PCR.

A:Reference number: 148934; M01D:44190621; PM:14804349

A:Accession: 148934

A&gt;Status: Preliminary; translated from GenBank/EMBL.

A:Molecule type: DNA

A:Residues: 18&lt;RES&gt;

A:Reference: EMBL:025691; NID:347610; PDB: A28047; PDB: 441456

Query Match 18.2%; Score 21; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 4 AK 5  
 lb 0 AK 8

## RESULT 49

A54824

c-fos-like receptor 17 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 24-Apr-1995 #sequence\_revision: 27-Apr-1995 #ext\_change: 17-Mar-1999

C:Accession: A54824

Schmidt, A., J. Schmitt, J. Gledits, H. J. Axelsen, R.

Cell 78: 823-834, 1994

A:Title: Altered induction, regulation, and expression of

A:Reference number: A54824; M01D:94438604; PM:14804349

A:Accession: A54824

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 18&lt;RES&gt;

Query Match 18.2%; Score 21; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 6 KP 7  
 lb 4 KP 4

## RESULT 50

P10595

c-fos-like receptor beta chain V-loop region (100-266) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision: 17-Jul-1992 #ext\_change: 06-Mar-1993

C:Accession: P10595

Kobayashi, A.J.

J. Exp. Med. 174: 125-124, 1991

A:Title: Functional sequences of total c-fos-like receptor beta chains have low N-terminus.

A:Reference number: P10509; M01D:91277601; PM:14711139

GeneCore version 5.1.5  
Copyright (c) 1993 - 2002 Compugen Ltd

OM protein: proteolite search, using sw model

Run on: September 30, 2003, 11:06:54 Search file: 41-083: Sequents  
(2) local alignment  
42.49% Mutation cell updates/sec

Title: US-09-787-443-15

Perfect score: 11

Sequence: 1 ASQAARPKGR 11

Scoring table: 0.0000  
Gap: 60.0 / Gapext: 60.0

Search: 1107663 seqs, 150720533 residues

Word size: 3

Total number of hits satisfying chosen parameters: 278824

Minimum LB seq length: 8

Maximum DB seq length: 35

Post-processing: testing first 500 summaries

Database:

- A\_Geneseq\_19Jun03:\*
- 1: /SIDSI/gcadata/geneseq/geneseq-cell/AA1983.DAT
  - 2: /SIDSI/gcadata/geneseq/geneseq-cell/AA1983.DAT
  - 3: /SIDSI/gcadata/geneseq/geneseq-cell/AA1982.DAT
  - 4: /SIDSI/gcadata/geneseq/geneseq-cell/AA1983.DAT
  - 5: /SIDSI/gcadata/geneseq/geneseq-cell/AA1984.DAT
  - 6: /SIDSI/gcadata/geneseq/geneseq-cell/AA1985.DAT
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  - 22: /SIDSI/gcadata/geneseq/geneseq-cell/AA2001.DAT
  - 23: /SIDSI/gcadata/geneseq/geneseq-cell/AA2002.DAT
  - 24: /SIDSI/gcadata/geneseq/geneseq-cell/AA2003.DAT

Foot. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	DB	Id	Description
1	11	100.0	11	21	AA198543	NCAM Igl binding p
2	11	100.0	11	23	ABC69443	Human neural cell
3	5	45.5	9	17	AA198425	Human heat shock p
4	5	45.5	10	14	AA198419	Hepatitis C Ab det
5	5	45.5	13	16	AA198412	H.V. StV. REV prot
6	5	45.5	13	21	AA198436	RNA binding peptid
7	5	45.5	13	21	AA198439	RNA binding peptid
8	5	45.5	13	21	AA198442	RNA binding peptid
9	5	45.5	13	21	AA198445	RNA binding peptid

10	5	45.5	13	21	AA198448	RNA binding peptid
11	5	45.5	13	21	AA198451	RNA binding peptid
12	5	45.5	13	21	AA198454	RNA binding peptid
13	5	45.5	13	21	AA198459	RNA binding peptid
14	5	45.5	13	21	AA198462	RNA binding peptid
15	5	45.5	13	21	AA198464	RNA binding peptid
16	5	45.5	13	21	AA198467	RNA binding peptid
17	5	45.5	13	21	AA198470	RNA binding peptid
18	5	45.5	13	22	AAU06073	RNA binding peptid
19	5	45.5	13	22	AAU05076	RNA binding peptid
20	5	45.5	13	22	AAU05079	RNA binding peptid
21	5	45.5	13	24	AAU06082	RNA binding peptid
22	5	45.5	13	22	AAU06085	RNA binding peptid
23	5	45.5	13	22	AAU05088	RNA binding peptid
24	5	45.5	13	22	AAU05091	RNA binding peptid
25	5	45.5	13	22	AAU05096	RNA binding peptid
26	5	45.5	13	22	AAU06099	RNA binding peptid
27	5	45.5	13	22	AAU06101	RNA binding peptid
28	5	45.5	13	22	AAU06104	RNA binding peptid
29	5	45.5	13	22	AAU06107	RNA binding peptid
30	5	45.5	15	19	AA120948	Human presenilin 1
31	5	45.5	15	21	AA14221	HIV US4 gp120 clea
32	5	45.5	15	21	AA14223	Mutant HIV cleavag
33	4	36.4	8	16	AA121239	Farnesyl Synthetas
34	4	36.4	8	16	AA121240	Farnesyl Synthetas
35	4	36.4	8	19	AA19185	Epitope of the Hep
36	4	36.4	8	19	AA19185	peptide modulating
37	4	36.4	8	21	AA19185	HIV A02 super moti
38	4	36.4	8	22	AB12017	HIV B58 Super moti
39	4	36.4	8	22	AB12017	Synthetic peptide,
40	4	36.4	8	22	AB12017	Synthetic peptide,
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42	4	36.4	8	22	AB12017	Synthetic peptide,
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82	4	36.4	8	22	AB12017	Synthetic peptide,

83	4	36.4	8	22	AA80701	Human glandular ka	156	4	36.4	9	24	ABJ22670	162P1E6 cancer gen
84	4	36.4	8	24	AB87455	DNA repair protein	157	4	36.4	9	24	ABJ22671	162P1E6 cancer gen
85	4	36.4	8	24	AB87456	Transcription factor	158	4	36.4	9	24	ABJ22676	162P1E6 cancer gen
86	4	36.4	9	11	AA875609	Peptide antigen	159	4	36.4	9	24	ABJ22684	162P1E6 cancer gen
87	4	36.4	9	14	AA87776	Transactivation do	160	4	36.4	9	24	ABJ22688	162P1E6 cancer gen
88	4	36.4	9	14	AA87777	Antic herpes pept	161	4	36.4	9	24	ABJ22693	162P1E6 cancer gen
89	4	36.4	9	14	AA87778	Antic herpes pept	162	4	36.4	9	24	ABJ22694	162P1E6 cancer gen
90	4	36.4	9	14	AA87779	HIV gp120 epitope	163	4	36.4	9	24	ABJ22695	162P1E6 cancer gen
91	4	36.4	9	16	AA87780	Anti-cytotoxicity	164	4	36.4	9	24	ABJ22696	162P1E6 cancer gen
92	4	36.4	9	16	AA87781	Anti-cytotoxicity	165	4	36.4	9	24	ABJ22697	162P1E6 cancer gen
93	4	36.4	9	17	AA87782	Hydrophobic lipid p	166	4	36.4	9	24	ABJ22698	162P1E6 cancer gen
94	4	36.4	9	17	AA87783	Cell modulatory	167	4	36.4	9	24	ABJ22699	162P1E6 cancer gen
95	4	36.4	9	18	AA87784	Peptide R10, R10a	168	4	36.4	9	24	ABJ22700	162P1E6 cancer gen
96	4	36.4	9	18	AA87785	Peptide R12, R12a	169	4	36.4	9	24	ABJ22701	162P1E6 cancer gen
97	4	36.4	9	18	AA87786	Anti-cytotoxicity	170	4	36.4	9	24	ABJ22702	162P1E6 cancer gen
98	4	36.4	9	19	AA87787	Anti-cytotoxicity	171	4	36.4	9	24	ABJ22703	162P1E6 cancer gen
99	4	36.4	9	19	AA87788	Human stem factor	172	4	36.4	9	24	ABJ22704	162P1E6 cancer gen
100	4	36.4	9	21	AA87789	Cytotoxic T lympho	173	4	36.4	9	24	ABJ22705	162P1E6 cancer gen
101	4	36.4	9	21	AA87790	Myeloid protein CA	174	4	36.4	9	24	ABJ22706	162P1E6 cancer gen
102	4	36.4	9	21	AA87791	HIV-1 derived GP12	175	4	36.4	9	24	ABJ22707	162P1E6 cancer gen
103	4	36.4	9	21	AA87792	HIV-1 derived GP12	176	4	36.4	9	24	ABJ22708	162P1E6 cancer gen
104	4	36.4	9	22	AA87793	HIV A02 super moti	177	4	36.4	9	24	ABJ22709	162P1E6 cancer gen
105	4	36.4	9	22	AA87794	HIV A03 super moti	178	4	36.4	9	24	ABJ22710	162P1E6 cancer gen
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108	4	36.4	9	22	AA87797	HIV B58 super moti	181	4	36.4	10	15	AA861371	Bradykinin recepto
109	4	36.4	9	22	AA87798	HIV B62 super moti	182	4	36.4	10	15	AA861382	Bradykinin recepto
110	4	36.4	9	22	AA87799	HIV A03 motif env	183	4	36.4	10	15	AA861391	Bradykinin recepto
111	4	36.4	9	22	AA87800	HIV A03 motif env	184	4	36.4	10	15	AA861392	Bradykinin recepto
112	4	36.4	9	22	AA87801	HIV A03 motif env	185	4	36.4	10	15	AA861393	Bradykinin recepto
113	4	36.4	9	22	AA87802	Human MHC molecule	186	4	36.4	10	15	AA861394	Bradykinin recepto
114	4	36.4	9	22	AA87803	HIV-1 gp120, gp120	187	4	36.4	10	15	AA861395	Bradykinin recepto
115	4	36.4	9	22	AA87804	Neurotrophic disease	188	4	36.4	10	15	AA861396	Human leukocyte an
116	4	36.4	9	22	AA87805	Neurotrophic disease	189	4	36.4	10	15	AA861397	Human leukocyte an
117	4	36.4	9	22	AA87806	Neurotrophic disease	190	4	36.4	10	15	AA861398	Human leukocyte an
118	4	36.4	9	23	AA87807	HIV-1 tat peptide	191	4	36.4	10	15	AA861399	Human leukocyte an
119	4	36.4	9	23	AA87808	Human immunodefici	192	4	36.4	10	15	AA861400	Human MHC molecule
120	4	36.4	9	24	AA87809	Human immunodefici	193	4	36.4	10	15	AA861401	Human MHC molecule
121	4	36.4	9	24	AA87810	Human immunodefici	194	4	36.4	10	20	AA861402	Immunogenic peptide
122	4	36.4	9	24	AA87811	Human immunodefici	195	4	36.4	10	20	AA861403	Antigenic peptide
123	4	36.4	9	24	AA87812	Human immunodefici	196	4	36.4	10	22	ABP12423	HIV A02 super moti
124	4	36.4	9	24	AA87813	Human immunodefici	197	4	36.4	10	22	ABP12424	HIV A03 super moti
125	4	36.4	9	24	AA87814	Human immunodefici	198	4	36.4	10	22	ABP12425	HIV B07 super moti
126	4	36.4	9	24	AA87815	Human immunodefici	199	4	36.4	10	22	ABP12426	HIV B58 super moti
127	4	36.4	9	24	AA87816	Human immunodefici	200	4	36.4	10	22	ABP12427	HIV B62 super moti
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138	4	36.4	9	24	AA87827	Human immunodefici	211	4	36.4	10	22	ABP12438	HIV A03 motif env
139	4	36.4	9	24	AA87828	Human immunodefici	212	4	36.4	10	22	ABP12439	HIV A03 motif env
140	4	36.4	9	24	AA87829	Human immunodefici	213	4	36.4	10	22	ABP12440	HIV A03 motif env
141	4	36.4	9	24	AA87830	Human immunodefici	214	4	36.4	10	22	ABP12441	HIV A03 motif env
142	4	36.4	9	24	AA87831	Human immunodefici	215	4	36.4	10	22	ABP12442	HIV A03 motif env
143	4	36.4	9	24	AA87832	Human immunodefici	216	4	36.4	10	22	ABP12443	HIV A03 motif env
144	4	36.4	9	24	AA87833	Human immunodefici	217	4	36.4	10	22	ABP12444	HIV A03 motif env
145	4	36.4	9	24	AA87834	Human immunodefici	218	4	36.4	10	22	ABP12445	HIV A03 motif env
146	4	36.4	9	24	AA87835	Human immunodefici	219	4	36.4	10	22	ABP12446	HIV A03 motif env
147	4	36.4	9	24	AA87836	Human immunodefici	220	4	36.4	10	22	ABP12447	HIV A03 motif env
148	4	36.4	9	24	AA87837	Human immunodefici	221	4	36.4	10	22	ABP12448	HIV A03 motif env
149	4	36.4	9	24	AA87838	Human immunodefici	222	4	36.4	10	22	ABP12449	HIV A03 motif env
150	4	36.4	9	24	AA87839	Human immunodefici	223	4	36.4	10	22	ABP12450	HIV A03 motif env
151	4	36.4	9	24	AA87840	Human immunodefici	224	4	36.4	10	22	ABP12451	HIV A03 motif env
152	4	36.4	9	24	AA87841	Human immunodefici	225	4	36.4	10	22	ABP12452	HIV A03 motif env
153	4	36.4	9	24	AA87842	Human immunodefici	226	4	36.4	10	22	ABP12453	HIV A03 motif env
154	4	36.4	9	24	AA87843	Human immunodefici	227	4	36.4	10	22	ABP12454	HIV A03 motif env
155	4	36.4	9	24	AA87844	Human immunodefici	228	4	36.4	10	22	ABP12455	HIV A03 motif env



437	4	36.4	13	21	AAV69756	RNA binding peptide	448	14	19	AAW79191	Synthetic peptide
438	4	36.4	13	21	AAV69757	RNA binding peptide	449	14	19	AAW56527	Antigenic HIV-1 pe
439	4	36.4	13	21	AAV69758	RNA binding peptide	450	14	19	AAW56528	Antigenic HIV-1 pe
440	4	36.4	13	21	AAV69759	RNA binding peptide	451	14	19	AAW56529	Myelin basic prote
441	4	36.4	13	21	AAV69760	RNA binding peptide	452	14	19	AAW56530	Type-1 collagen al
442	4	36.4	13	21	AAV69761	RNA binding peptide	453	14	21	AAH13789	HIV-1 gp 120 C5 re
443	4	36.4	13	21	AAV69762	RNA binding peptide	454	14	21	AAH13790	HIV-1 gp 120 C5 re
444	4	36.4	13	21	AAV69763	RNA binding peptide	455	14	21	AAH14094	Carboxy terminal p
445	4	36.4	13	21	AAV69764	RNA binding peptide	456	14	21	AAH14904	Human AKAP 79 pept
446	4	36.4	13	21	AAV69765	RNA binding peptide	457	14	21	AAH14904	Mutant peptide: AKA
447	4	36.4	13	21	AAV69766	RNA binding peptide	458	14	21	AAV91675	Human secreted pro
448	4	36.4	13	21	AAV69767	RNA binding peptide	459	14	21	AAV54490	HBV ORF 45-derive
449	4	36.4	13	21	AAV69768	RNA binding peptide	460	14	22	AAV57213	Human peptide: 4488
450	4	36.4	13	22	AAV69769	RNA binding peptide	461	14	22	AAV54200	Human peptide: 4147
451	4	36.4	13	22	AAV69770	RNA binding peptide	462	14	22	AAV54227	Human peptide: 4150
452	4	36.4	13	22	AAV69771	RNA binding peptide	463	14	22	AAV54227	Human peptide: 4150
453	4	36.4	13	22	AAV69772	RNA binding peptide	464	14	22	AAV54227	Synthetic peptide
454	4	36.4	13	22	AAV69773	RNA binding peptide	465	14	22	AAV54227	Synthetic peptide
455	4	36.4	13	22	AAV69774	RNA binding peptide	466	14	22	AAV54227	Protein encoded by
456	4	36.4	13	22	AAV69775	RNA binding peptide	467	14	23	AAH57614	IGFBP-1 displacer
457	4	36.4	13	22	AAV69776	RNA binding peptide	468	14	23	AAH57615	IGFBP-1 displacer
458	4	36.4	13	22	AAV69777	RNA binding peptide	469	14	23	AAH74667	Transcription fact
459	4	36.4	13	22	AAV69778	RNA binding peptide	470	14	24	AAV59119	HBV cell overexp
460	4	36.4	13	22	AAV69779	RNA binding peptide	471	15	19	AAV90224	Antigenic peptide
461	4	36.4	13	22	AAV69780	RNA binding peptide	472	15	19	AAV90225	Antigenic peptide
462	4	36.4	13	22	AAV69781	RNA binding peptide	473	15	12	AAV13066	HIV500 fusion prot
463	4	36.4	13	22	AAV69782	RNA binding peptide	474	15	12	AAV13066	HIV-1 gp120
464	4	36.4	13	22	AAV69783	RNA binding peptide	475	15	16	AAH5193	HTLV-III envelope
465	4	36.4	13	22	AAV69784	RNA binding peptide	476	15	16	AAH5193	HTLV-III envelope
466	4	36.4	13	22	AAV69785	RNA binding peptide	477	15	16	AAH5193	BPI-16, BPI domain
467	4	36.4	13	22	AAV69786	RNA binding peptide	478	15	17	AAV96884	Murine streptolisin-1
468	4	36.4	13	22	AAV69787	RNA binding peptide	479	15	17	AAV96885	Neisseria gonorrhoe
469	4	36.4	13	22	AAV69788	RNA binding peptide	480	15	17	AAV96886	Neisseria gonorrhoe
470	4	36.4	13	22	AAV69789	RNA binding peptide	481	15	18	AAV19332	SP-22 region of HI
471	4	36.4	13	22	AAV69790	RNA binding peptide	482	15	19	AAV72870	Polymerase epsilon
472	4	36.4	13	22	AAV69791	RNA binding peptide	483	15	19	AAV72870	HIV gp120 envelope
473	4	36.4	13	22	AAV69792	RNA binding peptide	484	15	20	AAV17986	Human heparanase p
474	4	36.4	13	22	AAV69793	RNA binding peptide	485	15	21	AAH14215	HIV SF162 gp120 cl
475	4	36.4	13	22	AAV69794	RNA binding peptide	486	15	21	AAH14220	Mutant HIV cleavag
476	4	36.4	13	22	AAV69795	RNA binding peptide	487	15	22	AAV24455	HIV DR super motif
477	4	36.4	13	22	AAV69796	RNA binding peptide	488	15	22	AAV24455	HIV DR super motif
478	4	36.4	13	22	AAV69797	RNA binding peptide	489	15	22	AAV24455	HIV DR super motif
479	4	36.4	13	22	AAV69798	RNA binding peptide	490	15	22	AAV24455	HIV DR super motif
480	4	36.4	13	22	AAV69799	RNA binding peptide	491	15	23	AAH24527	DNA repair protein
481	4	36.4	13	22	AAV69800	RNA binding peptide	492	15	23	AAH24527	DNA repair protein
482	4	36.4	13	22	AAV69801	RNA binding peptide	493	15	24	AAH24527	DNA repair protein
483	4	36.4	13	22	AAV69802	RNA binding peptide	494	15	24	AAH24527	DNA repair protein
484	4	36.4	13	22	AAV69803	RNA binding peptide	495	15	24	AAH24527	DNA repair protein
485	4	36.4	13	22	AAV69804	RNA binding peptide	496	15	24	AAH24527	DNA repair protein
486	4	36.4	13	22	AAV69805	RNA binding peptide	497	15	24	AAH24527	DNA repair protein
487	4	36.4	13	22	AAV69806	RNA binding peptide	498	15	24	AAH24527	DNA repair protein
488	4	36.4	13	22	AAV69807	RNA binding peptide	499	15	24	AAH24527	DNA repair protein
489	4	36.4	13	22	AAV69808	RNA binding peptide	500	15	24	AAH24527	DNA repair protein
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491	4	36.4	13	22	AAV69810	RNA binding peptide	502	15	24	AAH24527	DNA repair protein
492	4	36.4	13	22	AAV69811	RNA binding peptide	503	15	24	AAH24527	DNA repair protein
493	4	36.4	13	22	AAV69812	RNA binding peptide	504	15	24	AAH24527	DNA repair protein
494	4	36.4	13	22	AAV69813	RNA binding peptide	505	15	24	AAH24527	DNA repair protein
495	4	36.4	13	22	AAV69814	RNA binding peptide	506	15	24	AAH24527	DNA repair protein
496	4	36.4	13	22	AAV69815	RNA binding peptide	507	15	24	AAH24527	DNA repair protein
497	4	36.4	13	22	AAV69816	RNA binding peptide	508	15	24	AAH24527	DNA repair protein
498	4	36.4	13	22	AAV69817	RNA binding peptide	509	15	24	AAH24527	DNA repair protein
499	4	36.4	13	22	AAV69818	RNA binding peptide	510	15	24	AAH24527	DNA repair protein
500	4	36.4	13	22	AAV69819	RNA binding peptide	511	15	24	AAH24527	DNA repair protein
501	4	36.4	13	22	AAV69820	RNA binding peptide	512	15	24	AAH24527	DNA repair protein
502	4	36.4	13	22	AAV69821	RNA binding peptide	513	15	24	AAH24527	DNA repair protein
503	4	36.4	13	22	AAV69822	RNA binding peptide	514	15	24	AAH24527	DNA repair protein
504	4	36.4	13	22	AAV69823	RNA binding peptide	515	15	24	AAH24527	DNA repair protein
505	4	36.4	13	22	AAV69824	RNA binding peptide	516	15	24	AAH24527	DNA repair protein
506	4	36.4	13	22	AAV69825	RNA binding peptide	517	15	24	AAH24527	DNA repair protein
507	4	36.4	13	22	AAV69826	RNA binding peptide	518	15	24	AAH24527	DNA repair protein
508	4	36.4	13	22	AAV69827	RNA binding peptide	519	15	24	AAH24527	DNA repair protein
509	4	36.4	13	22	AAV69828	RNA binding peptide	520	15	24	AAH24527	DNA repair protein
510	4	36.4	13	22	AAV69829	RNA binding peptide	521	15	24	AAH24527	DNA repair protein
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516	4	36.4	13	22	AAV69835	RNA binding peptide	527	15	24	AAH24527	DNA repair protein
517	4	36.4	13	22	AAV69836	RNA binding peptide	528	15	24	AAH24527	DNA repair protein
518	4	36.4	13	22	AAV69837	RNA binding peptide	529	15	24	AAH24527	DNA repair protein
519	4	36.4	13	22	AAV69838	RNA binding peptide	530	15	24	AAH24527	DNA repair protein
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521	4	36.4	13	22	AAV69840	RNA binding peptide	532	15	24	AAH24527	DNA repair protein
522	4	36.4	13	22	AAV69841	RNA binding peptide	533	15	24	AAH24527	DNA repair protein
523	4	36.4	13	22	AAV69842	RNA binding peptide	534	15	24	AAH24527	DNA repair protein
524	4	36.4	13	22	AAV69843	RNA binding peptide	535	15	24	AAH24527	DNA repair protein
525	4	36.4	13	22	AAV69844	RNA binding peptide	536	15	24	AAH24527	DNA repair protein
526	4	36.4	13	22	AAV69845	RNA binding peptide	537	15	24	AAH24527	DNA repair protein
527	4	36.4	13	22	AAV69846	RNA binding peptide	538	15	24	AAH24527	DNA repair protein
528	4	36.4	13	22	AAV69847	RNA binding peptide	539	15	24	AAH24527	DNA repair protein
529	4	36.4	13	22	AAV69848	RNA binding peptide	540	15	24	AAH24527	DNA repair protein
530	4	36.4	13	22	AAV69849	RNA binding peptide	541	15	24	AAH24527	DNA repair protein
531	4	36.4	13	22	AAV69850	RNA binding peptide	542	15	24	AAH24527	DNA repair protein
532	4	36.4	13	22	AAV69851	RNA binding peptide	543	15	24	AAH24527	DNA repair protein
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536	4	36.4	13	22	AAV69855	RNA binding peptide	547	15	24	AAH24527	DNA repair protein
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539	4	36.4	13	22	AAV69858	RNA binding peptide	550	15	24	AAH24527	DNA repair protein
540	4	36.4	13	22	AAV69859	RNA binding peptide	551	15	24	AAH24527	DNA repair protein
541	4	36.4	13	22	AAV69860	RNA binding peptide	552	15	24	AAH24527	DNA repair protein
542	4	36.4	13	22	AAV69861	RNA binding peptide	553	15	24	AAH24527	DNA repair protein
543	4	36.4	13	22	AAV69862	RNA binding peptide	554	15	24	AAH24527	DNA repair protein
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548	4	36.4	13	22	AAV69867	RNA binding peptide	559	15	24	AAH24527	DNA repair protein
549	4	36.4	13	22	AAV69868	RNA binding peptide	560	15	24	AAH24527	DNA repair protein
550	4	36.4	13	22	AAV69869	RNA binding peptide	561	15	24	AAH24527	DNA repair protein
551	4	36.4	13	22	AAV69870	RNA binding peptide	562	15	24	AAH24527	DNA repair protein
552	4	36.4	13	22	AAV69871	RNA binding peptide	563	15	24	AAH24527	DNA repair protein
553	4	36.4	13	22							





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XX RESU11.4
XX AAK96624
XX 13 AAK96624 standard, peptide: 5 AA.
XX AC AAK96624
XX 29 NOV-1996 (first entry)
XX DE Human heat shock protein 47, homologous to Nucleosome core particle
XX 1A4 protease precursor: 1997 bacterial polyprotein, anti-hepatitis
XX viral infection; rheumatoid arthritis; AIDS; monoclonal antibody;
XX human heat shock protein 47, Hsp47; Nucleosome core particle; MS.1
XX amino sulfonates.
XX Key Location/Qualifiers
XX Ref 1
XX /note= "homologous to the sequence AKA526AKA in
XX Neisseria meningitidis serotype 4"
XX W09609155 AK5
XX 26 MAR-1996
XX 21 SEP-1996 95960-EP03726
XX 21 SEP-1996 945B 443768
XX (PLAN ) MAX PLANCK GES FÖRDERUNG WISSENSCHAFTLICH
XX Beck S.G., Jase J., Lorenzen DK., Meyer T., Wetzelsberger KB
XX Pöschner J., Weick J
XX WPI: 1996-186456/19
XX Requirements for treating with immune of viral diseases - vaccine
XX substances interfering with bacterial polyprotein function
XX Claim (2): Fig 4: 117pp: German
XX the present sequence from human heat shock protein hsp47 has been used
XX to a cleavage product from the car-terminal domain of the precursor of
XX hsp47 protease polyprotein (1997) of Neisseria meningitidis strain MS1.
XX The Neisseria hsp has been applied in rheumatoid arthritis and
XX other autoimmune diseases. The polyprotein also activates proteinases
XX and/or HIV. Substances which interfere with the function of hsp
XX from Neisseria will be used in the treatment of autoimmune diseases
XX and viral infections. Further, a peptide of the hsp47 sequence
XX sequences, whether from Neisseria or from other sources, is claimed.
XX Sequence 9 AA:
XX Query Match 45.5% Score 5: DB 14: Length 10:
XX Best Local Similarity 100.0% Pred. No. 82:
XX Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
XX QY 1 ASQAK 5
XX DE 4 ASQAK 8
XX RESU11.4
XX AAK94419
XX 13 AAK94419 standard, peptide: 10 AA.
XX AC AAK94419
XX 25 MAR-2003 (updated)
XX 05-AUG-1993 (first entry)
XX Hepatitis C Ab detection peptide #3.

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XX Test reagent: detection; antibody; hepatitis C; virus; HCV; epitope;
XX structural region; diagnosis; SS.
XX Synthetic
XX W09407488 AK1
XX 15-APR-1993
XX 02-OCT-1992 92W03JP01276
XX 02-OCT-1991 91JP 0255524
XX 26 MAR-1992 92J1-0608695
XX (EIKEN ) EIKEN KAZAKU KK
XX (TANA ) TANAKA SEIYAKU KK
XX (OSAE ) UNIV OSAKA
XX Ishibashi K., Ito M., Shibutani T., Takamizawa A., Yoshida I.
XX WPI: 1993-114624/16.
XX Reagent for detecting antibodies to hepatitis C virus - comprises
XX peptide(s) with the same sequence as an epitope of an HCV
XX structural region
XX Disclosure: Page 42: 51pp: Japanese.
XX The sequences given in AAK4417 25 are peptides which can be used in a
XX test reagent for the detection of antibodies against hepatitis C.
XX The peptides represent epitopes of an HCV structural region and they
XX react specifically with antibodies against the HCV structural region.
XX Detection is sensitive and accurate and allows diagnosis of the
XX infection at a very early stage.
XX (updated on 25 MAR-2003 to correct PN field.)
XX Sequence 10 AA:
XX Query Match 45.5% Score 5: DB 14: Length 10:
XX Best Local Similarity 100.0% Pred. No. 82:
XX Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
XX QY 7 RKQPR 11
XX 1 RKQPR 5
XX RESU11.4
XX AAW21512
XX 13 AAW21512 standard, peptide: 14 AA.
XX AC AAW21512
XX 30-JUN-1997 (first entry)
XX HIV, HIV, HIV protein derived signal oligopeptide #14.
XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; HIV;
XX competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
XX charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
XX hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
XX gonadotropin precursor; plasminogen activator inhibitor 2; prorenin;
XX Alzheimer amyloid A4; corticotropin releasing factor binding protein;
XX apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMV5;
XX herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
XX treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
XX fibroblast MMP1; schistosoma elastase precursor; schistosomin;
XX hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX Human immunodeficiency virus.
XX Simian immunodeficiency virus.

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XX W0996425-A2.  
 XX  
 XX 24 JUN 1999: 99W03P01741.  
 XX  
 XX 12 JAN 1995: 99W0-0S00575.  
 XX  
 XX 14 JAN 1994: 99W0-018224W.  
 XX  
 XX (RATER) RATER M.  
 XX  
 XX RATER M.  
 XX  
 XX WPI: 1999-253953/34.  
 XX  
 XX Identifying signal oligopeptides (S) in protein sequence (S) is shown as  
 XX regions of max. hydrophobicity, used in modulation of cell adhesion.  
 XX between protein(s)  
 XX  
 XX \*Page 5: Page 74: 88pp: English.  
 XX  
 XX The sequences given in AAW21201-500 represent hydrophobic signal oligo-  
 XX peptides. These signal oligopeptides are analysed on the surface  
 XX of the protein and are represented by the hydrophobicity maxima of  
 XX the protein. These peptides are enriched in charged amino acids  
 XX associated with neutral spacer amino acids. The specific signal  
 XX character of these oligopeptides is determined by a characteristic  
 XX combination of conformation and charge within the signal sequence.  
 XX These oligopeptides may be used as vaccines in the treatment of  
 XX local disease, as competitive inhibitors to prevent or reduce the  
 XX metabolic action or interaction of a selected protein by blocking  
 XX its specific signal sequences, or as treatment reagents to block  
 XX as feedback regulators to reduce synthesis rate of a selected protein.  
 XX These peptides may be modified by omitting one or more amino acids at  
 XX the N- and/or C-terminal, by substitution of one or more amino acids  
 XX without consideration of charge and polarity, by substitution and/or  
 XX more amino acids with amino acid residues with similar chemical and/or  
 XX polarity, by omitting one or more amino acids or a combination of these.  
 XX  
 XX Sequence 13 AA:  
 XX  
 XX Query Match: 45-58; Score 5; 2H 21; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 1c-02;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 6 KKKK 9  
 XX 111  
 XX 1 KKKK 6  
 XX  
 XX RESUME 2  
 XX AAY9749  
 XX AAY9749 standard; peptide: 13 AA.  
 XX  
 XX AC AAY9749;  
 XX  
 XX DE 11 APR 2000 (first entry)  
 XX  
 XX RNA binding peptide #5.  
 XX  
 XX DE RNA binding peptide #6.  
 XX  
 XX KW Antiviral; antibacterial; antitumoral; anticancer; detection; TAK: RRE;  
 XX KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 XX KW autoimmune disease; trans-activation regulatory region.  
 XX  
 XX SS Synthesis.  
 XX  
 XX FH Key Location/Qualifiers  
 XX Modified site 1 /note= "conjugated to DAPCYL  
 XX (4-(((dimethylamino)phenyl)azo)benzoic acid);"  
 XX  
 XX FT Modified-site 13 /note= "C-terminal amide"  
 XX  
 XX PN W0996425-A2.  
 XX  
 XX PO 14 JAN 1999.  
 XX  
 XX W0996425-A2.

XX 16 DEC 1999.  
 XX  
 XX 04 JUN 1999: 99W03P01741.  
 XX  
 XX 05 JUN 1998: 99W03-012175.  
 XX  
 XX 02 MAR 1999: 99W03-000479C.  
 XX  
 XX (RIDER) RIDE JARDETS LTD  
 XX  
 XX RIDE J. Present: CH.  
 XX  
 XX WPI: 2000-097545/06.  
 XX  
 XX Identifying compounds that bind to target RNA, potentially useful for  
 XX treating infections, tumors and autoimmune diseases -  
 XX  
 XX Examples: Page 50; 82pp; English.  
 XX  
 XX The invention relates to a method of determining if a compound binds to  
 XX a target RNA by treating a test compound with a reporter (R) labelled  
 XX with a donor or acceptor group and labelled target RNA, labelled with  
 XX the complementary donor or acceptor group, and measuring the  
 XX fluorescence from fluorescent groups associated with a compound; target  
 XX RNA complex in presence of the test compound and comparing the result  
 XX with a standard. This peptide represents a reporter molecule isolated  
 XX from a combinatorial peptide library having the generic sequence  
 XX AAY9749. Detection of the complex is by fluorescence resonance energy  
 XX transfer (FRET). The method is used to identify compounds that interfere  
 XX with interaction between the target RNA and ligands or proteins.  
 XX Compounds that are identified are potentially useful for treating  
 XX infections (viral, bacterial or fungal), cancer and autoimmune diseases.  
 XX The compounds are preferably directed to the TAR and RRE regions of human  
 XX immunodeficiency virus RNA and inhibit viral replication.  
 XX  
 XX Sequence 13 AA:  
 XX  
 XX Query Match: 45-58; Score 5; 2H 21; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 1c-02;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 6 KKKK 9  
 XX 111  
 XX 1 KKKK 11  
 XX  
 XX RESUME 2  
 XX AAY9749  
 XX AAY9749 standard; peptide: 13 AA.  
 XX  
 XX AC AAY9749;  
 XX  
 XX DE 11 APR 2000 (first entry)  
 XX  
 XX RNA binding peptide #6.  
 XX  
 XX KW Antiviral; antibacterial; antitumoral; anticancer; detection; TAK: RRE;  
 XX KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 XX KW autoimmune disease; trans-activation regulatory region.  
 XX  
 XX SS Synthesis.  
 XX  
 XX FH Key Location/Qualifiers  
 XX Modified site 1 /note= "conjugated to DAPCYL  
 XX (4-(((dimethylamino)phenyl)azo)benzoic acid);"  
 XX  
 XX FT Modified-site 13 /note= "C-terminal amide"  
 XX  
 XX PN W0996425-A2.  
 XX  
 XX PO 14 JAN 1999.  
 XX  
 XX W0996425-A2.



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XX      Karn J., Prescott CD;
XX      WPI: 2000-097545/08;
XX      Identifying compounds that bind to target RNA, potentially useful for
XX      treating infections, tumors and autoimmune diseases;
XX      Examples: Page 50, 62pp; English;
XX      The invention relates to a method of determining if a compound binds to
XX      a target RNA by treating a test compound with a reporter (R) labelled
XX      with a donor of acceptor group and labelled target RNA, labelled with
XX      the complementary donor of acceptor group, and measuring the
XX      fluorescence from fluorescent groups associated with a compound-target
XX      RNA complex in presence of the test compound and comparing the result
XX      with a standard. This peptide represents a reporter molecule isolated
XX      from a combinatorial peptide library having the generic sequence
XX      AAY6974. Detection of the complex is by fluorescence resonance energy
XX      transfer (FRET). The method is used to identify compounds that interfere
XX      with interaction between the target RNA and ligands or proteins.
XX      Compounds that are identified are potentially useful for treating
XX      infections (viral, bacterial or fungal), cancer and autoimmune diseases.
XX      The compounds are preferably directed to the TAR and RRE regions of human
XX      immunodeficiency virus RNA and inhibit viral replication.
XX      Sequence: 15 AA;
XX      Query Match: 45.5%; Score 5; DB 21; Length 15;
XX      Best Local Similarity: 100.0%; Pred. No. 1e+02;
XX      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      5 KKKK 9
XX      7 KKKK 11
XX      11 APR 2000 (first entry)
XX      RNA binding peptide #12;
XX      Activated, antibacterial, antifungal, anticancer; detection: TAR, RRE;
XX      Fluorescence resonance energy transfer; tat; HIV-1; Key response element;
XX      autoimmune disease; trans activation regulatory region.
XX      Synthesis;
XX      Key: Location/Qualifiers
XX      Modified site 1 /note: "conjugated to DABCYL
XX      (4-(((dimethylamino)phenyl)azo)benzoic acid)"
XX      Modified site 13 /note: "C-terminal amide"
XX      W5994625-AZ;
XX      16 DEC 1999;
XX      04 JUN 1999; 99WO-GB01761;
XX      05 JUN 1998; 98GB-0012196;
XX      02 MAR 1999; 99GB-0004790;
XX      (RIBO-) RIBOTARGETS LTD;
XX      Karn J., Prescott CD;
XX      WPI: 2000-097545/08;
XX      Identifying compounds that bind to target RNA, potentially useful for

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DB      WPI: 2000-097545/08;
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XX      treating infections, tumors and autoimmune diseases;
XX      Examples: Page 50, 62pp; English;
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XX      with a donor of acceptor group and labelled target RNA, labelled with
XX      the complementary donor of acceptor group, and measuring the
XX      fluorescence from fluorescent groups associated with a compound-target
XX      RNA complex in presence of the test compound and comparing the result
XX      with a standard. This peptide represents a reporter molecule isolated
XX      from a combinatorial peptide library having the generic sequence
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XX      transfer (FRET). The method is used to identify compounds that interfere
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XX      Compounds that are identified are potentially useful for treating
XX      infections (viral, bacterial or fungal), cancer and autoimmune diseases.
XX      The compounds are preferably directed to the TAR and RRE regions of human
XX      immunodeficiency virus RNA and inhibit viral replication.
XX      Sequence: 15 AA;
XX      Query Match: 45.5%; Score 5; DB 21; Length 15;
XX      Best Local Similarity: 100.0%; Pred. No. 1e+02;
XX      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      5 KKKK 9
XX      7 KKKK 11
XX      11 APR 2000 (first entry)
XX      RNA binding peptide #20;
XX      Activated, antibacterial, antifungal, anticancer; detection: TAR, RRE;
XX      Fluorescence resonance energy transfer; tat; HIV-1; Key response element;
XX      autoimmune disease; trans activation regulatory region.
XX      Synthesis;
XX      Key: Location/Qualifiers
XX      Modified site 1 /note: "conjugated to DABCYL
XX      (4-(((dimethylamino)phenyl)azo)benzoic acid)"
XX      Modified site 13 /note: "C-terminal amide"
XX      W5994625-AZ;
XX      16 DEC 1999;
XX      04 JUN 1999; 99WO-GB01761;
XX      05 JUN 1998; 98GB-0012196;
XX      02 MAR 1999; 99GB-0004790;
XX      (RIBO-) RIBOTARGETS LTD;
XX      Karn J., Prescott CD;
XX      WPI: 2000-097545/08;
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```

XX Treating infections, tumors and autoimmune diseases

PS Examples, Page 50: 82pp: English.

XX The invention relates to a method of determining if a compound binds to

CC a target RNA by treating a test compound with a reporter (R) labelled

CC with a donor or acceptor group and labelled target RNA, labelled with

CC the complementary donor or acceptor group, and measuring the

CC fluorescence from fluorescent dyes associated with a compound:target

CC RNA complex in presence of the test compound and comparing the result

CC with a standard. This peptide represents a reporter molecule isolated

CC from a combinatorial peptide library having the generic sequence

CC AAY69734. Detection of the complex is by fluorescence resonance energy

CC transfer (FRET). The method is used to identify compounds that interfere

CC with interaction between the target RNA and ligands or proteins.

CC Compounds that are identified are potentially useful for treating

CC infections (viral, bacterial or fungal), cancer and autoimmune diseases.

CC The compounds are preferably directed to the TAR and KEE regions of human

CC immunodeficiency virus RNA and inhibit viral replication.

XX Sequence: 13 AA:

SQ Query Match: 45.5%, Score 53, DB 21, Length 13;

Best Local Similarity: 100.0%, Pred. No. 1c+02;

Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 KRKKG 9

QD 7 KRKKG 11

RESUL: 12

AAAY69734

CC AAAY69734 standard; peptide: 13 AA

XX AAAY69734:

XX 11-APS 2006 (first entry)

XX RNA binding peptide #23.

XX Antiviral, antibacterial, antifungal, anticancer; detection; TAR, KEE;

KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;

KW autoimmune disease; trans-activation regulatory region.

XX Synthetic:

XX Key Location/Qualifiers

XX Modified-site 1

XX Modified-site 13 (4-((diethylamino)phenyl)azo)benzoic acid)\*

XX Modified-site 13 (4-((diethylamino)phenyl)azo)benzoic acid)\*

XX W09064625 A2

XX 16 Dec 1999

XX 04 JUN 1999; 99W03001761

XX 05 JUN 1998; 98G00012196

XX 02 MAR 1999; 99GB-0004790

XX (K1B6- ) K1B6-TARGETS LTD.

XX Karin J. Prescott CD;

XX WFL: 2000-097545/08

XX Identifying compounds that bind to target RNA, potentially useful for

XX Treating infections, tumors and autoimmune diseases

XX Examples, Page 50: 82pp: English.

XX The invention relates to a method of determining if a compound binds to

CC a target RNA by treating a test compound with a reporter (R) labelled

XX The invention relates to a method of determining if a compound binds to

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CC the complementary donor or acceptor group, and measuring the

CC fluorescence from fluorescent dyes associated with a compound:target

CC RNA complex in presence of the test compound and comparing the result

CC with a standard. This peptide represents a reporter molecule isolated

CC from a combinatorial peptide library having the generic sequence

CC AAY69734. Detection of the complex is by fluorescence resonance energy

CC transfer (FRET). The method is used to identify compounds that interfere

CC with interaction between the target RNA and ligands or proteins.

CC Compounds that are identified are potentially useful for treating

CC infections (viral, bacterial or fungal), cancer and autoimmune diseases.

CC The compounds are preferably directed to the TAR and KEE regions of human

CC immunodeficiency virus RNA and inhibit viral replication.

XX Sequence: 13 AA:

SQ Query Match: 45.5%, Score 53, DB 21, Length 13;

Best Local Similarity: 100.0%, Pred. No. 1c+02;

Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 KRKKG 9

QD 7 KRKKG 11

RESUL: 14

AAAY69734

CC AAAY69734 standard; peptide: 13 AA

XX AAAY69734:

XX 11-APS 2006 (first entry)

XX RNA binding peptide #23.

XX Antiviral, antibacterial, antifungal, anticancer; detection; TAR, KEE;

KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;

KW autoimmune disease; trans-activation regulatory region.

XX Synthetic:

XX Key Location/Qualifiers

XX Modified-site 1

XX Modified-site 13 (4-((diethylamino)phenyl)azo)benzoic acid)\*

XX Modified-site 13 (4-((diethylamino)phenyl)azo)benzoic acid)\*

XX W09064625 A2

XX 16 Dec 1999

XX 04 JUN 1999; 99W03001761

XX 05 JUN 1998; 98G00012196

XX 02 MAR 1999; 99GB-0004790

XX (K1B6- ) K1B6-TARGETS LTD.

XX Karin J. Prescott CD;

XX WFL: 2000-097545/08

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XX The invention relates to a method of determining if a compound binds to

CC a target RNA by treating a test compound with a reporter (R) labelled

CC with a donor or acceptor group and labeled target RNA, labelled with  
 CC the complementary donor or acceptor group, and measuring the  
 CC fluorescence from fluorescent groups associated with a compound:target  
 CC RNA complex in presence of the test compound and comparing the result  
 CC with a standard. This peptide represents a reporter molecule isolated  
 CC from a combinatorial peptide library having the generic sequence  
 CC AAY69733. Detection of the complex is by fluorescence resonance energy  
 CC transfer (FRET). The method is used to identify compounds that interfere  
 CC with interaction between the target RNA and ligands or proteins.  
 CC Compounds that are identified are potentially useful for treating  
 CC infections (viral, bacterial or fungal), cancer and autoimmune diseases.  
 CC The compounds are preferably directed to the TAR and RRE regions of human  
 CC immunodeficiency virus RNA and inhibit viral replication.

XX Sequence 13 AA;  
 SQ Query Match 45.5%; Score 5; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e-02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 5 KRKKG 9  
 UB 7 KRKKG 11

RESULT 14  
 AAY69762  
 ID AAY69762 standard; peptide: 13 AA.

XX AC AAY69762;  
 XX DT 11 APR 2000 (first entry)  
 XX DE RNA binding peptide #43.  
 XX KW Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;  
 XX KW fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 XX KW autoimmune disease; trans-activation regulatory region.  
 XX OS Synthetic.

XX Key Location/Qualifiers  
 XX Modified-site 1 /note "conjugated to DABCYL  
 XX (4-(((dimethylamino)phenyl)azo)benzoic acid)"  
 XX Modified-site 13 /note "C-terminal amide"

XX Modified-site 13 /note "C-terminal amide"  
 XX W0964625-A2  
 XX 16-DEC-1999;  
 XX 04-JUN 1999; 99WG-GB01761.  
 XX 05-JUN 1998; 98GB-0012196.  
 XX 02-MAR-1999; 99GB-0004790.  
 XX (RIBO-) RIBOTARGETS LTD.

XX Kato J., Prescott CD;  
 XX WPI: 2000-097545/08.

XX Identifying compounds that bind to target RNA, potentially useful for  
 XX treating infections, tumors and autoimmune diseases

XX Examples: Page 50; 82pp; English.

XX The invention relates to a method of determining if a compound binds to  
 CC a target RNA by treating a test compound with a reporter (R) labelled  
 CC with a donor or acceptor group and labeled target RNA, labelled with  
 CC the complementary donor or acceptor group, and measuring the  
 CC fluorescence from fluorescent groups associated with a compound:target  
 CC RNA complex in presence of the test compound and comparing the result  
 CC with a standard. This peptide represents a reporter molecule isolated  
 CC from a combinatorial peptide library having the generic sequence

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 CC with a standard. This peptide represents a reporter molecule isolated  
 CC from a combinatorial peptide library having the generic sequence  
 CC AAY69733. Detection of the complex is by fluorescence resonance energy  
 CC transfer (FRET). The method is used to identify compounds that interfere  
 CC with interaction between the target RNA and ligands or proteins.  
 CC Compounds that are identified are potentially useful for treating  
 CC infections (viral, bacterial or fungal), cancer and autoimmune diseases.  
 CC The compounds are preferably directed to the TAR and RRE regions of human  
 CC immunodeficiency virus RNA and inhibit viral replication.

XX Sequence 13 AA;  
 SQ Query Match 45.5%; Score 5; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e-02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 5 KRKKG 9  
 UB 7 KRKKG 11

RESULT 15  
 AAY69764  
 ID AAY69764 standard; peptide: 13 AA.

XX AC AAY69764;  
 XX DT 11 APR 2000 (first entry)  
 XX DE RNA binding peptide #43.  
 XX KW Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;  
 XX KW fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 XX KW autoimmune disease; trans-activation regulatory region.  
 XX OS Synthetic.

XX Key Location/Qualifiers  
 XX Modified-site 1 /note "conjugated to DABCYL  
 XX (4-(((dimethylamino)phenyl)azo)benzoic acid)"  
 XX Modified-site 13 /note "C-terminal amide"

XX Modified-site 13 /note "C-terminal amide"  
 XX W0964625-A2  
 XX 16-DEC-1999;  
 XX 04-JUN 1999; 99WG-GB01761.  
 XX 05-JUN 1998; 98GB-0012196.  
 XX 02-MAR-1999; 99GB-0004790.  
 XX (RIBO-) RIBOTARGETS LTD.  
 XX Kato J., Prescott CD;  
 XX WPI: 2000-097545/08.

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 XX treating infections, tumors and autoimmune diseases

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 CC a target RNA by treating a test compound with a reporter (R) labelled  
 CC with a donor or acceptor group and labeled target RNA, labelled with  
 CC the complementary donor or acceptor group, and measuring the  
 CC fluorescence from fluorescent groups associated with a compound:target  
 CC RNA complex in presence of the test compound and comparing the result  
 CC with a standard. This peptide represents a reporter molecule isolated  
 CC from a combinatorial peptide library having the generic sequence

CC AAY6733... detection of the complex is by fluorescence resonance energy transfer (FRET). The method is used to identify compounds that interfere with interaction between the target RNA and ligands of proteins.

CC The compounds are preferably directed to the TAR and RRE regions of human infections (viral, bacterial or fungal), cancer and autoimmune diseases.

CC The compounds are preferably directed to the TAR and RRE regions of human immunodeficiency virus RNA and inhibit viral replication.

XX Sequence 13 AA:

Query Match 45.5% Score 57 DB 211 Length 13

Best Local Similarity 100.0% Pred. No. 1002

Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Q7 5 KRKK 9

DE 7 KRKK 11

RESID 17

AAAY6770

10 AAY6770 standard; peptide: 13 AA.

XX AAY6770:

AC

XX 11-APR 2000 (first entry)

XX RNA binding peptide #49.

XX Antiviral; antibacterial; antitumor; anticancer; detection: TAR; RRE;

XX fluorescence resonance energy transfer; tat; HIV-1; Rev response element;

XX autoimmune disease; trans-activation regulatory region.

XX Synthetic.

XX Key Location/qualifiers

XX Modified site 1

XX Modified site 13 /note- "conjugated to DABCYL (4-(((dimethylamino)phenyl)azo)benzoic acid)"

XX Modified site 13 /note- "C-terminal amide"

XX W09954625-A2.

XX 16-DEC-1999.

XX 04-JUN-1999; 99W0-0801761.

XX 05-JUN-1998; 99GB-0012196.

XX 02-MAR-1999; 99GB-0004790.

XX (RIBO) REBOTARGETS LTD.

XX Karin J. Prescott CD;

XX WPI: 2000-097545/08.

XX Identifying compounds that bind to target RNA, potentially useful for treating infections, tumors and autoimmune diseases.

XX Examples: Page 50; 82pp; English.

XX The invention relates to a method of determining if a compound binds to a target RNA by treating a test compound with a reporter (R) labelled with a donor or acceptor group and labelled target RNA, labelled with the complementary donor or acceptor group, and measuring the fluorescence from fluorescent groups associated with a compound-target RNA complex in presence of the test compound and comparing the result with a standard. This peptide represents a reporter molecule isolated from a combinatorial peptide library having the generic sequence AAY6733... Detection of the complex is by fluorescence resonance energy transfer (FRET). The method is used to identify compounds that interfere with interaction between the target RNA and ligands or proteins.

CC Compounds that are identified are potentially useful for treating infections (viral, bacterial or fungal), cancer and autoimmune diseases.

CC The compounds are preferably directed to the TAR and RRE regions of human immunodeficiency virus RNA and inhibit viral replication.

XX Sequence 13 AA:

Query Match 45.5% Score 57 DB 211 Length 13

Best Local Similarity 100.0% Pred. No. 1002

Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Q7 5 KRKK 9

DE 7 KRKK 11

RESID 17

AAAY6770

10 AAY6770 standard; peptide: 13 AA.

XX AAY6770:

AC

XX 11-APR 2000 (first entry)

XX RNA binding peptide #49.

XX Antiviral; antibacterial; antitumor; anticancer; detection: TAR; RRE;

XX fluorescence resonance energy transfer; tat; HIV-1; Rev response element;

XX autoimmune disease; trans-activation regulatory region.

XX Synthetic.

XX Key Location/qualifiers

XX Modified site 1

XX Modified site 13 /note- "conjugated to DABCYL (4-(((dimethylamino)phenyl)azo)benzoic acid)"

XX Modified site 13 /note- "C-terminal amide"

XX W09954625-A2.

XX 16-DEC-1999.

XX 04-JUN-1999; 99W0-0801761.

XX 05-JUN-1998; 99GB-0012196.

XX 02-MAR-1999; 99GB-0004790.

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XX Karin J. Prescott CD;

XX WPI: 2000-097545/08.

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CC Compounds that are identified are potentially useful for treating infections (viral, bacterial or fungal), cancer and autoimmune diseases.

CC The compounds are preferably directed to the TAR and RRE regions of human

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XX  Query Match 45.5% Score 5; DB 22; Length 13;
XX  Best Local Similarity 100.0% Pred. No. 10-02;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KRKG 4
   1 1
SD 7 KRKG 11

RESULT 19
AAU06073
XX AAU06073 Standard; peptide: 15 AA.
XX AC
XX 24-007-2501 (first entry)
XX RNA binding peptide #8 tested for binding to HCV IRES RNA.
XX RNA binding peptide; Hepatitis C virus; HCV 5'-UTR; minimal IRES; IRES;
XX internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX HCV translation initiation; antiviral.
XX Synthetic.
XX Key Location/Qualifiers
XX Region 4-18
XX /note= "Variable pentapeptide core"
XX W220144266-A2.
XX 21 JUN 2001
XX 16 DEC 2000 2000W000486Z.
XX 16 DEC 1999 993B-00296Z.
XX 22 DEC 1999 990S-0171804.
XX (P1500) HIV-TARGETS LTD.
XX Kato, J. Marker: S.
XX W21 2001 465050/50.
XX Nucleotide sequences derived from Hepatitis C virus. useful for
XX identifying candidate antiviral compounds.
XX Description Page 29; 46pp; English.
XX The present sequence represents RNA binding peptide #8 tested for
XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a
XX library of synthetic peptides with a variable pentapeptide core and
XX constant flanking neutral and basic amino acids were tested for
XX binding to HCV IRES RNA. The present sequence is described in an
XX invention relating to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated region
XX (5'UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX eIF3 (eukaryotic initiation factor 3). The invention particularly
XX relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX IRES (mIRES) which can be used to identify drugs which inhibit HCV
XX translation initiation. The compounds of the invention may be used to
XX screen for potential HCV antiviral compounds. Assays based on the
XX mIRES enable potential antivirals to be screened in a cheaper and easier
XX way. It allows rapid assaying with a small volume of material and are
XX suitable to parallel processing.
XX Sequence 15 AA.

QY 5 KRKG 4
   1 1
SD 7 KRKG 11

RESULT 19
AAU06073
XX AAU06073 Standard; peptide: 15 AA.
XX AC
XX 24-007-2501 (first entry)
XX RNA binding peptide #8 tested for binding to HCV IRES RNA.
XX RNA binding peptide; Hepatitis C virus; HCV 5'-UTR; minimal IRES; IRES;
XX internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX HCV translation initiation; antiviral.
XX Synthetic.
XX Key Location/Qualifiers
XX Region 4-18
XX /note= "Variable pentapeptide core"
XX W220144266-A2.
XX 21 JUN 2001
XX 16 DEC 2000 2000W000486Z.
XX 16 DEC 1999 993B-00296Z.
XX 22 DEC 1999 990S-0171804.
XX (P1500) HIV-TARGETS LTD.
XX Kato, J. Marker: S.
XX W21 2001 465050/50.
XX Nucleotide sequences derived from Hepatitis C virus. useful for
XX identifying candidate antiviral compounds.
XX Description Page 29; 46pp; English.
XX The present sequence represents RNA binding peptide #8 tested for
XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a
XX library of synthetic peptides with a variable pentapeptide core and
XX constant flanking neutral and basic amino acids were tested for
XX binding to HCV IRES RNA. The present sequence is described in an
XX invention relating to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated region
XX (5'UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX eIF3 (eukaryotic initiation factor 3). The invention particularly
XX relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX IRES (mIRES) which can be used to identify drugs which inhibit HCV
XX translation initiation. The compounds of the invention may be used to
XX screen for potential HCV antiviral compounds. Assays based on the
XX mIRES enable potential antivirals to be screened in a cheaper and easier
XX way. It allows rapid assaying with a small volume of material and are
XX suitable to parallel processing.
XX Sequence 15 AA.
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Q7      5 KRKKG 9
Q8      111 1
Q9      7 KRKKG 11

RESULT 21
AAU06082 standard: peptide: 14 AA
XX      AAU06082
XX      AAU06082
XX      24-00T-2001 (first entry)
XX      RNA binding peptide #11 tested for binding to REV IRES RNA
XX      RNA binding peptide #11 tested for binding to REV IRES RNA
XX      RNA binding peptide: hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX      internal ribosome entry site (IRES) eukaryotic initiation factor 3
XX      HCV translation initiation and viral
XX      Synthesized
XX      Key      Location/Qualifiers
XX      Residues 4-18
XX      /note "Variable pentapeptide core"
XX      WC200144266-A2
XX      21 JUN 2001
XX      18 DEC 2000; Z000W0 3003412
XX      18 DEC 1999; 96S-0029820
XX      22 DEC 1999; 96S-0272514
XX      (KIBS) KIBJTARGETS LTD.
XX      Kuhn J., Walker S.
XX      WP1: 2001 46550/50
XX      Nucleotide sequences derived from Hepatitis C virus, useful for
XX      identifying candidate antiviral compounds
XX      Disclosed: Page 29; 48pp; English
XX      The present sequence represents RNA binding peptide #14 tested for
XX      binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX      RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a
XX      library of synthetic peptides with a variable pentapeptide core and
XX      constant flanking neutral and basic amino acids were tested for
XX      binding to REV IRES RNA. The present sequence is described in an
XX      invention relating to a novel compound comprising nucleotide sequences
XX      capable of annealing and which is derived from a 5'-untranslated region
XX      (UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX      eukaryotic initiation factor 3). The invention particularly
XX      relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX      IRES (mIRES) which can be used to identify drugs which inhibit HCV
XX      translation initiation. The compounds of the invention may be used to
XX      screen for potential HCV antiviral compounds. Assays based on the
XX      mIRES enable potential antivirals to be screened in a cheaper and easier
XX      way. It allows rapid assaying with a small volume of material and are
XX      suitable to parallel processing.
XX      Sequence 14 AA:
XX      Query Match      45.0%; Score 5; DB 22; Length 13;
XX      Best Local Similarity 10.0%; Fred. No. 1e-02;
XX      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      Q7      5 KRKKG 9
XX      111 1
XX      7 KRKKG 11

RESULT 22
AAU06085
XX      AAU06085 standard: peptide: 14 AA

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Q7      5 KRKKG 9
Q8      111 1
Q9      7 KRKKG 11

RESULT 21
AAU06079 standard: peptide: 14 AA
XX      AAU06079
XX      24-00T-2001 (first entry)
XX      RNA binding peptide #11 tested for binding to REV IRES RNA
XX      RNA binding peptide: hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX      internal ribosome entry site (IRES) eukaryotic initiation factor 3
XX      HCV translation initiation and viral
XX      Synthesized
XX      Key      Location/Qualifiers
XX      Residues 4-18
XX      /note "Variable pentapeptide core"
XX      WC200144266-A2
XX      21 JUN 2001
XX      18 DEC 2000; Z000W0 3003412
XX      18 DEC 1999; 96S-0029820
XX      22 DEC 1999; 96S-0272514
XX      (KIBS) KIBJTARGETS LTD.
XX      Kuhn J., Walker S.
XX      WP1: 2001 46550/50
XX      Nucleotide sequences derived from Hepatitis C virus, useful for
XX      identifying candidate antiviral compounds
XX      Disclosed: Page 29; 48pp; English
XX      The present sequence represents RNA binding peptide #14 tested for
XX      binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX      RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a
XX      library of synthetic peptides with a variable pentapeptide core and
XX      constant flanking neutral and basic amino acids were tested for
XX      binding to REV IRES RNA. The present sequence is described in an
XX      invention relating to a novel compound comprising nucleotide sequences
XX      capable of annealing and which is derived from a 5'-untranslated region
XX      (UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX      eukaryotic initiation factor 3). The invention particularly
XX      relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX      IRES (mIRES) which can be used to identify drugs which inhibit HCV
XX      translation initiation. The compounds of the invention may be used to
XX      screen for potential HCV antiviral compounds. Assays based on the
XX      mIRES enable potential antivirals to be screened in a cheaper and easier
XX      way. It allows rapid assaying with a small volume of material and are
XX      suitable to parallel processing.
XX      Sequence 14 AA:
XX      Query Match      45.0%; Score 5; DB 22; Length 13;
XX      Best Local Similarity 10.0%; Fred. No. 1e-02;
XX      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      Q7      5 KRKKG 9
XX      111 1
XX      7 KRKKG 11

```





```

XX  W2 0144266-A2.
XX  21-JUN-2001.
XX  18-DEC-2000: 2000W0-GB04862.
XX  16-DEC-1999: 99GB-0029820.
XX  22-DEC-1999: 99US-071834.
XX  (HCV) RIB TARGETS LIG.
XX  Kato J, Walker S.
XX  W01: 2001-46505/50.
XX  Nucleotide sequences derived from Hepatitis C virus, useful for
XX  identifying candidate antiviral compounds
XX  Discourse: Page 29: 48pp; English.
XX  The present sequence represents RNA binding peptide #33 tested for
XX  binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX  RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a
XX  library of synthetic peptides with a variable pentapeptide core and
XX  constant flanking neutral and basic amino acids were tested for
XX  binding to HCV IRES RNA. The present sequence is described in an
XX  invention relating to a novel compound comprising nucleotide sequences
XX  capable of annealing and which is derived from a 5'-untranslated region
XX  (5'UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX  eIF3 (eukaryotic initiation factor 3). The invention particularly
XX  relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX  IRES (mIRES) which can be used to identify drugs which inhibit HCV
XX  translation initiation. The compounds of the invention may be used to
XX  screen for potential HCV antiviral compounds. Assays based on the
XX  mIRES enable potential antivirals to be screened in a cheaper and easier
XX  way. It allows rapid assaying with a small volume of material and are
XX  suitable to parallel processing.
XX  Sequence 13 AA:
XX  Query Match: 45.5%, Score 5; DB 22; Length 13;
XX  Best Local Similarity 100.0%; Pred. No. Ident:
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 5 KRRKG 9
XX  11111
XX  7 KRRKG 11
XX  RESULT 27
XX  AAU06101
XX  ID AAU06101 standard; peptide: 13 AA.
XX  AC AAU06101;
XX  24-OCT-2001 (first entry)
XX  RNA binding peptide #33 tested for binding to HCV IRES RNA.
XX  RNA binding peptide; Hepatitis C virus; HCV 5'-UTR; minimal IRES; mIRES;
XX  internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX  HCV translation initiation; antiviral.
XX  Synthetic.
XX  Key Location/Qualifiers
XX  Region 4..8
XX  /note= "Variable pentapeptide core"
XX  W200144266-A2.
XX  21-JUN-2001.

```

```

XX  18-DEC-2000: 2000W0-GB04862.
XX  16-DEC-1999: 99GB-0029820.
XX  22-DEC-1999: 99US-071834.
XX  (HCV) RIB TARGETS LIG.
XX  Kato J, Walker S.
XX  W01: 2001-46505/50.
XX  Nucleotide sequences derived from Hepatitis C virus, useful for
XX  identifying candidate antiviral compounds
XX  Discourse: Page 29: 48pp; English.
XX  The present sequence represents RNA binding peptide #33 tested for
XX  binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX  RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a
XX  library of synthetic peptides with a variable pentapeptide core and
XX  constant flanking neutral and basic amino acids were tested for
XX  binding to HCV IRES RNA. The present sequence is described in an
XX  invention relating to a novel compound comprising nucleotide sequences
XX  capable of annealing and which is derived from a 5'-untranslated region
XX  (5'UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX  eIF3 (eukaryotic initiation factor 3). The invention particularly
XX  relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX  IRES (mIRES) which can be used to identify drugs which inhibit HCV
XX  translation initiation. The compounds of the invention may be used to
XX  screen for potential HCV antiviral compounds. Assays based on the
XX  mIRES enable potential antivirals to be screened in a cheaper and easier
XX  way. It allows rapid assaying with a small volume of material and are
XX  suitable to parallel processing.
XX  Sequence 13 AA:
XX  Query Match: 45.5%, Score 5; DB 22; Length 13;
XX  Best Local Similarity 100.0%; Pred. No. Ident:
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 5 KRRKG 9
XX  11111
XX  7 KRRKG 11
XX  RESULT 28
XX  AAU06104
XX  ID AAU06104 standard; peptide: 13 AA.
XX  AC AAU06104;
XX  24-OCT-2001 (first entry)
XX  RNA binding peptide #46 tested for binding to HCV IRES RNA.
XX  RNA binding peptide; Hepatitis C virus; HCV 5'-UTR; minimal IRES; mIRES;
XX  internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX  HCV translation initiation; antiviral.
XX  Synthetic.
XX  Key Location/Qualifiers
XX  Region 4..8
XX  /note= "Variable pentapeptide core"
XX  W200144266-A2.
XX  21-JUN-2001.
XX  18-DEC-2000: 2000W0-GB04862.
XX  16-DEC-1999: 99GB-0029820.

```







CC These oligopeptides may be used as vaccines in the treatment of  
CC human disease, as competitive inhibitors to prevent or reduce the  
CC metabolic action of a selected protein by blocking  
CC its specific signal sequences, or as therapeutic agents to function  
CC as feedback regulators to reduce synthesis rate of a selected protein.  
CC These peptides may be modified by adding one or more amino acids at  
CC the N and/or C-terminal, by substituting one or more amino acids  
CC without consideration of charge and polarity, by substituting one or  
CC more amino acids with amino acid residues with a similar charge and/or  
CC polarity, by omitting one or more amino acids or a combination of these.  
XX  
SQ Sequence: 5 AA;

Query Match 46.4%; Score 4; DB 19; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KRRK R

DB 5 KRRK R

#### RESULT 4c

AAW791B5  
AAW791B5 standard: peptide: 8 AA;

XX AAW791B5

DE 25 JAN-1999 (first entry)

DE HIV gp120 C5 region B cell epitope peptide

XX B cell: T cell; epitope: immunoglobulin heavy chain gp120 C5 region  
KW human immune deficiency virus; HIV; tolerance: treatment: therapy;  
KW prophylaxis: vaccine; chemotherapy; immune response; modified; human;  
KW microbial infection; autoimmune disease; antibody; diagnosis;  
KW antiviral: cell immunity;

US Mas SP

US Homo sapiens

XX W0086627-A1

DE 20-AUG-1998

DE 13-FEB-1994 94WO-0802766

DE 13-FEB-1994 97US-0040084

XX (APNA : AMERICAN NAT REL TRUSS)

XX Scott D; Zaidi:dis E;

XX W01199656-A1/5/43

DE New fusion immunoglobulin heavy chain containing gp120 epitopes and  
DE related complete antibodies : DNA vectors and transfectants are  
DE used to induce tolerance to the epitopes for treatment of human  
DE immune deficiency virus infection

ES Example 11: Page 73; 154pp; English

XX This sequence is an epitope used to the construction of a novel fusion  
XX immunoglobulin heavy chain (IgH) protein with a mammalian, especially  
XX human, IgH chain fused in frame at its N terminus to one or more human  
XX immune deficiency virus (HIV) gp120 epitopes. Fused Ig proteins and/or  
XX transfectant cells are used to tolerate subjects to gp120 epitopes and to  
XX maintain this tolerance, particularly for treatment of HIV infection;  
XX optionally together with other therapeutic/prophylactic agents such as  
XX vaccines, chemotherapeutic agents and immune response modifiers. Such  
XX proteins can be used against other diseases where an immune response is  
XX deleterious, e.g. microbial infection, cancers or autoimmune disease.  
XX Induction of tolerance suppresses production of antibodies against gp120.

CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that  
CC are bound to gp120 protein, maximising induction of protective antiviral  
CC T cell immunity.  
XX  
SQ Sequence: 8 AA;

Query Match 46.4%; Score 4; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7

DB 5 AKRR 7

#### RESULT 4d

AAW59607  
AAW59607 standard: peptide: 8 AA;

XX AAW59607

DE 23-OCT-1998 (first entry)

DE Epitope of the Hepatitis C virus

XX Epitope: HCV; envelope protein E2; HCV antibody; anti-idiotype;  
KW vaccine: HCV infection; treatment: diagnosis;

XX Synthetic

XX Hepatitis C virus

XX W09816647-A1

DE 25-APR-1998

DE 03-OCT-1997 97WO-0045511

DE 03-MAR-1997 97JP-0065448

DE 14-OCT-1996 96JP-0294399

XX (KAGA ) CHEMO-SEPO-THERAPEUTIC RES INST.

XX Makizumi K, Mizuno K, Nishihara T, Nishimura S;

XX Nozaki O, Kikuhisa I;

XX W011998 241644/24

XX Hepatitis C virus envelope antigen epitope peptide(s) useful for,  
XX e.g. treatment, vaccination and detection of hepatitis C virus  
XX infection(s)

XX Disclosure: E14 14; 99pp; Japanese

XX AAW59504-609 represent epitopes of the Hepatitis C virus (HCV). The  
XX peptides are derived from the HCV envelope protein E2 (384-414 region)  
XX and are capable of binding to HCV antibodies. The epitope peptides and  
XX anti-idiotype antibodies can be used to produce effective vaccines  
XX against HCV infection. The antibodies recognising the epitope peptides  
XX can be used in the treatment of HCV infection. The epitope peptides,  
XX DNA and antibodies can be used for diagnosis of HCV infection, detection  
XX of the presence of HCV and for HCV neutralising antibody assay.

XX Sequence: 8 AA;

Query Match 46.4%; Score 4; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ASQA 4

DB 4 ASQA 4



```

RESULT 17
AB06148
ID  AA06148 standard; peptide; 8 AA.
AC
XX
XX
XX 04-SEP-2002 (first entry)
XX
XX peptide modulating activity of hepatitis and other viruses.
XX
XX glycosaminoglycan; proteoglycan; heparin; heparan sulfate;
XX cell attachment; cell adhesion; cell migration; tumor cell metastasis;
XX cartilage differentiation; wound healing
XX
XX Synthetic.
XX
XX Key location/Qualifiers
XX Rise difference 1-8
XX /note: "this peptide may be related to an
XX unspecified number of 1-8"
XX
XX W-2001-4541-A1.
XX
XX 10 AUG-2002.
XX
XX G2-F26-2002; 2000W-US02853.
XX
XX G2-F26-1999; 990S-0118276.
XX
XX (UWJE ) UNIV JEFFERSON THOMAS.
XX
XX San Antonio, Ab. Verrechia A. Schick BP.
XX
XX WPI: 2001-54446/49.
XX
XX Novel synthetic peptides with high affinity for glycosaminoglycans and
XX proteoglycans, useful for modulating heparin promoting cell
XX attachment, modulating tumor metastasis and modulating wound healing.
XX
XX Chesnut R. Page 24; 76pp; English.
XX
XX The present sequence represents a synthetic peptide which has a high
XX affinity for glycosaminoglycans and proteoglycans. The peptide is useful
XX in methods for modulating heparin or other glycosaminoglycans with
XX anticoagulant activity, promoting cell attachment of adenocarcinoma
XX natural or synthetic surfaces (especially hemostatic), modulation
XX tumor cell metastasis, modulation with the 4 potential cell targeting
XX proteoglycans, modulation enzymes that are glycosaminoglycan
XX substrates, affinity purification of glycosaminoglycans and
XX glycosaminoglycan, modifying endothelial cell permeability and
XX anticoagulant functions mediated through glycosaminoglycans, and
XX modulation wound healing. The peptide may also be used for blocking
XX tissue uptake of heparin or other glycosaminoglycans in a normal to
XX increase heparin half-life in circulation
XX
XX Sequence 8 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 RRGK 9
XX III
XX 2 RRGK 5
XX
XX RESULT 18
AB012017
ID  AB012017 standard; Peptide; 8 AA.
XX
XX AC
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV p24 Super Cyt c11 env peptide #117.
XX

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```

D4 15-JUL-2002 (first entry)
XX
XX HIV AC2 Super Cyt c11 env peptide #74.
DE
XX
XX HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vpr; tat; cytochrome b lymphocyte; CTL; immune response; epitope;
XX antisense; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX W-2001-4810-A1
XX
XX 12 APR-2002.
XX
XX 05-JUL-2000; 2000W-US2756.
XX
XX 06-JUL-1999; 990S-0412453.
XX
XX (EP:9-) ESTIMINE (N).
XX
XX Sette A, Sidney J. Southwood S, Livingston BD, Chesnut R,
XX Baker LM, Ellis P, Kubo R, Grey HM;
XX
XX WPI: 2001-3548#7/7.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32; Page 115; 448pp; English.
XX
XX The present invention describes a composition (1) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 91 defined amino acid sequences (AHL25347 to
XX ABP25397); (1) has virucide activity and can be used in vaccines. (1)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group based vaccine may be selected from conserved regions of viral or
XX tumor-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 8 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 AKRR 7
XX III
XX 4 AKRR 7
XX
XX DB
XX
XX RESULT 19
ABP17716
ID  ABP17716 standard; Peptide; 8 AA.
XX
XX AC
XX
XX ABP17716;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV p24 Super Cyt c11 env peptide #117.
XX

```





AA366201

21 NOV 2001 (first entry)

p21 derived cyclin A binding peptide #2

Human p21WAF1, cyclin dependent protein kinase, CDK2, cyclin A, inhibitor, proliferative disorder; cancer; leukaemia; drug screening; mutant; putative.

Host sources:

Synthetic.

Key Location/Qualifiers

Modified site 1 /note "Hydrogenated N-terminus"

Misc-difference 2 /note "Optimally active domain residue"

Misc-difference 3 /note "Optimally active domain residue"

Misc-difference 4 /note "Optimally active domain residue"

Misc-difference 5 /note "Optimally active domain residue"

Misc-difference 7 /note "Optimally active domain residue"

Misc-difference 8 /note "Optimally active domain residue"

Modified-site 8 /note "Optimally active domain residue"

Modified-site 8 /note "C-terminal amide"

W200140142 A2.

07 JUN 2001

29 NOV 2001 Z00000-GR04550

30 NOV 1999 9903B-0428424

CYCCLIN CYCLINIC LTD.

Zheleva D, Fischer PM, McInnes C, Andrews MJ, Chan WC, Atkinson GE.

W200140142 A2.

New p21 derived peptides and their variants, particularly useful as selective inhibitors of CDK2/cyclin interaction for treating proliferative disorders e.g. cancers and leukaemias, and in assays for identifying CDK/cyclin inhibitors.

Example 12, Page 53; 102pp; English.

The invention relates to peptide and their variants derived from p21WAF1, which are inhibitors of CDK2 activity by binding to G1 and S phase specific cyclins which activate CDK2; selective inhibitors of CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes. The variants of the peptide may have further amino acids at either end or have up to 7 amino acids deleted, provided the motif XLXF is retained. The peptides are specific regions of p21WAF1 that bind to G1 and S phase specific cyclins, preferably cyclins which activate CDK2, one of the products of screening for screening in the assays include antibody products for screening for p21 or cyclin binding regions.

combinatorial libraries and single compound collections. The present sequence is a peptide derived from the C-terminus of p21 and used in a cyclin A binding experiment, the effect on cyclin A binding of replacing each residue with its chiral alternative was tested.

Query Match 96.4% Score 41 DB 22 Length 87  
Best Label Similarity 100.0% Pred. No. 9,36+05;  
Matches 41 Conservative 0 Mismatches 0 Indels 0 Gaps 0

4 AKKK  
111  
2 AKKK

RESULT 44  
AA366201  
ID AA366201 Standard; peptide; 8 AA.  
XX  
XX AA366201  
XX  
XX 21 NOV 2001 (first entry)  
XX  
XX p21 derived peptide, p21(152)Ser153Ala.  
XX  
XX Human; p21WAF1; cyclin dependent protein kinase; CDK2; cyclin A;  
XX inhibitor; proliferative disorder; cancer; leukaemia;  
XX drug screening; p21(152)Ser153Ala.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX  
XX Misc-difference 1 /label Ala, Ser, CysR  
XX  
XX /note "other: 4-pyridylalanine, Thiophenylalanine,  
XX Homoserine, 2,4-bisaminobutyric acid or absent and  
XX the N-terminus is hydrogenated"

Modified site 8 /note "C-terminal amide"

W200140142 A2.

07 JUN 2001

29 NOV 2001 Z00000-GR04550.

30 NOV 1999 9903B-0428424

CYCCLIN CYCLINIC LTD.

Zheleva D, Fischer PM, McInnes C, Andrews MJ, Chan WC, Atkinson GE.

W200140142 A2.

New p21 derived peptides and their variants, particularly useful as selective inhibitors of CDK2/cyclin interaction for treating proliferative disorders e.g. cancers and leukaemias, and in assays for identifying CDK/cyclin inhibitors.

Example 13, Page 54; 102pp; English.

The invention relates to peptide and their variants derived from p21WAF1, which are inhibitors of CDK2 activity by binding to G1 and S phase specific cyclins which activate CDK2; selective inhibitors of CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes. The variants of the peptide may have further amino acids at either end or have up to 7 amino acids deleted, provided the motif XLXF is retained. The peptides are specific regions of p21WAF1 that bind to G1 and S phase specific cyclins, preferably cyclins which activate CDK2, one of the products of screening for screening in the assays include antibody products for screening for p21 or cyclin binding regions.

XX Treating proliferative disorders, e.g., cancers and leukaemias, the  
 CC peptides are also for identifying substances which interfere with  
 CC protein-protein interactions involving cyclins (e.g., cyclin A, E or D),  
 CC especially CLK/cyclin interactions, and which are capable of inhibiting  
 CC CLK2 and/or CLK4 activity. p21 peptides other than p21(149-159)  
 CC competitively inhibit the binding of peptide p21(149-159) to cyclin and  
 CC may be used to identify substances that bind to, or inhibit, peptide-  
 CC cyclin interactions. Substances for screening in the assays include  
 CC antibody products specific for p21 or cyclin 1, and reagents  
 CC combinatorial libraries and single compound libraries. The present  
 CC sequence is a peptide derived from the C-terminus of p21 and used in  
 CC a cyclin A binding experiment. The effect on cyclin A binding of  
 CC replacing the His residue at position 1 was assessed.

XX  
 SQ Sequence # AA.

Query Match 36.4%, Score 4, Db 22, Length 8;  
 Best Local Similarity 100.0%, Pos. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SY 4 AKRR ?  
 IL I I I I I I I I

DE 2 AKRR 5

RESUL 46  
 AA362267  
 ID AA362267 standard: peptide, 8 AA  
 XX  
 AC AA362267  
 XX  
 SI 21 NOV 2001 (FIRST ENTRY)  
 XX  
 DE p21 derived peptide, p21(152)Ser155Ala #7.  
 XX  
 KW Human, p21WAF1, cyclin dependent protein kinase; CLK2; cyclin A;  
 KW inhibitor; proliferative disorders; cancer; leukaemia;  
 KW drug screening; p21(152)Ser155Ala.  
 XX  
 SS Basic Synthesis  
 SS Synthesis  
 XX  
 EH K07 Location/Qualifiers  
 FI Modified Site 1 /note "The N-terminus is hydrogenated"  
 FI Miscellaneous 7 /label "Ile, Ala, OTHER, Ieu, Val, Phe, Nva, IVal  
 FI /note "data: cyclohexylalanine or absent"  
 FI Modified Site 8 /note "N-terminal amide"  
 FI  
 XX  
 FN W020143142-A2  
 XX  
 EQ 07-JUN-2001  
 XX  
 XX 29-NOV-2000, 2000W020143142-A2  
 XX  
 PR 30 NOV-1999, 1999B0028323  
 XX  
 PA (CYCL) CYCLOA2611110  
 XX  
 FI Zaslavsky L, Fischer IM, Rittner C, Andrews ML, Chan WC,  
 FI Aleksanov GE

XX The invention relates to peptide and their variants derived from p21WAF1,  
 CC which are inhibitors of CLK2 activity by binding to G1 and  
 CC S phase specific cyclins which activate CLK2; selective inhibitors of  
 CC CLK2/cyclin complexes, particularly CLK2/cyclin A or E complexes.  
 CC the variants of the peptide may have further amino acids at either end  
 CC or have up to 7 amino acids deleted, provided the motif XLRF is retained.  
 CC The peptides are specific reagents of p21WAF1 that bind to G1 and S  
 CC phase specific cyclins, preferably cyclins which activate CLK2, one  
 CC of the peptides corresponds to p21(149-159). The peptides are used for  
 CC treating proliferative disorders, e.g., cancers and leukaemias. The  
 CC peptides are also for identifying substances which interfere with  
 CC protein-protein interactions involving cyclins (i.e., cyclin A, E or D),  
 CC especially CLK2/cyclin interactions, and which are capable of inhibiting  
 CC CLK2 and/or CLK4 activity. p21 peptides other than p21(149-159)  
 CC competitively inhibit the binding of peptide p21(149-159) to cyclin and  
 CC may be used to identify substances that bind to, or inhibit, peptide-  
 CC cyclin interactions. Substances for screening in the assays include  
 CC antibody products specific for p21 or cyclin binding regions. The present  
 CC sequence is a peptide derived from the C-terminus of p21 and used in  
 CC a cyclin A binding experiment. The effect on cyclin A binding of  
 CC replacing the Leu residue at position 6 was assessed.

XX  
 SQ Sequence # AA.

Query Match 36.4%, Score 4, Db 22, Length 8;  
 Best Local Similarity 100.0%, Pos. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SY 4 AKRR ?  
 IL I I I I I I I I

DE 2 AKRR 5

RESUL 46  
 AA362267  
 ID AA362267 standard: peptide, 8 AA  
 XX  
 AC AA362267  
 XX  
 SI 21 NOV 2001 (FIRST ENTRY)  
 XX  
 DE p21 derived peptide, p21(152)Ser155Ala #7.  
 XX  
 KW Human, p21WAF1, cyclin dependent protein kinase; CLK2; cyclin A;  
 KW inhibitor; proliferative disorders; cancer; leukaemia;  
 KW drug screening; p21(152)Ser155Ala.  
 XX  
 SS Basic Synthesis  
 SS Synthesis  
 XX  
 EH K07 Location/Qualifiers  
 FI Modified Site 1 /note "The N-terminus is hydrogenated"  
 FI Miscellaneous 7 /label "Ile, Ala, OTHER, Ieu, Val, Phe, Nva, IVal  
 FI /note "data: cyclohexylalanine or absent"  
 FI Modified Site 8 /note "N-terminal amide"  
 FI  
 XX  
 FN W020143142-A2  
 XX  
 EQ 07-JUN-2001  
 XX  
 XX 29-NOV-2000, 2000W020143142-A2  
 XX  
 PR 30 NOV-1999, 1999B0028323  
 XX  
 PA (CYCL) CYCLOA2611110  
 XX  
 FI Zaslavsky L, Fischer IM, Rittner C, Andrews ML, Chan WC,  
 FI Aleksanov GE

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XX WP1: 2001-48644/53.
XX
XX New p21 derived peptides and their variants, particularly useful as
XX selective inhibitors of CDK2/cyclin interaction for treating
XX proliferative disorders e.g. cancers and leukaemias, and in assays for
XX identifying CDK/cyclin inhibitors.
XX
XX Example 20: Page 57; 102pp; English.
XX
XX The invention relates to peptide and their variants derived from p21WAF1,
XX which are inhibitors of CDK2 activity by binding to G1 and
XX S phase specific cyclins which activate CDK2; selective inhibitors of
XX CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes.
XX The variants of the peptide may have further amino acids at either end
XX or have up to 7 amino acids deleted, provided the motif XLRF is retained.
XX The peptides are specific regions of p21WAF1 that bind to G1 and S
XX phase specific cyclins, preferably cyclins which activate CDK2. One
XX of the peptides corresponds to p21(149-159). The peptides are used for
XX treating proliferative disorders, e.g. cancers and leukaemias. The
XX peptides are also for identifying substances which interfere with
XX protein-protein interactions involving cyclins (i.e. cyclin A, E or D),
XX especially CDK2/cyclin interactions, and which are capable of inhibiting
XX CDK2 and/or CDK4 activity. p21 peptides other than p21(149-159)
XX competitively inhibit the binding of peptide p21(149-159) to cyclin and
XX may be used to identify substances that bind to, or inhibit peptide-
XX cyclin interactions. Substances for screening in the assays include
XX antibody products specific for p21 or cyclin binding regions,
XX combinatorial libraries and single compound collections. The present
XX sequence is a peptide derived from the C-terminus of p21 and used in
XX a Cyclin A binding experiment, the effect on cyclin A binding of
XX replacing the Ile residue at position 7 was assessed.
XX
XX Sequence 8 AA:
XX
XX Query Match 36.4% Score 4; DB 22; Length 8;
XX Best local Similarity 100.0%; Pred. No. 9, 1e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 AKRP 7
XX I.
XX Zb 2 AKRR 5
XX
XX RESULT 1:
XX AAG66208 standard; Peptide: 8 AA
XX
XX AAG66208:
XX
XX 21-NOV-2001 (first entry)
XX
XX p21 derived peptide, p21(152)Ser154A.
XX
XX Human, p21WAF1; cyclin dependent protein kinase; CDK2; cyclin A;
XX inhibitor; proliferative disorder; cancer; leukaemia;
XX drug screening; p21(152)Ser154A.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX
XX Modified-site 1
XX
XX Note= "The N-terminus is hydroxylated"
XX
XX Miscellaneous 8
XX
XX /label= lys, Tyr, Glu, Leu, Trp, 2Rd1, Phe, Ibal
XX /note= "Other: Cyclohexylalanine, norphenylalanine,
XX para-fluorohexylalanine, meta-fluorophenylalanine
XX or biphenylalanine"
XX
XX Modified-site 8
XX
XX /note= "C-terminal amide"
XX
XX W.200140:42-AZ.

```

```

XX QY 07-JUN-2001.
XX
XX 29-NOV-2001: 2003W00360450.
XX
XX 30-NOV-1999: 9903b 002R424.
XX
XX (Cyclin A) CYCLIN A. L10.
XX
XX Zhelova D, Fischer PE, Mellows G, Andrews MJL, Chan WC,
XX Alkanson GE.
XX
XX WP1: 2001-48644/53.
XX
XX New p21 derived peptides and their variants, particularly useful as
XX selective inhibitors of CDK2/cyclin interaction for treating
XX proliferative disorders e.g. cancers and leukaemias, and in assays for
XX identifying CDK/cyclin inhibitors.
XX
XX Example 20: Page 57; 102pp; English.
XX
XX The invention relates to peptide and their variants derived from p21WAF1,
XX which are inhibitors of CDK2 activity by binding to G1 and
XX S phase specific cyclins which activate CDK2; selective inhibitors of
XX CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes.
XX The variants of the peptide may have further amino acids at either end
XX or have up to 7 amino acids deleted, provided the motif XLRF is retained.
XX The peptides are specific regions of p21WAF1 that bind to G1 and S
XX phase specific cyclins, preferably cyclins which activate CDK2. One
XX of the peptides corresponds to p21(149-159). The peptides are used for
XX treating proliferative disorders, e.g. cancers and leukaemias. The
XX peptides are also for identifying substances which interfere with
XX protein-protein interactions involving cyclins (i.e. cyclin A, E or D),
XX especially CDK2/cyclin interactions, and which are capable of inhibiting
XX CDK2 and/or CDK4 activity. p21 peptides other than p21(149-159)
XX competitively inhibit the binding of peptide p21(149-159) to cyclin and
XX may be used to identify substances that bind to, or inhibit peptide-
XX cyclin interactions. Substances for screening in the assays include
XX antibody products specific for p21 or cyclin binding regions,
XX combinatorial libraries and single compound collections. The present
XX sequence is a peptide derived from the C-terminus of p21 and used in
XX a Cyclin A binding experiment, the effect on cyclin A binding of
XX replacing the Phe residue at position 8 was assessed.
XX
XX Sequence 8 AA:
XX
XX Query Match 46.4% Score 4; DB 22; Length 8;
XX Best local Similarity 100.0%; Pred. No. 9, 1e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 AKRP 7
XX I.
XX Zb 2 AKRR 5
XX
XX RESULT 1:
XX AAG66252 standard; Peptide: 8 AA.
XX
XX AAG66252:
XX
XX 21-NOV-2001 (first entry)
XX
XX p21 C-terminus derived peptide #44.
XX
XX Human, p21WAF1; cyclin dependent protein kinase; CDK2; cyclin A;
XX inhibitor; proliferative disorder; cancer; leukaemia;
XX drug screening.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers

```







Genre version 6.1.2  
Copyright: (c) 1994 - 2004 - Copyright: 114

**Abstract**

[illegible]

Title: US-09-787-443-17  
 Perfect Score: 11  
 Score: 1 AKKERPNKPN: 13

Series	Value	Series	Value
Capital	60.0	Export	40.0

Sequences: 1197863 seqs, 158726578 positions.

Word size : 6

Total number of hits satisfying chosen parameters: 27,422

Minimum: 13 seq	length: 8
Max, min: 13 seq	length: 15

Post hoc analyses indicated that the first 500 symptoms

Database : A\_Geneseq\_19Jun03:\*

1	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-80	AAI
2	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-88	AAI
4	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-82	AAI
5	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-83	AAI
6	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-84	AAI
7	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-85	AAI
8	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-86	AAI
9	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-87	AAI
10	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-88	AAI
11	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-89	AAI
12	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-90	AAI
13	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-91	AAI
14	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-92	AAI
15	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-93	AAI
16	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-94	AAI
17	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-95	AAI
18	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-96	AAI
19	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-97	AAI
20	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-98	AAI
21	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-99	AAI
22	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-00	AAI
23	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-01	AAI
24	/SIDSI/acqdat/a/qemeseq/qaesce	H	emb./AAI-02	AAI

Prod. No. is the number of results produced by a group to have a score greater than or equal to the score of the subject being printed and is derived by analysis of the total score distribution.

SEQUENCES									
Seq. ID	Score		Match		Length	DB	IL		Description
	Seq	Ref	Seq	Ref					
1	11	100.0	11	21	AAV86545				NCAM 141 binding p
2	13	100.0	11	23	ABG59345				Human neural cell
3	5	45.5	9	22	AAE7918				Formalin for heparin
4	5	45.5	12	15	AAR57069				Nerve and heparin
5	5	45.5	14	21	AAV44548				Hepatitis C virus
6	5	45.5	14	24	AAE7964				HARP derived peppt
7	5	45.5	15	24	APR4336				Human derived total
8	5	45.5	15	24	APR43719				Human derived total
9	5	45.5	15	24	APR43726				Human derived total

[illegible]

429	8	22	AA098972	Varicella-related ME	322	9	14	AA024666	Immunomodulatory p
240	8	22	AA014714	Preferred peptide	323	9	14	AA024667	Immunomodulatory p
241	8	22	AA067297	Peptide encoded by	324	9	14	AA024668	Immunomodulatory p
242	8	22	AA007259	Peptide #24 from 1	325	9	14	AA024670	Immunomodulatory p
243	8	22	AA008151	Peptide #50 from 1	326	9	14	AA024671	Immunomodulatory p
244	8	22	AA006429	Human leukocyte An	327	9	14	AA024672	Immunomodulatory p
245	8	22	AA009419	HLA-B*07:01:01	328	9	14	AA024673	Immunomodulatory p
246	8	22	AA009897	HLA-B*07:01:01	329	9	14	AA024674	Immunomodulatory p
247	8	22	AA010514	HLA-B*07:01:01	330	9	14	AA024675	Immunomodulatory p
248	8	22	AA004914	Human immunodef	331	9	14	AA036851	Insulin-like growt
249	8	22	AA007147	Lactylin-like peptid	332	9	14	AA043455	Ro/SSA epitope 212
250	8	22	AA070478	Peptide #22, beta	333	9	14	AA043456	Cytotoxic T lympho
251	8	22	AA070655	Bacillus stearother	334	9	14	AA043457	MHC Class I allele
252	8	22	AA072698	Newcastle disease	335	9	14	AA043458	Haemostatic, bioc
253	8	22	AA011064	Peptide derived fr	336	9	14	AA059442	Protein-kinase inh
254	8	22	AA031113	Polypeptide fragm	337	9	14	AA059741	Peptide (241) inh
255	8	22	AA031153	A polypeptide fra	338	9	14	AA061061	Dynorphin-like pol
256	8	22	AA075735	HLA class I bindin	339	9	14	AA071753	Neurotensin recept
257	8	22	AA075736	Human kallikrein 1	340	9	14	AA071754	Neurotensin recept
258	8	22	AA075737	HLA activation cum	341	9	14	AA087283	Plasmodium falcipa
259	8	22	AA085475	Neurotensin peptid	342	9	14	AA087284	Plasmodium falcipa
260	8	22	AA057489	HLA cytotoxic lymph	343	9	14	AA087285	Plasmodium falcipa
261	8	22	AA057490	Myristoylation ord	344	9	14	AA087286	Plasmodium falcipa
262	8	22	AA079942	HLA class I molecu	345	9	14	AA087287	Plasmodium falcipa
263	8	22	AA079943	Hepatitis B virus	346	9	14	AA087288	Template peptide f
264	8	22	AA079944	Hepatitis B virus	347	9	14	AA087289	Partial sequence f
265	8	22	AA079945	Hepatitis B virus	348	9	14	AA087290	Synthetic HTLV pep
266	8	22	AA079946	Hepatitis B virus	349	9	14	AA087291	Cyclin R/p33(cdc2)
267	8	22	AA079947	Hepatitis B virus	350	9	14	AA087292	Human leucocyte an
268	8	22	AA079948	Hepatitis B virus	351	9	14	AA087293	Compacting peptide
269	8	22	AA079949	Hepatitis B virus	352	9	14	AA087294	Antifungal peptide
270	8	22	AA079950	Hepatitis B virus	353	9	14	AA087295	NS2 receptor alte
271	8	22	AA079951	Hepatitis B virus	354	9	14	AA087296	Bradykinin analogo
272	8	22	AA079952	Hepatitis B virus	355	9	14	AA087297	HPV16 E6 peptide (
273	8	22	AA079953	Hepatitis B virus	356	9	14	AA087298	Anti-fungal peptide
274	8	22	AA079954	Hepatitis B virus	357	9	14	AA087299	Bactericidal/perme
275	8	22	AA079955	Hepatitis B virus	358	9	14	AA087300	Mycobacterium tube
276	8	22	AA079956	Hepatitis B virus	359	9	14	AA087301	Mycobacterium tube
277	8	22	AA079957	Hepatitis B virus	360	9	14	AA087302	HLIV-1a, c.m. deriv
278	8	22	AA079958	Hepatitis B virus	361	9	14	AA087303	PECAM-1 inhibitor
279	8	22	AA079959	Hepatitis B virus	362	9	14	AA087304	PECAM-1 inhibitor
280	8	22	AA079960	Hepatitis B virus	363	9	14	AA087305	PECAM-1 inhibitor
281	8	22	AA079961	Hepatitis B virus	364	9	14	AA087306	PECAM-1 inhibitor
282	8	22	AA079962	Hepatitis B virus	365	9	14	AA087307	PECAM-1 inhibitor
283	8	22	AA079963	Hepatitis B virus	366	9	14	AA087308	PECAM-1 inhibitor
284	8	22	AA079964	Hepatitis B virus	367	9	14	AA087309	Epitope C-terminal
285	8	22	AA079965	Hepatitis B virus	368	9	14	AA087310	K4, a nucleic acid
286	8	22	AA079966	Hepatitis B virus	369	9	14	AA087311	Thrombin receptor
287	8	22	AA079967	Hepatitis B virus	370	9	14	AA087312	Peptide GP61: C-9
288	8	22	AA079968	Hepatitis B virus	371	9	14	AA087313	Helicobacter pylor
289	8	22	AA079969	Hepatitis B virus	372	9	14	AA087314	M. tuberculosis po
290	8	22	AA079970	Hepatitis B virus	373	9	14	AA087315	Dengue virus type-
291	8	22	AA079971	Hepatitis B virus	374	9	14	AA087316	Dengue virus type-
292	8	22	AA079972	Hepatitis B virus	375	9	14	AA087317	PECAM-1 inhibitor
293	8	22	AA079973	Hepatitis B virus	376	9	14	AA087318	PECAM-1 inhibitor
294	8	22	AA079974	Hepatitis B virus	377	9	14	AA087319	PECAM-1 inhibitor
295	8	22	AA079975	Hepatitis B virus	378	9	14	AA087320	PECAM-1 inhibitor
296	8	22	AA079976	Hepatitis B virus	379	9	14	AA087321	PECAM-1 inhibitor
297	8	22	AA079977	Hepatitis B virus	380	9	14	AA087322	PECAM-1 inhibitor
298	8	22	AA079978	Hepatitis B virus	381	9	14	AA087323	PECAM-1 inhibitor
299	8	22	AA079979	Hepatitis B virus	382	9	14	AA087324	PECAM-1 inhibitor
300	8	22	AA079980	Hepatitis B virus	383	9	14	AA087325	PECAM-1 inhibitor
301	8	22	AA079981	Hepatitis B virus	384	9	14	AA087326	PECAM-1 inhibitor
302	8	22	AA079982	Hepatitis B virus	385	9	14	AA087327	PECAM-1 inhibitor
303	8	22	AA079983	Hepatitis B virus	386	9	14	AA087328	PECAM-1 inhibitor
304	8	22	AA079984	Hepatitis B virus	387	9	14	AA087329	PECAM-1 inhibitor
305	8	22	AA079985	Hepatitis B virus	388	9	14	AA087330	PECAM-1 inhibitor
306	8	22	AA079986	Hepatitis B virus	389	9	14	AA087331	PECAM-1 inhibitor
307	8	22	AA079987	Hepatitis B virus	390	9	14	AA087332	PECAM-1 inhibitor
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311	8	22	AA079991	Hepatitis B virus	394	9	14	AA087336	PECAM-1 inhibitor
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317	8	22	AA079997	Hepatitis B virus	400	9	14	AA087342	PECAM-1 inhibitor
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319	8	22	AA079999	Hepatitis B virus	402	9	14	AA087344	PECAM-1 inhibitor
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321	8	22	AA080001	Hepatitis B virus	404	9	14	AA087346	PECAM-1 inhibitor
322	8	22	AA080002	Hepatitis B virus	405	9	14	AA087347	PECAM-1 inhibitor
323	8	22	AA080003	Hepatitis B virus	406	9	14	AA087348	PECAM-1 inhibitor
324	8	22	AA080004	Hepatitis B virus	407	9	14	AA087349	PECAM-1 inhibitor
325	8	22	AA080005	Hepatitis B virus	408	9	14	AA087350	PECAM-1 inhibitor
326	8	22	AA080006	Hepatitis B virus	409	9	14	AA087351	PECAM-1 inhibitor
327	8	22	AA080007	Hepatitis B virus	410	9	14	AA087352	PECAM-1 inhibitor
328	8	22	AA080008	Hepatitis B virus	411	9	14	AA087353	PECAM-1 inhibitor
329	8	22	AA080009	Hepatitis B virus	412	9	14	AA087354	PECAM-1 inhibitor
330	8	22	AA080010	Hepatitis B virus	413	9	14	AA087355	PECAM-1 inhibitor
331	8	22	AA080011	Hepatitis B virus	414	9	14	AA087356	PECAM-1 inhibitor
332	8	22	AA080012	Hepatitis B virus	415	9	14	AA087357	PECAM-1 inhibitor
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335	8	22	AA080015	Hepatitis B virus	418	9	14	AA087360	PECAM-1 inhibitor
336	8	22	AA080016	Hepatitis B virus	419	9	14	AA087361	PECAM-1 inhibitor
337	8	22	AA080017	Hepatitis B virus	420	9	14	AA087362	PECAM-1 inhibitor
338	8	22	AA080018	Hepatitis B virus	421	9	14	AA087363	PECAM-1 inhibitor
339	8	22	AA080019	Hepatitis B virus	422	9	14	AA087364	PECAM-1 inhibitor
340	8	22	AA080020	Hepatitis B virus	423	9	14	AA087365	PECAM-1 inhibitor
341	8	22	AA080021	Hepatitis B virus	424	9	14	AA087366	PECAM-1 inhibitor
342	8	22	AA080022	Hepatitis B virus	425	9	14	AA087367	PECAM-1 inhibitor
343	8	22	AA080023	Hepatitis B virus	426	9	14	AA087368	PECAM-1 inhibitor
344	8	22	AA080024	Hepatitis B virus	427	9	14	AA087369	PECAM-1 inhibitor
345	8	22	AA080025	Hepatitis B virus	428	9	14	AA087370	PECAM-1 inhibitor
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347	8	22	AA080027	Hepatitis B virus	430	9	14	AA087372	PECAM-1 inhibitor
348	8	22	AA080028	Hepatitis B virus	431	9	14	AA087373	PECAM-1 inhibitor
349	8	22	AA080029	Hepatitis B virus	432	9	14	AA087374	PECAM-1 inhibitor
350	8	22	AA080030	Hepatitis B virus	433	9	14	AA087375	PECAM-1 inhibitor
351	8	22	AA080031	Hepatitis B virus	434	9	14	AA087376	PECAM-1 inhibitor
352	8	22	AA080032	Hepatitis B virus	435	9	14	AA087377	PECAM-1 inhibitor
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359	8	22	AA080039	Hepatitis B virus	442	9	14	AA087384	PECAM-1 inhibitor
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361	8	22	AA080041	Hepatitis B virus	444	9	14	AA087386	PECAM-1 inhibitor
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364	8	22	AA080044	Hepatitis B virus	447	9	14	AA087389	PECAM-1 inhibitor
365	8	22	AA080045	Hepatitis B virus	448	9	14	AA087390	PECAM-1 inhibitor
366	8	22	AA080046	Hepatitis B virus	449	9	14	AA087391	PECAM-1 inhibitor
367	8	22	AA080047	Hepatitis B virus	450	9	14	AA087392	PECAM-1 inhibitor
368	8	22	AA080048	Hepatitis B virus	451	9	14	AA087393	PECAM-1 inhibitor
369	8	22	AA080049	Hepatitis B virus	452	9	14	AA087394	PECAM-1 inhibitor
370	8	22	AA080050	Hepatitis B virus	453	9	14	AA087395	PECAM-1 inhibitor
371	8	22	AA080051	Hepatitis B virus	454	9	14	AA087396	PECAM-1 inhibitor
372	8	22	AA080052	Hepatitis B virus	455	9	14	AA087397	PECAM-1 inhibitor
373	8	22	AA080053	Hepatitis B virus	456	9	14	AA087398	PECAM-1 inhibitor





```

RESULT 3
AA0627416
ID AA0627416 standard; peptide: 9 AA
XX
XX AA0627416
AC
XX
XX 29 JUN 2003 (first entry)
DE
XX Formula for hepatitis regulatory peptide region in peptides.
XX
XX Hepatitis regulatory peptide (HARP) sequence peptide activity.
XX immune response; cellular growth; cellular response; cellular death;
XX creatinase; immunosuppressive disease; human; immunoreactivity; HIV;
XX HIV infection; antiviral.
XX
XX Synthetic
XX
XX Key Location/Variant
XX
XX Miscellaneous: /note: "any amino acid in positions 1-29, where the
XX sum of the residues represented by amino acids
XX 1 and 9 is 0.20. Preferably 0.15, and most
XX preferably 0.10"
XX
XX Miscellaneous: /note: "any amino acid in positions 1-29, where the
XX sum of the residues represented by amino acids
XX 1 and 9 is 0.20. Preferably 0.15, and most
XX preferably 0.10"
XX
XX W200127416A2.
XX
XX In AA0627416
XX
XX 06 AUG 2003, 23:00W PR02764
XX
XX 12 SEP 2003, 09:00W PR02764
XX
XX (CNRS) CNRS CENT NAT RECH SCL
XX
XX Bartsch, D., Achard, A., Courty, J
XX
XX W200128197/29.
XX
XX New hepatitis regulatory peptide (HARP) region used for
XX regenerative muscle cells, and in regenerative, protective and
XX feeding immunosuppressive disease (e.g., HIV, multiple sclerosis and
XX tissue regeneration).
XX
XX Claim 2, Page 42: 43pt French.
XX
XX The present sequence represents a 10 amino acid hepatitis regulatory
XX regulatory peptide (HARP) antigenic epitope that stimulates the
XX response, cellular growth, and regeneration in the peptides are used
XX for regenerative cells, such as muscle cells, and in addition
XX creatinase, as well as in the treatment of muscle degenerative
XX diseases. The peptides amplify the regenerative capacity of muscle
XX virus (HIV) in vitro, and are active in the treatment of HIV infection
XX when used with anti-viral agents. They render the HIV more accessible
XX to the antiviral agents, and therefore are more easily destroyed.
XX
XX Sequence 9 AA:
XX
XX Quality Match: 45.5%; Score 5; Db 15; length 12;
XX Best Local Similarity: 100.0%; Pred. No. 42;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 KKEKP 6
XX
XX DE 11111
XX
XX 5 KKEKP 9
XX
XX
XX
XX RESULT 5
XX
XX AA044548 standard; peptide: 14 AA.
XX
XX AA044548
XX
XX AA044548
XX
XX 04 APR 2000 (first entry)
XX
XX Hepatitis C virus antigenic peptide ASF #1.
XX
XX Hepatitis C virus; HIV; ASF #1; alternate reading frame; hepatitis C;
XX antigenic peptide; immunogenic vaccine; HIV infection; antibody;
XX protective; diagnosis; therapeutic target; anti-HCV therapy.
XX
XX Hepatitis C virus

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AA057969
ID AA057969 standard; peptide: 12 AA.
XX
XX AA057969
AC
XX
XX 25 MAR 2003 (updated)
XX
XX 13 APR 1995 (first entry)
DE
XX N-terminal fragment of HARP like growth factor.
XX
XX Mitogen-activated tyrosine kinase factor: tyrosine hydroxylase; HARP;
XX wound healing; bone regeneration; osteoporosis; osteoporosis; neurons.
XX
XX Bone synthesis.
XX
XX PR270195A2.
XX
XX 02 SEP 1994
XX
XX 25 FEB 1995; 94PR0002270.
XX
XX 25 FEB 1995; 94PR0002270.
XX
XX (CNRS) CNRS CENT NAT RECH SCL
XX
XX Bartsch, D., Courty, J., Lacroix, K.
XX
XX W200128197/5756.
XX
XX New growth factor peptide of HARP type - with mitogenic,
XX angiogenic, neurotrophic and tyrosine hydrolase stimulating
XX activity.
XX
XX Claim 1, Page 10: 24pt French.
XX
XX The sequence from which this N terminal fragment was derived is
XX described in AA057970. The protein has sequence similarity to HARP
XX peptide and has a molecular weight of 18 kD. The peptide and
XX fragments of the protein comprising the peptide at their N-terminal
XX have mitogenic, angiogenic and neurotrophic activity and stimulate
XX tyrosine hydroxylase activity. They may be used to promote wound
XX healing and bone regeneration, to maintain homeostasis in skin and
XX bone tissue (especially to combat osteoporosis), to promote
XX vascularisation of cerebral CNS structures, and to induce growth of
XX nerve cells. Note: HARP is undefined in the specification.
XX (Updated on 25 MAR 2003 to correct PN field.)
XX
XX Sequence 12 AA.
XX
XX Quality Match: 45.5%; Score 5; Db 15; length 12;
XX Best Local Similarity: 100.0%; Pred. No. 42;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 KKEKP 6
XX
XX DE 11111
XX
XX 5 KKEKP 9
XX
XX
XX
XX
XX RESULT 5
XX
XX AA044548 standard; peptide: 14 AA.
XX
XX AA044548
XX
XX AA044548
XX
XX 04 APR 2000 (first entry)
XX
XX Hepatitis C virus antigenic peptide ASF #1.
XX
XX Hepatitis C virus; HIV; ASF #1; alternate reading frame; hepatitis C;
XX antigenic peptide; immunogenic vaccine; HIV infection; antibody;
XX protective; diagnosis; therapeutic target; anti-HCV therapy.
XX
XX Hepatitis C virus

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XX FN W 099 0941 A2
XX FI 16 JUN 1999
XX FE 29 JUN 1999 0900 US:2929
XX FR 09 JUN 1999 0805 0088679
XX FS 11 JUN 1999 0805 0089138
XX GA (GRAN/) KRANCH A D
XX FA (WALE/) WALEWSKI J L
XX LA (SOM/) STUMP D D
XX PI Bruch A, Walewski JL, Stump D
XX DR WPI: 2000-12641/13
XX FI Novel hepatitis C virus peptides useful in vaccine compositions for
XX FI diagnosing HCV infection and as therapeutic agents
XX FS Claim 11: Page 44: 50pp; English
XX CC The present sequence is a Hepatitis C virus (HCV) antigenic
XX CC peptide AEP #1. The novel HCV peptide is
XX CC encoded by a reading frame +1 or +2 relative to the standard HCV open
XX CC reading frame hence not derived from the standard HCV polyprotein.
XX CC The peptide elicits an immune response in patients infected with HCV and
XX CC are produced during HCV infection. The present sequence is used as
XX CC an immunogen to generate antibodies against HCV protein which are
XX CC useful for diagnosing HCV infection. The peptide is also
XX CC useful in vaccine compositions for preventing HCV infection
XX CC and as a target for anti HCV therapy
XX SQ Sequence 14 AA:
XX
XX Query Match 45.5%; Score 5; DB 22; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 48;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KKEKN 7
XX QL III I
XX
XX RESULT 7
XX AAB67904
XX GB AAB67904 standard; peptide: 14 AA
XX
XX AC AAB79004
XX FI 29 JUN 2001 (first entry)
XX FE BACG derived peptide which is rich in basic amino acids
XX FR Hepatitis affinity regulatory peptide (BACG) modulates the structure of
XX FW immune response; cellular growth; cellular growth; cellular growth;
XX KW cellular growth; cellular growth; cellular growth; cellular growth;
XX KW HIV infection; antiviral
XX
XX PS Embedded.
XX FN W0200127136-A2
XX
XX PD 19 APR 2001
XX PF 09 OCT 2000: 200UWO-FR02786
XX PS 12 OCT 1999: 99FR-0012714
XX PA (CNRS ) CNRS CERT NAT RECH SCL
XX FI BATTAGLIA D, Achour A, Gerty D

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XX
XX DR WPI: 2001-261970/29
XX FI New Heparin Affinity Regulatory Peptide angiotensin peptides, useful for
XX FE regenerating muscle cells, aiding cicatrization, detecting and
XX FE treating immunosuppressive diseases, stimulate immune response and
XX FE tissue regeneration
XX FS Disclosure: Page 4: 4pp; French
XX
XX AAB67904-16 represent peptides which rich in basic amino acids. The
XX CC specification describes heparin affinity regulatory peptide (HARP)
XX CC angiotensin peptides that stimulate immune response, cellular growth
XX CC and regeneration. The peptides are useful for regenerating cells, such
XX CC as muscle cells, and in aiding cicatrization, as well as in the
XX CC treatment of immunosuppressive diseases. The peptides amplify the
XX CC replication of human immunodeficiency virus (HIV) in vitro, and are
XX CC useful in the detection of HIV infections. When used with antiviral
XX CC agents, they render the HIV more accessible to the antiviral agent,
XX CC and therefore are more easily destroyed.
XX SQ Sequence 14 AA:
XX
XX Query Match 45.5%; Score 5; DB 22; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 48;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 KKEKP 6
XX QL III I
XX
XX RESULT 7
XX ABR30556
XX ID ABR30556 standard; peptide: 15 AA
XX
XX AC ABR30556
XX FI 14-MAY-2003 (first entry)
XX FE Human cancer-related protein R30488 HLA peptide #1618
XX FR Human cancer-related protein R30488 HLA peptide #1618
XX KW Human cytotoxic vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen
XX
XX CS Homo sapiens
XX
XX FN W0200263921-A2
XX
XX PQ 24 OCT 2002
XX FF 10 APR 2002: 2002WO-US11054
XX
XX PR 10 APR 2001: 2001US-252799
XX PR 10 APR 2001: 2001US-261129
XX PR 25-APR-2001: 2001US-286609
XX
XX PA (AGEN ) AGENSYS INC
XX
XX PI Jakobovits A, Chaillet-Eld PM, Faris M, Ge W, Hubert RS;
XX FI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI: 2003-075559/e7
XX
XX FI New composition comprising a substance that modulates the structure of
XX FE proteins and polypeptides, useful for therapeutic, prognostic and
XX FE diagnostic reagents for eliciting cellular or humoral immune response
XX FE in cancer patients
XX PS Claim 13, Page 477: 102pp; English
XX
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (AB078423-AB078618 and AB078499-AB078611). The genes and

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XX Proteins are useful for eliciting a cellular immune response.  
 XX The genes are useful as probes and primers for the amplification and/or  
 XX detection of genes, mRNAs or their transcripts as reagents for the  
 XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX directing the expression of the protein, as tools for modulation of  
 XX inhibiting the expression of genes and/or translation of transcripts and  
 XX as therapeutic agents. The proteins and peptides are useful as  
 XX diagnostic reagents for eliciting cellular or humoral immune response  
 XX in cancer patients.  
 XX Sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX from the invention.

XX Sequence 15 AA:

Query Match 45.5% Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 KKEKP 6  
 XX I I I I  
 XX K KKEKP 12

RESLI 9

ABR0720  
 ID ABR0720 standard; Peptide: 15 AA

XX ABR0719;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein RA789 HLA peptide #1762.

XX Human cytotoxic vaccine; cancer; immune response; HLA

XX human leukocyte antigen.

XX Homo sapiens.

XX W020283921-A2.

XX 24 OCT 2002.

XX 10-APR-2002: 2502WS-US11654.

XX 10-APR-2001: 2501US-282749.

XX 10-APR-2001: 2501US-284129.

XX 25-APR-2001: 2501US-286606.

XX (AGEN) AGENSYS INC.

XX Jakubovits A., Chaillat-Eld IM, Paris M, Ge W, Hubert RS;

XX Morrison K., Morrison RK, Kalland AB;

XX WPI: 2003 075555/07.

XX New composition comprising a substance that modulates the structure of  
 XX proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX diagnostic reagents for eliciting cellular or humoral immune response  
 XX in cancer patients.

XX claim 13; Page 480; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 XX proteins (AB278120-AB278168 and AB278169-AB278186). The genes and  
 XX proteins are useful for eliciting a humoral or cellular immune response  
 XX The genes are useful as probes and primers for the amplification and/or  
 XX detection of genes, mRNAs or their transcripts as reagents for the  
 XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX directing the expression of the protein, as tools for modulation of  
 XX inhibiting the expression of genes and/or translation of transcripts, and  
 XX as therapeutic agents. The proteins and peptides are useful as  
 XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
 XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX from the invention.

XX Sequence 15 AA:

Query Match 45.5% Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 KKEKP 6  
 XX I I I I  
 XX K KKEKP 9

RESLI 9

ABR0720  
 ID ABR0720 standard; Peptide: 15 AA.

XX ABR0720;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein RA7488 HLA peptide #1762.

XX Human cytotoxic vaccine; cancer; immune response; HLA;

XX human leukocyte antigen.

XX Homo sapiens.

XX W0200283921-A2.

XX 24 OCT 2002.

XX 10-APR-2002: 2502WS-US11654.

XX 10-APR-2001: 2501US-282749.

XX 10-APR-2001: 2501US-284129.

XX 25-APR-2001: 2501US-286606.

XX (AGEN) AGENSYS INC.

XX Jakubovits A., Chaillat-Eld IM, Paris M, Ge W, Hubert RS;

XX Morrison K., Morrison RK, Kalland AB;

XX WPI: 2003 075555/07.

XX New composition comprising a substance that modulates the structure of  
 XX proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX diagnostic reagents for eliciting cellular or humoral immune response  
 XX in cancer patients.

XX claim 13; Page 480; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 XX proteins (AB278120-AB278168 and AB278169-AB278186). The genes and  
 XX proteins are useful for eliciting a humoral or cellular immune response.  
 XX The genes are useful as probes and primers for the amplification and/or  
 XX detection of genes, mRNAs or their transcripts, as reagents for the  
 XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX directing the expression of the protein, as tools for modulation of  
 XX inhibiting the expression of genes and/or translation of transcripts, and  
 XX as therapeutic agents. The proteins and peptides are useful as  
 XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
 XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX from the invention.

XX Sequence 15 AA:

Query Match 45.5% Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 KKEKP 6  
 XX I I I I  
 XX K KKEKP 6







CC unlabeled cytotoxic T lymphocytes. It may be useful to have data against  
 CC labeled.  
 CC (Updated on 25-MAR-2003 to correct IR field.)  
 XX  
 SC Sequence: 8 AA:

Query Match: 36.4%, Score 4; DB 16; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 QY 8 KPN0 1;  
 DB 1;  
 ID 1 KPN0 4

RESULT 16  
 AAR76842  
 ID AAR76842 standard; peptide: 8 AA;  
 AC AAR76842;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 26 JUN 1996 (first entry)  
 XX  
 TF Fibrinolytic peptide EP-SEPL (2044) peptide: 8 AA;  
 XX  
 KW Fibrinolytic peptide; EP SEPL (2044) streptokinase treatment;  
 KW cardiovascular diseases; clot dissolution; fibrinolysis; hemostasis;  
 KW thrombosis; haemostasis; myocardial infarction; stroke; cancer;  
 KW constitutive conformation; interaction site

OS Synthesis;  
 XX  
 PR W09522417-A1;  
 XX  
 DT 16 NOV 1994;  
 DT 21 APR 1994; 94WO 0504241;  
 XX  
 PR 21 APR 1994; 94US-0051741;  
 PR 24 OCT 1994; 94US-0143364;  
 XX  
 PA (UNAK); EVANS J J;  
 PA (LIN); SIKI R M;  
 XX  
 PT Evans JJ, SIKI RM;  
 XX  
 PR WPI: 1994-06186/44;  
 XX  
 PT Peptide homologous or analogous with constitutive conformation; it has  
 PT proline residues flanking the interaction site (compared to)  
 XX  
 PT of more stable, biological activity  
 XX  
 CS Example 2; Page 23; 57pp; English.

AA0675344 are fibrinolytic peptides derived from naturally occurring  
 CC polypeptides that contain proline at position 2, which are flanked by  
 CC prolines that are shortened to form tripeptides that contain one or more  
 CC interaction sites of interest. AA0675344 also comprise the streptokinase  
 CC and bind to plasminogen and non-proteinolytic activators plasminogen,  
 CC which dissolves fibrin clots. These are also described in the data  
 CC collected demonstrates that interaction sites possess activity when  
 CC present in a polypeptide that differs from the native form. Inclusion  
 CC of information constraining monomers can have dramatic effects on an  
 CC interaction site. (Also see AA067011 at 200; AA067012 for analogues  
 CC of other biologically active peptides that contain interaction site flanked  
 CC by conformational constraint (see also AA067013).  
 CC (Updated on 25-MAR-2003 to correct IR field.)

XX Sequence: 8 AA;  
 Query Match: 36.4%, Score 4; DB 16; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 QY 4 KKP 4;  
 DB 1;  
 ID 4 KKP 7

RESULT 16  
 AAR76842  
 ID AAR76842 standard; peptide: 8 AA;  
 AC AAR76842;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 27 MAR 1996 (first entry)  
 XX  
 DE P. talciparum liver Ag 1850-1857 cytotoxic T lymphocyte epitope;  
 XX  
 KW liver Ag 1850-1857; cytotoxic T cell epitope; helper T cell;  
 KW lymphocyte; viruses; parasites; tumours; antigens; treatment;  
 KW disease prevention; cell;  
 XX  
 OS Plasmodium talciparum

XX  
 PN W09522417-A1;  
 XX  
 DT 24-APR 1996;  
 PR 16 FEB 1996; 95WO 0502121;  
 XX  
 PR 16 FEB 1994; 94US-197484;  
 XX  
 PA (CYTE); CYHEL 08P;  
 XX  
 PT Vittiello MA, Chaslat RW, Sette AG, Celis E, Grey H;  
 XX  
 PR WPI: 1995-302545/49;

XX  
 PT Compn. induced cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX  
 OS Disclosed: Page 17; 10pp; English.

AA0675344 which induces a cytotoxic T lymphocyte (CTL) response to  
 CC an antigen (Ag) in a mammal comprises a CTL Ag response inducing  
 CC peptide (1..6) AAR76842-878664) and a lipid conjugated helper T cell  
 CC inducing peptide. The complex induces a CTL response to bacterial,  
 CC viral or tumour Ags, and is therefore useful in the treatment and  
 CC prevention of diseases associated with the Ag.  
 CC (Updated on 25-MAR-2003 to correct PT field.)

XX Sequence: 8 AA;

Query Match: 36.4%, Score 4; DB 16; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e-05;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 8 KPN0 1;  
 DB 1 KPN0 4

RESULT 17  
 AAW54665  
 ID AAW54665 standard; peptide: 8 AA;  
 AC AAW54665;  
 XX  
 DT 25-SEP-1998 (first entry)

XX  
 XX  
 DB Peptide from P. talciparum IS 1850-1857;



06-MAR-1995; 95US 04994-11.  
 (L.A.B.) LA JOLLA CANCER RES FOUND.  
 Human S:  
 WPI: 2000-41879/45.  
 New IR domain peptides comprising amino acid sequences from 1-11  
 example of retinoblastoma interacting zinc finger and carboxy protein for  
 regulating gene transcription and controlling cell proliferation and  
 differentiation.  
 Disclosure: Column 9; 9pp; English.  
 The present sequence of the G1/G2S motif from R1Z, R1Z is  
 retinoblastoma (RB)-interacting zinc finger (RIZ) protein. RIZ is a  
 nuclear phosphoprotein that acts as a cell differentiation factor. RIZ  
 can modulate cell growth by binding to Rb protein, which is involved in  
 regulating cell proliferation. In addition, RIZ can act to regulate  
 transcription. RIZ functions to maintain cells in the G1 phase of the  
 cell cycle, by interacting with Rb through the C-terminal domain of RIZ. RIZ  
 protein is a 98 domain protein and is present primarily in the cell  
 nucleus. RIZ gene mutations may be implicated in various cancers such as  
 melanoma, neuroblastoma, leukaemia and breast cancer. Also, the RIZ gene  
 may be used in gene therapy for these disorders. Since RIZ protein is  
 implicated in cell cycle arrest, inhibition of RIZ activity may be useful  
 in neurodegenerative disorder therapy e.g. for Parkinson's, Huntington's  
 or Alzheimer's disease, paralysis of motor neurone disorders, or partial  
 disorders e.g. heart disease, where the ability to induce neural/cardiac  
 tissue proliferation would be useful.  
 Sequence: 8 AA:  
 Query Match 36.4%; Score 4; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0.  
 QY 8 KPNQ 11  
 ID 111  
 2 KPNQ 5  
 REFSEQ 20  
 AAB24657  
 ID AAB24657 Standard; Peptide: # AA  
 A:  
 AAB24657:  
 05 JAN 2001 (first entry)  
 Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO 19  
 Amino Asp70; heat shock protein 70; cytotoxic T lymphocyte CTL  
 immune response; infectious disease; malaria; cytotoxic T cells;  
 cytostatic; immunostimulant; cellular immune response inducer;  
 protozoasidae; leukaemia; cancer.  
 Homo Sapiens.  
 W0200049041-AL.  
 24 AUG 2000.  
 18 FEB 2000, 2000WO JP00941.  
 19 FEB 1999; 99JP-0041535.  
 (SOME) SUMITOMO ELECTRIC IND CO.  
 Shikibuia N. Uono B. Yuki K.  
 WPI: 2000-54544/49.

Fused protein capable of inducing cellular immune response, useful as  
 active ingredient for drug compositions in preventing and/or treating  
 infectious diseases such as malaria or cancer.  
 Claim 5; Page 5; 22pp; Japanese.  
 The present invention describes a fused protein (1) prepared from a  
 peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 cytotoxic T cells and a protein containing the ATPase domain of a heat  
 shock protein. Also described are: (1) a drug composition containing (1)  
 as active ingredient; (2) a DNA encoding (1); (3) an expression vector  
 containing the DNA of (2); and (4) a transformant which can retain the  
 expression vector of (3). (1) has cytostatic, immunostimulant and  
 protozoasidae activities, and can be used as a cellular immune response  
 inducer. The protein is useful as an active ingredient for drug  
 compositions in preventing and/or treating infectious diseases such as  
 malaria or cancer; e.g. to provide systemic immunity against leukaemia.  
 The present sequence represents a specifically claimed CTL epitope  
 for use in a fused protein of the present invention.  
 Sequence: 6 AA:  
 Query Match 36.4%; Score 4; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0.  
 QY 8 KPNQ 11  
 ID 111  
 1 KPNQ 4  
 RESULT 21  
 AAY70286  
 ID AAY70286 Standard; peptide: 8 AA.  
 AC AAY70286:  
 06 JUN 2000 (first entry)  
 Plasmodium falciparum ISA-1 antigenic epitope, P596.  
 Recombinant protein; CLR/NIIMALVAC-1; multivalent; malaria; vaccine;  
 T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
 circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;  
 liver stage antigen-1; ISA-1; merozoite surface protein-1; MSP-1; MSP-2;  
 apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
 EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
 Pf27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.  
 Plasmodium falciparum.  
 W0200011179-AL.  
 02 MAR 2000.  
 19 AUG 1999; 99WO-US18669.  
 21 AUG 1998; 98US-0097703.  
 (NAIN) NAT INST IMMUNOLOGY.  
 (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Lai AA, Shi YF, Hasnain SE.  
 WPI: 2000-237654/20.  
 Novel recombinant protein as vaccine for treating malarial infection  
 comprises antigenic peptides obtained from different stages of  
 plasmodium falciparum life cycle.  
 Claim 2; Page 17; 52pp; English.





XX In whole antigens can be avoided with the use of group based vaccines.  
 XX An additional advantage of an group-based vaccine may be the ability to combine selected groups (CTL and HTL) and further to modify the composition of the groups, achieving an exact response against a particular antigenity. Accordingly, the immune response can be tailored as appropriate for the target disease. Such an approach is not possible with traditional approaches. Similarly, the use of group-based vaccines is not possible with traditional approaches. And finally, group-based vaccines represent peptide sequences used in the development of the present invention.

XX Sequence: # AA.  
 SU Query Match: 64% (first entry)  
 Best Local Similarity: 100.0%, (first entry)  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0

XX 2 KKKK 5  
 XX III  
 XX 2 KKKK 5

RES011 26  
 ABP19257  
 U3 ABP19257 standard; Peptides: # AA  
 XX  
 XX ABP19257  
 XX  
 XX 15 JUL 2002 (first entry)  
 XX HIV 862 Super motif pol peptide #263  
 XX HIV: HIV-1, human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpx; vpr; tat; cytochrome 1 lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1  
 XX W20124870 AI  
 XX 12 APR 2001  
 XX 05 JUL 2001 240090-US27766  
 XX 05 JUL 2001 240090-US27766  
 XX (P018) 10180000-INC

XX Sette A, Stacey D, Southwood S, Livingston HC, Chesnut R  
 XX Baker SM, Collins E, Kuhn M, Gray RM  
 XX W01 2001 04887/02  
 XX Vaccine compositions comprising for use in a group-based vaccine against HIV-1  
 XX peptide groups, useful for vaccinating against HIV-1

XX Class 42: Page 224: 488pp: English  
 XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus 1 (HIV-1) antigen comprising an amino acid sequence selected from 51 defined amino acid sequences (AB25447 to AB25497). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens may be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response to combine selected groups (CTL and HTL) and further to modify the

XX In whole antigens can be avoided with the use of group based vaccines.  
 XX An additional advantage of an group-based vaccine may be the ability to combine selected groups (CTL and HTL) and further to modify the composition of the groups, achieving an exact response against a particular antigenity. Accordingly, the immune response can be tailored as appropriate for the target disease. Such an approach is not possible with traditional approaches. Similarly, the use of group-based vaccines is not possible with traditional approaches. And finally, group-based vaccines represent peptide sequences used in the development of the present invention.

XX Sequence: # AA.  
 SU Query Match: 64% (first entry)  
 Best Local Similarity: 100.0%, (first entry)  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0

XX 2 KKKK 5  
 XX III  
 XX 2 KKKK 5

RES011 27  
 ABP19257  
 U3 ABP19257 standard; Peptides: # AA  
 XX  
 XX ABP19257  
 XX  
 XX 15 JUL 2002 (first entry)  
 XX HIV 862 Super motif pol peptide #263  
 XX HIV: HIV-1, human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpx; vpr; tat; cytochrome 1 lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1  
 XX W20124870 AI  
 XX 12 APR 2001  
 XX 05 JUL 2001 240090-US27766  
 XX 05 JUL 2001 240090-US27766  
 XX (P018) 10180000-INC  
 XX Sette A, Stacey D, Southwood S, Livingston HC, Chesnut R  
 XX Baker SM, Collins E, Kuhn M, Gray RM  
 XX W01 2001 04887/02  
 XX Vaccine compositions comprising for use in a group-based vaccine against HIV-1  
 XX peptide groups, useful for vaccinating against HIV-1

XX Class 42: Page 224: 488pp: English  
 XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus 1 (HIV-1) antigen comprising an amino acid sequence selected from 51 defined amino acid sequences (AB25447 to AB25497). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens may be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the

XX In whole antigens can be avoided with the use of group based vaccines.  
 XX An additional advantage of an group-based vaccine may be the ability to combine selected groups (CTL and HTL) and further to modify the composition of the groups, achieving an exact response against a particular antigenity. Accordingly, the immune response can be tailored as appropriate for the target disease. Such an approach is not possible with traditional approaches. Similarly, the use of group-based vaccines is not possible with traditional approaches. And finally, group-based vaccines represent peptide sequences used in the development of the present invention.

XX Sequence: # AA.  
 SU Query Match: 64% (first entry)  
 Best Local Similarity: 100.0%, (first entry)  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0

XX 2 KKKK 5  
 XX III  
 XX 2 KKKK 5

RES011 27  
 ABP19257  
 U3 ABP19257 standard; Peptides: # AA  
 XX  
 XX ABP19257  
 XX  
 XX 15 JUL 2002 (first entry)  
 XX HIV 862 Super motif pol peptide #263  
 XX HIV: HIV-1, human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpx; vpr; tat; cytochrome 1 lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1  
 XX W20124870 AI  
 XX 12 APR 2001  
 XX 05 JUL 2001 240090-US27766  
 XX 05 JUL 2001 240090-US27766  
 XX (P018) 10180000-INC

XX Sette A, Stacey D, Southwood S, Livingston HC, Chesnut R  
 XX Baker SM, Collins E, Kuhn M, Gray RM  
 XX W01 2001 04887/02  
 XX Vaccine compositions comprising for use in a group-based vaccine against HIV-1  
 XX peptide groups, useful for vaccinating against HIV-1

XX Class 42: Page 224: 488pp: English  
 XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus 1 (HIV-1) antigen comprising an amino acid sequence selected from 51 defined amino acid sequences (AB25447 to AB25497). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens may be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response

XX In whole antigens can be avoided with the use of group based vaccines.  
 XX An additional advantage of an group-based vaccine may be the ability to combine selected groups (CTL and HTL) and further to modify the composition of the groups, achieving an exact response against a particular antigenity. Accordingly, the immune response can be tailored as appropriate for the target disease. Such an approach is not possible with traditional approaches. Similarly, the use of group-based vaccines is not possible with traditional approaches. And finally, group-based vaccines represent peptide sequences used in the development of the present invention.

XX Sequence: # AA.  
 SU Query Match: 64% (first entry)  
 Best Local Similarity: 100.0%, (first entry)  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0

XX 2 KKKK 5  
 XX III  
 XX 2 KKKK 5

RES011 27  
 ABP19257  
 U3 ABP19257 standard; Peptides: # AA  
 XX  
 XX ABP19257  
 XX  
 XX 15 JUL 2002 (first entry)  
 XX HIV 862 Super motif pol peptide #263  
 XX HIV: HIV-1, human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpx; vpr; tat; cytochrome 1 lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1  
 XX W20124870 AI  
 XX 12 APR 2001  
 XX 05 JUL 2001 240090-US27766  
 XX 05 JUL 2001 240090-US27766  
 XX (P018) 10180000-INC

XX Sette A, Stacey D, Southwood S, Livingston HC, Chesnut R  
 XX Baker SM, Collins E, Kuhn M, Gray RM  
 XX W01 2001 04887/02  
 XX Vaccine compositions comprising for use in a group-based vaccine against HIV-1  
 XX peptide groups, useful for vaccinating against HIV-1

XX Class 42: Page 224: 488pp: English  
 XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus 1 (HIV-1) antigen comprising an amino acid sequence selected from 51 defined amino acid sequences (AB25447 to AB25497). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens may be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response



US and possible with traditional approaches. Add'l info to ABP25412  
represent peptide sequences used in the exemplification of the present  
invention.

XX Sequence R AA:  
SQ Query Match 36.4% Score 47 DB 22 Length 87  
Best Local Similarity 100.0% Pred. No. 9 3e-05;  
Matches 47 Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKEK 5  
II III  
II

II 4 KKEK 7

RESULTS 29  
ABP21507  
ID ABP21507 standard: peptide; R AA:  
XX AC ABP21507;  
XX DT 15-JUL-2002 (first entry)  
XX DE HIV AC3 motif pol peptide #552;  
XX KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
XX KM vif; tat; cytoxic T lymphocyte; cll; immune response; epitope;  
XX KW antigen; vaccine; HIV infection; immunisation; virucide;  
XX US Human immunodeficiency virus type 1;  
XX PN W02001448:10-A1;  
XX XX  
XX 12 APR-2001;  
XX PF 05-OCT-2000; 2000WO-US27756;  
XX PR 05-OCT-1999; 990S-0412853;  
XX XX  
XX (EPIM) EPIMUNE INC;  
XX PI Scott A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
XX PI Baker DM, Collins E, Kubo RT, Grey RM;  
XX XX  
XX WPI, 2001 054877/57;  
XX XX  
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
peptide groups, useful for vaccinating against HIV-1;  
XX XX  
XX CLAIM 32, Page 254; 44pp; English;  
XX XX  
XX The present invention describes a composition (i) comprising a prepared  
human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
sequence selected from 51 defined amino acid sequences (ABP25412 to  
ABP25497); (i) has virucide activity and can be used in vaccines; (i)  
may be used for immunising subjects against HIV-1 infections. The use of  
group-based vaccines has several advantages over traditional vaccines,  
particularly when compared to the use of whole antigens in vaccine  
compositions. There is evidence that the immune response to whole  
antigens is directed largely toward variable regions of the antigen,  
allowing for immune escape due to mutations. The groups for inclusion in  
a group-based vaccine may be selected from conserved regions of viral or  
tumour-associated antigens, which therefore reduces the likelihood of  
escape mutants. Furthermore, immunosuppressive groups that may be present  
in whole antigens can be avoided with the use of group-based vaccines.  
An additional advantage of a group-based vaccine approach is the ability  
to combine selected groups (C1, and H1), and further, to modify the  
composition of the groups, achieving, for example, enhanced  
immunogenicity. Accordingly, the immune response can be modulated, as  
appropriate, for the target disease. Similar engineering of the response  
is not possible with traditional approaches. ABP1501 to ABP25412  
represent peptide sequences used in the exemplification of the present  
invention.

US and possible with traditional approaches. Add'l info to ABP25412  
represent peptide sequences used in the exemplification of the present  
invention.

XX Sequence R AA:  
SQ Query Match 36.4% Score 47 DB 22 Length 87  
Best Local Similarity 100.0% Pred. No. 9 3e-05;  
Matches 47 Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKEK 5  
II III  
II

II 4 KKEK 7

RESULTS 29  
ABP21507  
ID ABP21507 standard: peptide; R AA:  
XX AC ABP21507;  
XX DT 15-JUL-2002 (first entry)  
XX DE HIV AC3 motif pol peptide #552;  
XX KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
XX KM vif; tat; cytoxic T lymphocyte; cll; immune response; epitope;  
XX KW antigen; vaccine; HIV infection; immunisation; virucide;  
XX US Human immunodeficiency virus type 1;  
XX PN W02001448:10-A1;  
XX XX  
XX 12 APR-2001;  
XX PF 05-OCT-2000; 2000WO-US27756;  
XX PR 05-OCT-1999; 990S-0412853;  
XX XX  
XX (EPIM) EPIMUNE INC;  
XX PI Scott A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
XX PI Baker DM, Collins E, Kubo RT, Grey RM;  
XX XX  
XX WPI, 2001 054877/57;  
XX XX  
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
peptide groups, useful for vaccinating against HIV-1;  
XX XX  
XX CLAIM 32, Page 254; 44pp; English;  
XX XX  
XX The present invention describes a composition (i) comprising a prepared  
human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
sequence selected from 51 defined amino acid sequences (ABP25412 to  
ABP25497); (i) has virucide activity and can be used in vaccines; (i)  
may be used for immunising subjects against HIV-1 infections. The use of  
group-based vaccines has several advantages over traditional vaccines,  
particularly when compared to the use of whole antigens in vaccine  
compositions. There is evidence that the immune response to whole  
antigens is directed largely toward variable regions of the antigen,  
allowing for immune escape due to mutations. The groups for inclusion in  
a group-based vaccine may be selected from conserved regions of viral or  
tumour-associated antigens, which therefore reduces the likelihood of  
escape mutants. Furthermore, immunosuppressive groups that may be present  
in whole antigens can be avoided with the use of group-based vaccines.  
An additional advantage of a group-based vaccine approach is the ability  
to combine selected groups (C1, and H1), and further, to modify the  
composition of the groups, achieving, for example, enhanced  
immunogenicity. Accordingly, the immune response can be modulated, as  
appropriate, for the target disease. Similar engineering of the response  
is not possible with traditional approaches. ABP1501 to ABP25412  
represent peptide sequences used in the exemplification of the present  
invention.

Query Match: 36.4%, Score 41, DB 22, Length 87  
 Best Local Similarity: 100.0%, Pred. No. 9, Jacc 5,  
 Matches: 4, Conservative 0, Mismatches 0, Indels 0,  
 Gaps 0

2 KKEK 5  
 1 1 1  
 3 KKEK 6

RESULT 40  
 ABE24417  
 ID: ABE24417 standard: Peptide: 8 AA.

XX AC  
 XX AC  
 XX AC

XX 24-JAN 2002 (first entry)

XX Human peptide #204 encoded by a SNP oligonucleotide.

XX HIV A11 motif: pol peptide #359.

XX HIV, HIV 1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpx; tat; cytotoxic T lymphocyte (CTL) immune response epitopes;  
 KW anti-hepatocellular carcinoma vaccine; HIV infection; immunisation; vaccine;  
 KW anti-hepatocellular carcinoma vaccine; HIV infection; immunisation; vaccine;

XX Human immunodeficiency virus type 1.

XX W:240124812-AA.

XX 12 APR 2001.

XX 05 OCT 2002; 2002WJ-9S27766.

XX 05 OCT 2002; 940S-041286A.

XX (FPM) EPIPHONE INC.

XX Setti A, Schrey J, Southwood S, Johnson J, New, Vincent M,  
 PI Baker LM, Collins E, Kube PL, Gray HG  
 XX WPI: 2001-04887/37.

XX Vaccine compositions comprising human immunodeficiency virus (HIV) 1 peptide groups, useful for vaccination and diagnosis HIV 1.  
 PS Claim 42: Page 348; 448pp; English.

XX The present invention describes a composition for immunizing a prepared human immunodeficiency virus (HIV) 1 vaccine comprising an antigen and sequence selected from 51 defined amino acid residues (ABE25417 to ABE25437). (i) has virulence activity and can be used in vaccines. (ii) may be used for immunized subjects against HIV infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations in the groups for inclusion in an group-based vaccine may be selected from a series of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (cell and viral) and further to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Such an composition of the resp use is not possible with traditional approaches. ABE1190; to ABE25412 represent peptide sequences used in the experimental of the present invention.

XX Sequence: 8 AA.

Query Match: 36.4%, Score 41, DB 22, Length 87  
 Best Local Similarity: 100.0%, Pred. No. 9, Jacc 5,  
 Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

2 KKEK 5  
 1 1 1  
 3 KKEK 6

QY 2 KKEK 5  
 1 1 1  
 3 KKEK 6

RESULT 41

AAM98771

ID: AAM98771 standard: Peptide: 8 AA.

XX AC

XX AAM98771.

XX 24-JAN 2002 (first entry)

XX Human peptide #204 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX Homo sapiens.

XX W:200147944-AA.

XX 05-JUL-2001.

XX 28-DEC 2000; 2000WJ-9S6498.

XX 28-DEC 1999; 990S-017447.

XX 27-DEC-2000; 20000S-0173419.

XX (CERA-1) CURAGEN CORP.

XX SHUKKETSU RA, Leach M.

XX WPI: 2001-465216/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

PS Biosciences; Page 416; 414pp; English.

XX The present invention relates to oligonucleotides (see AAI26793-AA14659) encoding polymorphic variants of proteins related to amylases, amylid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in: the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

XX Sequence: 8 AA.

Query Match: 36.4%, Score 41, DB 22, Length 87  
 Best Local Similarity: 100.0%, Pred. No. 9, Jacc 5,  
 Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

2 KKEK 5  
 1 1 1  
 3 KKEK 6









WP1: 2001-054887/37.

Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

Claim 32: Page 197: 448pp: English.

The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABL25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABL1501 to ABL25412 represent peptide sequences used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 46.4% Score 47 DP 22 Length 97  
 Best Local Similarity 100.0% Pred. No. 9, 10-05  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 KKKK 5  
 1111

DB 4 KKKK 7

RESULT 41

ABL1501

ID ABL1501 standard; Peptide: 9 AA.

AC ABL1501

DE 15 JUN 2002 (first entry)

XX HIV A24 super motif pol peptide #103.

XX HIV: HIV-1: human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX W0200124810-A1.

XX 12-APR 2001.

XX 05-OCT-1999: 2000WO-US27766.

XX 05-OCT-1999: 99US-0412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R, Baker DM, Cellis E, Kubo RT, Grey HM.

XX WP1: 2001-054887/37.

Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

PT peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32: Page 197: 448pp: English.

XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABL25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABL1501 to ABL25412 represent peptide sequences used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 46.4% Score 47 DP 22 Length 97  
 Best Local Similarity 100.0% Pred. No. 9, 10-05  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 KKKK 5  
 1111

DB 4 KKKK 7

RESULT 42

ABL17369

ID ABL17369 standard; Peptide: 9 AA.

AC ABL17369

DE 15 JUN 2002 (first entry)

XX HIV B27 super motif pol peptide #103.

XX HIV: HIV-1: human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX W0200124810-A1.

XX 12-APR 2001.

XX 05-OCT-1999: 2000WO-US27766.

XX 05-OCT-1999: 99US-0412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R, Baker DM, Cellis E, Kubo RT, Grey HM.

XX WP1: 2001-054887/37.

Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32: Page 224: 448pp: English.

XX The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumor-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunocompetency. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABL1501 to ABL25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:  
 CC  
 CC Empty Match 96.4% Score 41 DB 22 Length 9;  
 CC Best Local Similarity 100.0% Pred. No. 9.4e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5  
 DE 1 KKER 4

RESULT 4:  
 ABL1570  
 ID ABL1570 standard: peptide: 9 AA  
 AC ABL15261:  
 XX 15-JUL-2002 (first entry)  
 XX HIV B62 super motif pol peptide #267.  
 XX HIV: HIV-1; human immunodeficiency virus: env: pol: gag: nef: vif:  
 XX vpr: vpr: tat: cytochrome P lymphocyte; CTL: immune response: epitope;  
 XX antigen: vaccine: HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus Type 1  
 XX W0200124810-A1  
 XX 12-APR-2001.  
 XX 05-JUL-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412853.  
 XX (EPIMV) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chestnut R;  
 XX Baker DM, Coats E, Kubo RT, Grey HM;  
 XX WPI: 2001-454887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 42: Page 24: 448pp; English.  
 XX The present invention describes a composition (1) comprising a prepared  
 XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 XX sequence selected from 51 defined amino acid sequences (ABL25447 to  
 XX ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 XX may be used for immunising subjects against HIV-1 infections. The use of

CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumor-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunocompetency. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABL1501 to ABL25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:  
 CC  
 CC Empty Match 96.4% Score 41 DB 22 Length 9;  
 CC Best Local Similarity 100.0% Pred. No. 9.4e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5  
 DE 1 KKER 4

RESULT 4:  
 ABL15261:  
 ID ABL15261 standard: peptide: 9 AA  
 AC ABL15261:  
 XX 15-JUL-2002 (first entry)  
 XX HIV B62 super motif pol peptide #267.  
 XX HIV: HIV-1; human immunodeficiency virus: env: pol: gag: nef: vpr:  
 XX vpr: vpr: tat: cytochrome P lymphocyte; CTL: immune response: epitope;  
 XX antigen: vaccine: HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus Type 1  
 XX W0200124810-A1  
 XX 12-APR-2001.  
 XX 05-JUL-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412853.  
 XX (EPIMV) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chestnut R;  
 XX Baker DM, Coats E, Kubo RT, Grey HM;  
 XX WPI: 2001-454887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 42: Page 24: 448pp; English.  
 XX The present invention describes a composition (1) comprising a prepared  
 XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 XX sequence selected from 51 defined amino acid sequences (ABL25447 to  
 XX ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 XX may be used for immunising subjects against HIV-1 infections. The use of



CC group based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumor associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HIV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA:  
 Query Match 36.4% Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pos. No. 9; 40-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 QY 2 KKEK 5  
 ID 1 1 1 1 1  
 4 KKEK 7  
 RESULT 4b  
 ABP25445  
 ID ABP25445 Standard; Peptide: 9 AA.  
 AC ABP25445;  
 XX  
 QY 15 JUL 2002 (first entry)  
 XX  
 DE HIV A93 motif; pol. peptide #440  
 XX  
 KW HIV; HIV 1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; vpr; tat; cytototoxic lymphocyte; ccr5; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 IN W-25012487.0 A1  
 XX  
 CL 12-APR 2001.  
 XX  
 FF 05-OCT 2000; 2003W0 US27766.  
 XX  
 PR 05-OCT 1999; 99US 0412063.  
 XX  
 PA (EPIM ) EPIMUNE INC.  
 XX  
 PI Scott A, Sidney J, Southwood S, Livingston BD, Chestnut K,  
 PI Baker DM, Curtis E, Kubo RT, Gray HM;  
 XX  
 DR WP1: 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 42; Page 263; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or

CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumor associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HIV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA:  
 Query Match 36.4% Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pos. No. 9; 40-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 QY 2 KKEK 5  
 ID 1 1 1 1 1  
 4 KKEK 7  
 RESULT 4b  
 ABP25445  
 ID ABP25445 Standard; Peptide: 9 AA.  
 AC ABP25445;  
 XX  
 QY 15 JUL 2002 (first entry)  
 XX  
 DE HIV A93 motif; pol. peptide #440  
 XX  
 KW HIV; HIV 1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; vpr; tat; cytototoxic lymphocyte; ccr5; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 IN W-25012487.0 A1  
 XX  
 CL 12-APR 2001.  
 XX  
 FF 05-OCT 2000; 2003W0 US27766.  
 XX  
 PR 05-OCT 1999; 99US 0412063.  
 XX  
 PA (EPIM ) EPIMUNE INC.  
 XX  
 PI Scott A, Sidney J, Southwood S, Livingston BD, Chestnut K,  
 PI Baker DM, Curtis E, Kubo RT, Gray HM;  
 XX  
 DR WP1: 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 42; Page 302; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or







17M proteins protein search using sw-mem.  
 Release: September 30, 2003, 11:06:58, Search time: 11:43:55, Seqs: 6  
 Copyright (c) 1994-2003, Gappedata, Inc.  
 (sw-mem algorithm)  
 98.54% Residue, cell updates/sec

Title: US-09-787-443-17

Perfect score: 11

Sequence: 1 AKKKPKPNQ 11

Scoring table: CL100

Gapped 60.0, Gapped: 4.0

Searches: 283387 seqs, 96158682 residues

Word size: 3

Total number of hits satisfying chosen parameters: 2054

Minimum gap seq length: 6

Maximum hit seq length: 19

FAST processing: listing first 500 summaries

Database: PIR76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Prod. No. is the number of results produced by chance to have a  
 Score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4	45.4	15	2	PA233.6	Protein, Q22000.6
2	3	27.3	8	2	PA233.6	Protein, Q22000.6
3	3	27.3	9	2	PA233.6	Protein, Q22000.6
4	3	27.3	10	2	PA233.6	Protein, Q22000.6
5	3	27.3	11	2	PA233.6	Protein, Q22000.6
6	3	27.3	11	2	PA233.6	Protein, Q22000.6
7	3	27.3	11	2	PA233.6	Protein, Q22000.6
8	3	27.3	12	2	PA233.6	Protein, Q22000.6
9	3	27.3	12	2	PA233.6	Protein, Q22000.6
10	3	27.3	12	2	PA233.6	Protein, Q22000.6
11	3	27.3	13	1	QNRK	Protein, Q22000.6
12	3	27.3	13	2	S2115.2	Protein, Q22000.6
13	3	27.3	13	2	A0512.4	Protein, Q22000.6
14	3	27.3	13	2	10653.3	Protein, Q22000.6
15	3	27.3	13	2	S2294.6	Protein, Q22000.6
16	3	27.3	13	2	Q2233.9	Protein, Q22000.6
17	3	27.3	13	2	Q2233.9	Protein, Q22000.6
18	3	27.3	13	2	A0512.6	Protein, Q22000.6
19	3	27.3	14	1	QWAVV	Protein, Q22000.6
20	3	27.3	14	1	QWVHK	Protein, Q22000.6
21	3	27.3	14	1	QWVHK	Protein, Q22000.6
22	3	27.3	14	1	QWVHK	Protein, Q22000.6
23	3	27.3	14	2	S2294.2	Protein, Q22000.6
24	3	27.3	14	2	14975.3	Protein, Q22000.6
25	3	27.3	14	2	9441.6	Protein, Q22000.6
26	3	27.3	14	2	A0110.6	Protein, Q22000.6
27	3	27.3	14	2	6610.6	Protein, Q22000.6
28	3	27.3	14	2	S143.6	Protein, Q22000.6
29	3	27.3	14	2	1672.9	Protein, Q22000.6

dehydrin 4.5K poly	14	2	PA448.2	27.3	3	40
hydrogensulfite re	15	2	S212.8	27.3	3	31
cellulase (EC 3.2.	15	2	A631.6	27.3	3	32
22K protein p1. mi	15	2	A491.7	27.3	3	33
small granule S6 c	15	2	PC111.3	27.3	3	34
cytochrome-c oxida	15	2	S7798.7	27.3	3	35
hypertrehalosemic	8	2	S6899.6	16.2	2	36
hypertrehalosemic	8	2	S6899.6	16.2	2	37
adipokinetic hormo	8	2	A498.2	16.2	2	38
adipokinetic hormo	8	2	A498.2	16.2	2	39
neuropeptide led-C	8	2	A4496.0	16.2	2	40
neuropeptide led-C	8	2	A4496.0	16.2	2	41
hypertrehalosemic	8	2	A497.6	16.2	2	42
hypertrehalosemic	8	2	A497.6	16.2	2	43
leghemoglobin 11f	8	2	S2016.2	16.2	2	44
rpsA protein - Erw	8	2	S471.1	16.2	2	45
glycine reductase	8	2	A910.8	16.2	2	46
variant surface ql	8	2	A2144.0	16.2	2	47
neuropeptide M-1 -	8	2	AC516.9	16.2	2	48
callitremamide 8 -	8	2	H4197.8	16.2	2	49
acetylcholinestera	8	2	A4111.7	16.2	2	50
apolipoprotein A-1	8	2	14893.4	16.2	2	51
cytochrome P450 AL	8	2	A6159.7	16.2	2	52
major postsynaptic	8	2	A4268.9	16.2	2	53
thymic factor - pi	8	2	YF82	16.2	2	54
thymocyte growth p	8	2	A6095.7	16.2	2	55
cat gene leader po	8	2	S304.9	16.2	2	56
chloramphenicol O-	8	2	B2436.2	16.2	2	57
quinoline 2-oxidor	8	2	S6660.8	16.2	2	58
orf AB protein - S	8	2	S1952.3	16.2	2	59
ribosomal protein	8	2	SP507.3	16.2	2	60
tetrameric protein	8	2	S6441.9	16.2	2	61
amine oxidase (cop	8	2	S7034.5	16.2	2	62
hypothetical prote	8	2	13161.2	16.2	2	63
callitremamide 10	8	2	A4478.7	16.2	2	64
cytochrome-c oxida	8	2	S7798.4	16.2	2	65
118K stomach cance	8	2	A6315.6	16.2	2	66
lg heavy chain CRD	8	2	PI027.2	16.2	2	67
macrophage inhibit	8	2	A6138.6	16.2	2	68
zymogen granule me	8	2	PC219.7	16.2	2	69
alpha-2-macroglobu	8	2	S6653.6	16.2	2	70
spectrin alpha cha	8	2	PC707.6	16.2	2	71
unidentified 48.7K	8	2	PC707.8	16.2	2	72
52.5K protein - SP	8	2	S7842.6	16.2	2	73
gonadotrophin - se	10	2	RH5MGS	16.2	2	74
alpha-2-macroglobu	10	2	S3384.4	16.2	2	75
hypertrehalosemic	10	2	JC141.6	16.2	2	76
hypertrehalosemic	10	2	S041.8	16.2	2	77
caerulein-like pep	10	2	A1468.7	16.2	2	78
scyllorhizin 1 - s	10	2	A2486.7	16.2	2	79
phyllomedulin - tw	10	2	S0720.2	16.2	2	80
hypothetical prote	10	2	D3739.7	16.2	2	81
urease (EC 3.5.1.5	10	2	C3538.9	16.2	2	82
bacterioterritin -	10	2	S4818.2	16.2	2	83
neurotoxin-associa	10	2	F4464.4	16.2	2	84
glycine reductase	10	2	B3930.8	16.2	2	85
ribosomal protein	10	2	JP067.2	16.2	2	86
polyferredoxin - M	10	2	S6220.8	16.2	2	87
polygalacturonase	10	2	S6288.0	16.2	2	88
transcription fact	10	2	A4208.9	16.2	2	89
gonadotropin-relea	10	2	A4918.7	16.2	2	90
cytochrome-c oxida	10	2	S4362.5	16.2	2	91
cytochrome-c oxida	10	2	S4363.1	16.2	2	92
bradykinin-potent	10	2	H3719.6	16.2	2	93
platelet activatin	10	2	H4548.2	16.2	2	94
T-cell receptor al	10	2	S2337.0	16.2	2	95
T-cell receptor ga	10	2	F4903.3	16.2	2	96
matrix metalloprot	10	2	S7194.8	16.2	2	97
lg heavy chain C r	10	2	A3726.8	16.2	2	98
olfactory receptor	10	2	C5482.3	16.2	2	99
T-cell receptor al	10	2	PT021.3	16.2	2	100
olfactory receptor	10	2	D5482.3	16.2	2	101
cytochrome-c oxida	10	2	S6538.7	16.2	2	102



253	2	18.2	2	PA0045	protein for 1 - Arabi	322	2	18.2	15	2	P00862	protein G600023 -
250	2	18.2	2	PA0116	protein G600044 -	323	2	18.2	15	2	PA0007	seed storage prote
251	2	18.2	2	PA0307	lectin B1 - Isoflav	324	2	18.2	15	2	S43521	RNA-binding protei
252	2	18.2	2	PA0306	phosphogluco isom	325	2	18.2	15	2	PA0008	lectin B2 - psopho
253	2	18.2	2	PA0307	phosphogluco isom	326	2	18.2	15	2	PS0276	phospholipid kinase
254	2	18.2	2	PA0307	phosphogluco isom	327	2	18.2	15	2	PA0057	adenylate isopente
255	2	18.2	2	PA0307	phosphogluco isom	328	2	18.2	15	2	PA0064	cytochrome c3 - 1
256	2	18.2	2	PA0307	phosphogluco isom	329	2	18.2	15	2	PA0087	cytochrome c2 - fu
257	2	18.2	2	PA0307	phosphogluco isom	330	2	18.2	15	2	PA0093	emulatin synthetas
258	2	18.2	2	PA0307	phosphogluco isom	331	2	18.2	15	2	PA0076	fructose biphosph
259	2	18.2	2	PA0307	phosphogluco isom	332	2	18.2	15	2	PA0105	heat shock protein
260	2	18.2	2	PA0307	phosphogluco isom	333	2	18.2	15	2	PA0091	methionine adenosy
261	2	18.2	2	PA0307	phosphogluco isom	334	2	18.2	15	2	PA0056	protein G200002 -
262	2	18.2	2	PA0307	phosphogluco isom	335	2	18.2	15	2	PA0052	protein G200015 -
263	2	18.2	2	PA0307	phosphogluco isom	336	2	18.2	15	2	PA0051	protein G200016 -
264	2	18.2	2	PA0307	phosphogluco isom	337	2	18.2	15	2	PA0086	protein G200044 -
265	2	18.2	2	PA0307	phosphogluco isom	338	2	18.2	15	2	PA0088	protein G200051 -
266	2	18.2	2	PA0307	phosphogluco isom	339	2	18.2	15	2	PA0106	protein G200076 -
267	2	18.2	2	PA0307	phosphogluco isom	340	2	18.2	15	2	PA0097	starch phosphoryla
268	2	18.2	2	PA0307	phosphogluco isom	341	2	18.2	15	2	PA0097	starch phosphoryla
269	2	18.2	2	PA0307	phosphogluco isom	342	2	18.2	15	2	PA0097	starch phosphoryla
270	2	18.2	2	PA0307	phosphogluco isom	343	2	18.2	15	2	PA0097	starch phosphoryla
271	2	18.2	2	PA0307	phosphogluco isom	344	2	18.2	15	2	PA0097	starch phosphoryla
272	2	18.2	2	PA0307	phosphogluco isom	345	2	18.2	15	2	PA0097	starch phosphoryla
273	2	18.2	2	PA0307	phosphogluco isom	346	2	18.2	15	2	PA0097	starch phosphoryla
274	2	18.2	2	PA0307	phosphogluco isom	347	2	18.2	15	2	PA0097	starch phosphoryla
275	2	18.2	2	PA0307	phosphogluco isom	348	2	18.2	15	2	PA0097	starch phosphoryla
276	2	18.2	2	PA0307	phosphogluco isom	349	2	18.2	15	2	PA0097	starch phosphoryla
277	2	18.2	2	PA0307	phosphogluco isom	350	2	18.2	15	2	PA0097	starch phosphoryla
278	2	18.2	2	PA0307	phosphogluco isom	351	2	18.2	15	2	PA0097	starch phosphoryla
279	2	18.2	2	PA0307	phosphogluco isom	352	2	18.2	15	2	PA0097	starch phosphoryla
280	2	18.2	2	PA0307	phosphogluco isom	353	2	18.2	15	2	PA0097	starch phosphoryla
281	2	18.2	2	PA0307	phosphogluco isom	354	2	18.2	15	2	PA0097	starch phosphoryla
282	2	18.2	2	PA0307	phosphogluco isom	355	2	18.2	15	2	PA0097	starch phosphoryla
283	2	18.2	2	PA0307	phosphogluco isom	356	2	18.2	15	2	PA0097	starch phosphoryla
284	2	18.2	2	PA0307	phosphogluco isom	357	2	18.2	15	2	PA0097	starch phosphoryla
285	2	18.2	2	PA0307	phosphogluco isom	358	2	18.2	15	2	PA0097	starch phosphoryla
286	2	18.2	2	PA0307	phosphogluco isom	359	2	18.2	15	2	PA0097	starch phosphoryla
287	2	18.2	2	PA0307	phosphogluco isom	360	2	18.2	15	2	PA0097	starch phosphoryla
288	2	18.2	2	PA0307	phosphogluco isom	361	2	18.2	15	2	PA0097	starch phosphoryla
289	2	18.2	2	PA0307	phosphogluco isom	362	2	18.2	15	2	PA0097	starch phosphoryla
290	2	18.2	2	PA0307	phosphogluco isom	363	2	18.2	15	2	PA0097	starch phosphoryla
291	2	18.2	2	PA0307	phosphogluco isom	364	2	18.2	15	2	PA0097	starch phosphoryla
292	2	18.2	2	PA0307	phosphogluco isom	365	2	18.2	15	2	PA0097	starch phosphoryla
293	2	18.2	2	PA0307	phosphogluco isom	366	2	18.2	15	2	PA0097	starch phosphoryla
294	2	18.2	2	PA0307	phosphogluco isom	367	2	18.2	15	2	PA0097	starch phosphoryla
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299	2	18.2	2	PA0307	phosphogluco isom	372	2	18.2	15	2	PA0097	starch phosphoryla
300	2	18.2	2	PA0307	phosphogluco isom	373	2	18.2	15	2	PA0097	starch phosphoryla
301	2	18.2	2	PA0307	phosphogluco isom	374	2	18.2	15	2	PA0097	starch phosphoryla
302	2	18.2	2	PA0307	phosphogluco isom	375	2	18.2	15	2	PA0097	starch phosphoryla
303	2	18.2	2	PA0307	phosphogluco isom	376	2	18.2	15	2	PA0097	starch phosphoryla
304	2	18.2	2	PA0307	phosphogluco isom	377	2	18.2	15	2	PA0097	starch phosphoryla
305	2	18.2	2	PA0307	phosphogluco isom	378	2	18.2	15	2	PA0097	starch phosphoryla
306	2	18.2	2	PA0307	phosphogluco isom	379	2	18.2	15	2	PA0097	starch phosphoryla
307	2	18.2	2	PA0307	phosphogluco isom	380	2	18.2	15	2	PA0097	starch phosphoryla
308	2	18.2	2	PA0307	phosphogluco isom	381	2	18.2	15	2	PA0097	starch phosphoryla
309	2	18.2	2	PA0307	phosphogluco isom	382	2	18.2	15	2	PA0097	starch phosphoryla
310	2	18.2	2	PA0307	phosphogluco isom	383	2	18.2	15	2	PA0097	starch phosphoryla
311	2	18.2	2	PA0307	phosphogluco isom	384	2	18.2	15	2	PA0097	starch phosphoryla
312	2	18.2	2	PA0307	phosphogluco isom	385	2	18.2	15	2	PA0097	starch phosphoryla
313	2	18.2	2	PA0307	phosphogluco isom	386	2	18.2	15	2	PA0097	starch phosphoryla
314	2	18.2	2	PA0307	phosphogluco isom	387	2	18.2	15	2	PA0097	starch phosphoryla
315	2	18.2	2	PA0307	phosphogluco isom	388	2	18.2	15	2	PA0097	starch phosphoryla
316	2	18.2	2	PA0307	phosphogluco isom	389	2	18.2	15	2	PA0097	starch phosphoryla
317	2	18.2	2	PA0307	phosphogluco isom	390	2	18.2	15	2	PA0097	starch phosphoryla
318	2	18.2	2	PA0307	phosphogluco isom	391	2	18.2	15	2	PA0097	starch phosphoryla
319	2	18.2	2	PA0307	phosphogluco isom	392	2	18.2	15	2	PA0097	starch phosphoryla
320	2	18.2	2	PA0307	phosphogluco isom	393	2	18.2	15	2	PA0097	starch phosphoryla
321	2	18.2	2	PA0307	phosphogluco isom	394	2	18.2	15	2	PA0097	starch phosphoryla





[illegible]



Cite: 10-Jan-1997 #sequence\_revision 05-Jun-1997 #text\_change 16-Feb-2000

C:Accession: A05174  
 C:Species: Escherichia coli  
 C:Title: Purification and transfer of the cloned *swtA* gene from *Escherichia coli* strain 8639  
 C:Accession: J02409  
 C:Species: Escherichia coli  
 C:Title: Purification and transfer of the cloned *swtA* gene from *Escherichia coli* strain 8639  
 C:Accession: J02409  
 C:Species: Escherichia coli  
 C:Title: Purification and transfer of the cloned *swtA* gene from *Escherichia coli* strain 8639

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
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QY 4 KEK 6  
 II  
 DB 2 KEK 4

Query Match: 27.3% Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6  
 II  
 DB 2 KEK 4







Query Match 27.3% Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3; 4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EKP 6  
 DL 1 EKP 3

RESULT 15  
 S77987  
 cytochrome c oxidase (EC 1.9.3.1) chain VIII-2; Eupye 100 (14-peptides)  
 C:Species: Thaumococcus bigeysii (fungus)  
 C:Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 04-Sep-1998  
 C:Accession: S77987  
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Lindell, D.; Gottschalk, F.; Kadenbach, B.  
 submitted to the Protein Sequence Database, June 1997  
 A:Reference number: S77980  
 A:Accession: S77987  
 A:Molecule type: protein  
 A:Residues: 18; 9-15 <ARN>  
 A:Experimental source: heart  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Pathway: oxidative phosphorylation, respiratory chain  
 C:Keywords: electron transfer; membrane-associated complex; mitochondria; inner membrane

Query Match 27.3% Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3; 4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKK 4  
 DL 7 AKK 9

RESULT 16  
 S80995  
 hyperreninase hormone 1 - - - - - of central cockroach  
 N:Alternate names: periplanetin CC-1  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 30-Jan-1992 #sequence\_revision 24-Oct-1997 #text\_change 07-Oct-1997  
 C:Accession: S08995  
 R:Gaede, G.; Rinehart, K.L.  
 and J. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A:Title: Primary structures of hypertrichalosemic neuropeptides isolated from the c  
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
 A:Reference number: S08995; MUID:90253659; PMID:2340112  
 A:Accession: S08995  
 A:Molecule type: protein  
 A:Residues: 18; 9-15 <GAE>  
 A:Note: the amino terminal residue forms pyrrolidone carboxylic acid, therefore, we  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2; 8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PN 7  
 DL 6 PN 7

RESULT 17  
 S08996  
 hyperreninase hormone 1 - - - - - of central cockroach  
 N:Alternate names: periplanetin CC-1  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C:Accession: A49823  
 R:Scarborough, K.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory am  
 A:Reference number: A49823; MUID:84298179; PMID:6591205  
 A:Accession: A49823  
 A:Molecule type: protein  
 A:Residues: 18; 9-15 <GAE>  
 A:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglu  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2; 8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PN 7  
 DL 6 PN 7

RESULT 19  
 S89923  
 adipokinetic hormone 1 - - - - - American cockroach  
 N:Alternate names: neuropeptide M-11; periplanetin CC-1  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C:Accession: B49823; A05170  
 R:Scarborough, K.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory am  
 A:Reference number: A49823; MUID:84298179; PMID:6591205  
 A:Accession: B49823  
 A:Molecule type: protein  
 A:Residues: 18; 9-15 <GAE>  
 R:Witten, J.L.; Schaffer, M.H.; Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr.,  
 Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
 A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment  
 A:Reference number: A99118; MUID:85046530; PMID:6548628  
 A:Accession: A05170  
 A:Molecule type: protein

C:Date: 30-Jan-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997

C:Accession: S08996

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrichalosemic neuropeptides isolated from the c  
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bon

A:Reference number: S08995; MUID:90253659; PMID:2340112

A:Accession: S08996

A:Molecule type: protein

A:Residues: 18 <GAE>

A:Note: the amino terminal residue forms pyrrolidone carboxylic acid, therefore, we

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2; 8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PN 7

DL 6 PN 7







Leucoperoxidase: carboxylic ester hydrolase

Query Match: 18.2% SC 20 21 16 25 100% 40  
 Best Local Similarity: 100.0% Pos 1 3 2 80 2 1  
 Matching: 23 Conservative: 30 Misplaced: 00 Gaps: 00

SV 6 FN 7  
 DE 11  
 7 FN 8

Source: Uniprot/RefSeq/TrEMBL  
 Job Time: 12.4167 secs



107	2	18.2	13	1	RS13_ASHVAP	243542	ash yellow	180	1	9.1	8	1	CAN1_ENTFA	P13268 entecocarcu
108	2	18.2	13	1	TEJA_RANJA	280002	racca papua	181	1	9.1	8	1	CKK1_MAGSU	P10369 macropus eu
109	2	18.2	14	1	CALL_CAGLI	220128	calibri pis	182	1	9.1	8	1	CLP1_THICU	P80488 thiobaciliu
110	2	18.2	14	1	ETU1_CANFA	246435	caelis lami	183	1	9.1	9	1	CMZ2_CONPU	P58785 conus purpu
111	2	18.2	14	1	KPPI_SEIMI	225903	selicostidiu	184	1	9.1	8	1	COXG_RAT	P80440 rattus norv
112	2	18.2	14	1	CRG1_ESGSI	222963	esopocarcipa	185	1	9.1	8	1	FAR1_PENNO	P83316 penaeus mon
113	2	18.2	14	1	MASI_TAPIT	212715	tasapocarpa	186	1	9.1	8	1	FAR2_MACRS	P81275 macrobrachi
114	2	18.2	14	1	MASI_TALJA	260512	taliosus la	187	1	9.1	8	1	FAR3_HUMAM	P41486 homarus ame
115	2	18.2	14	1	MASI_VESPA	212208	vespa cicco	188	1	9.1	8	1	FAR4_HUMAM	P41487 homarus ame
116	2	18.2	14	1	KPK1_KPITIM	238813	kapah lara	189	1	9.1	8	1	FAR4_MACRS	P81277 macrobrachi
117	2	18.2	14	1	RS14_TALIP	240228	talipus foli	190	1	9.1	8	1	FAR7_ASCSU	P43171 ascaris suu
118	2	18.2	14	1	RS14_TALIP	240228	talipus foli	191	1	9.1	8	1	FUSS_FUSSO	P81010 fusarium so
119	2	18.2	14	1	RS15_TLWBP	246876	talipus foli	192	1	9.1	8	1	SEUR_HUMAN	P02729 homo sapien
120	2	18.2	14	1	RS15_TLWBP	246876	talipus foli	193	1	9.1	8	1	LEK1_LEUMA	P21140 leucophaea
121	2	18.2	14	1	TAL_HVW2	212509	talipus foli	194	1	9.1	8	1	LEK2_LEUMA	P21141 leucophaea
122	2	18.2	14	1	TAT_HVW2	212511	talipus foli	195	1	9.1	8	1	LEK3_LEUMA	P21142 leucophaea
123	2	18.2	14	1	TKN1_SHUGS	282470	schistopore	196	1	9.1	8	1	LEK4_LEUMA	P21143 leucophaea
124	2	18.2	14	1	UN17_TLIDA	281562	talipus foli	197	1	9.1	8	1	LEK5_LEUMA	P19989 leucophaea
125	2	18.2	14	1	UN17_TLIDA	281562	talipus foli	198	1	9.1	8	1	LEK6_LEUMA	P19990 leucophaea
126	2	18.2	15	1	ABZ_EKUSE	229260	prucis sero	199	1	9.1	8	1	LEK7_LEUMA	P22396 locusta mig
127	2	18.2	15	1	ASPL_LACSN	282649	lactobacilli	200	1	9.1	8	1	LEK8_LEUMA	P13049 leucophaea
128	2	18.2	15	1	COA1_RAT	241320	rattus norv	201	1	9.1	8	1	LEK9_LEUMA	P23211 staphylococ
129	2	18.2	15	1	CHIT_FEA	221225	pus am sili	202	1	9.1	8	1	LEK10_LEUMA	P15507 bos taurus
130	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	203	1	9.1	8	1	LEK11_LEUMA	P82455 orconectes
131	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	204	1	9.1	8	1	LEK12_LEUMA	P82692 periplaneta
132	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	205	1	9.1	8	1	LEK13_LEUMA	P82618 periplaneta
133	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	206	1	9.1	8	1	LEK14_LEUMA	P08949 pandanus bo
134	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	207	1	9.1	8	1	LEK15_LEUMA	P33564 mycobacteri
135	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	208	1	9.1	8	1	LEK16_LEUMA	P82929 bos taurus
136	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	209	1	9.1	8	1	LEK17_LEUMA	P80642 zea mays (m
137	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	210	1	9.1	8	1	LEK18_LEUMA	P38644 mus muscula
138	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	211	1	9.1	8	1	LEK19_LEUMA	P56575 rattus norv
139	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	212	1	9.1	8	1	LEK20_LEUMA	P30687 homo sapien
140	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	213	1	9.1	8	1	LEK21_LEUMA	P40096 homo sapien
141	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	214	1	9.1	8	1	LEK22_LEUMA	P81780 herpes simp
142	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	215	1	9.1	8	1	LEK23_LEUMA	P83195 perkinsus a
143	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	216	1	9.1	8	1	LEK24_LEUMA	P81813 carcarius ma
144	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	217	1	9.1	8	1	LEK25_LEUMA	P82678 chlamydomon
145	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	218	1	9.1	8	1	LEK26_LEUMA	P83375 serratia pl
146	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	219	1	9.1	8	1	LEK27_LEUMA	P81337 clostridium
147	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	220	1	9.1	8	1	LEK28_LEUMA	P38556 carcarius ma
148	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	221	1	9.1	8	1	LEK29_LEUMA	P05487 conus geogr
149	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	222	1	9.1	8	1	LEK30_LEUMA	P05487 conus geogr
150	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	223	1	9.1	8	1	LEK31_LEUMA	P24816 nephrops no
151	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	224	1	9.1	8	1	LEK32_LEUMA	P16339 locusta mig
152	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	225	1	9.1	8	1	LEK33_LEUMA	P01186 eryctolagus
153	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	226	1	9.1	8	1	LEK34_LEUMA	P41856 calliphora
154	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	227	1	9.1	8	1	LEK35_LEUMA	P41857 calliphora
155	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	228	1	9.1	8	1	LEK36_LEUMA	P41858 calliphora
156	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	229	1	9.1	8	1	LEK37_LEUMA	P83276 macrobrachi
157	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	230	1	9.1	8	1	LEK38_LEUMA	P83318 penaeus mon
158	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	231	1	9.1	8	1	LEK39_LEUMA	P83319 penaeus mon
159	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	232	1	9.1	8	1	LEK40_LEUMA	P41860 calliphora
160	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	233	1	9.1	8	1	LEK41_LEUMA	P82661 paragrillus
161	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	234	1	9.1	8	1	LEK42_LEUMA	P81320 penaeus mon
162	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	235	1	9.1	8	1	LEK43_LEUMA	P41861 calliphora
163	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	236	1	9.1	8	1	LEK44_LEUMA	P83279 macrobrachi
164	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	237	1	9.1	8	1	LEK45_LEUMA	P41862 calliphora
165	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	238	1	9.1	8	1	LEK46_LEUMA	P83281 macrobrachi
166	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	239	1	9.1	8	1	LEK47_LEUMA	P43172 ascaris suu
167	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	240	1	9.1	8	1	LEK48_LEUMA	P41868 calliphora
168	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	241	1	9.1	8	1	LEK49_LEUMA	P38495 callinectes
169	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	242	1	9.1	8	1	LEK50_LEUMA	P19346 erythrocybu
170	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	243	1	9.1	8	1	LEK51_LEUMA	P19345 macaca fusc
171	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	244	1	9.1	8	1	LEK52_LEUMA	P19344 papio anubi
172	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	245	1	9.1	8	1	LEK53_LEUMA	P19343 papio anubi
173	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	246	1	9.1	8	1	LEK54_LEUMA	P19342 theropithec
174	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	247	1	9.1	8	1	LEK55_LEUMA	P80159 treponema h
175	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	248	1	9.1	8	1	LEK56_LEUMA	P83350 sarcophaga
176	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	249	1	9.1	8	1	LEK57_LEUMA	P12381 klebsiella
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178	2	18.2	15	1	CRJA_CROQU	258841	crocus spore	251	1	9.1	8	1	LEK59_LEUMA	P42993 cyprinus ca
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Query Match: 100.0%; Pred. No. 1,8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DI 10 AKK 12

RESULT 11
MAST_VESMA
ID MAST_VESMA STANCAKO: PRI: 14 AA.
AC P04205;
DI 20-MAR-1987 (rel. 04, last sequence update)
DI 20-MAR-1987 (rel. 04, last sequence update)
DI 28-FEB-2003 (rel. 41, last annotation update)
DE Mastoparan M [Mast cell-degranulating peptide].
OS Vespa mandarina (hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID:7445;
RN [1]
RP SEQUENCE.
RC MEDLINE:84285 (rel. 04, last sequence update)
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide, mastoparan-M, in the venom of
RT the hornet Vespa mandarina."
RC Abstr. Res. 2:447-449 (1981).
CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: A01777; QMVHP2.
KW Mast cell degranulation; Amidation.
FT MGLPES 14 AA: 1480 MW; C85A7ECA1D7R00DD CRC64.
SQ SEQUENCE 14 AA: 27.1%; Score 3; DB 1; Length 14;

Query Match: 100.0%; Pred. No. 1,8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DI 10 AKK 12

RESULT 12
MAST_VESMA
ID MAST_VESMA STANCAKO: PRI: 14 AA.
AC P04205;
DI 21-JUN-1986 (rel. 01, last sequence update)
DI 21-JUN-1986 (rel. 01, last sequence update)
DI 28-FEB-2003 (rel. 41, last annotation update)
DE Mastoparan X (MX).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID:7446;
RN [1]
RP SEQUENCE.
RC MEDLINE:80553 (rel. 01, last sequence update)
RA Hirai Y., Kowada M., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide homologous to mastoparan in
RT the venom of Japanese hornet (Vespa xanthoptera)."
RC Chem. Pharm. Bull. 27:1945-1946 (1979).
CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: A01776; QMAYV.
KW Mast cell degranulation; Amidation.
FT MGLPES 14 AA: 1480 MW; C85A7ECA1D7R00DD CRC64.
SQ SEQUENCE 14 AA: 27.1%; Score 3; DB 1; Length 14;

Query Match: 100.0%; Pred. No. 1,8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DI 10 AKK 12

RESULT 13
MAST_VESMA
ID MAST_VESMA STANCAKO: PRI: 14 AA.
AC P04205;
DI 21-JUN-1986 (rel. 01, last sequence update)
DI 21-JUN-1986 (rel. 01, last sequence update)
DI 28-FEB-2003 (rel. 41, last annotation update)
DE Mastoparan Y (MY).
OS Vespa velutina (Yellow jacket) (wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID:7452;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC MEDLINE:80155 (rel. 01, last sequence update)
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Yoshida H.,
RT "A new mast cell degranulating peptide (mastoparan-Y) in the venom of
RT Vespa velutina."
RC Chem. Pharm. Bull. 27:1942-1944 (1979).
CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: A01776; QMAYV.
KW Mast cell degranulation; Amidation; DB structure.
FT MGLPES 14 AA: 1480 MW; C85A7ECA1D7R00DD CRC64.
SQ SEQUENCE 14 AA: 27.1%; Score 3; DB 1; Length 14;

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RP STRUCTURE BY NMR.
RX MEDLINE 9626894. PubMed:9547994.
RA Kusunoki H, Kakimoto K, Sato K, Miyazawa T, Kuno T.
RI "G Protein-bound conformation of mas/gp130K1: reconstitution of
RI multidimensional transferred nuclear overhauser effect analysis of
RI peptide uniformly enriched with 13C and 15N".
RL Biochemistry 37:4782-4790(1998)
CC -1 FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
CP PIR: A01796; QM00XK.
CR PUB: 1411; 16-FEB-99.
KW Mast cell degranulation; Activation; G structure.
FT MISC_RES 14 24 ACETATION
SQ SEQUENCE 14 AA: 1557 MW: 2045672AA/ASDLS CK 642

Query Match 27.4% Score 3; BB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1 8024;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3
DB 1; AKK 12

RESULT 13
TSNK_PANNA
ID TSNK_PANNA STANDARD; PRI: 14 AA.
AC P40953
DI 01-FEB-1995 (Rev. 31; Created)
DI 01-FEB-1995 (Rev. 31; Last sequence update)
DI 15-SEP-2003 (Rev. 42; Last annotation update)
DE Pancreatic.
OS Rana maculata (Chinese frog).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Bufoninae.
CX NCBI_TaxID:121156;
RN SEQUENCE.
RP TISSUE: Skin secretion.
RX MEDLINE 96265652; PubMed:2405543.
RA Bao Y Q, Tian S B, Wu S X, Guo L Q, Wu L F, Chen E M, Li Y A,
RA Zhu Y Q, Zou G, Tsou K.
RI "Isolation and structure of ranamartinin, a new tachykinin from the
RI skin of Chinese frog Rana maculata".
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 42(5):574(1999)
RN 121
RP SYNOPSIS.
RX MEDLINE 96265650; PubMed:2405542.
RA Gu Y A, Bao Y Q, Zou Y Q, Wu S X, Guo L Q, Wu L F, Chen E M, Li Y A,
RI "Synthesis and biological activity of a new tachykinin peptide,
RI ranamartinin".
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 42(5):574(1999)
CC -1 FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKES BEHAVIORAL RESPONSES, ARE POLYMERIZABLE AND
CC SEREACTAGILES, AND CONTRACT (DEPENDENT ON THE POLYMERIZABLE
CC MESLES).
CC -2 SUBCELLULAR LOCATION: Secreted.
CC -3 TISSUE SPECIFICITY: SKIN.
CC -4 SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CR InterPro: IPR022640; Tachykinin.
CR Peptide: P50257; TACHYKININ_1.
KW Asphidian defense peptide; Tachykinin; Neuropeptide; Acetation.
FT MISC_RES 14 14 ACETATION
SQ SEQUENCE 14 AA: 1617 MW: 1459463066/6230 3664

Query Match 27.38% Score 3; BB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1 8024;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3
DB 7 AKK 9

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RESULT 14
COXI_THUOB
ID COXI_THUOB STANDARD; PRI: 15 AA.
AC P80978;
DI 01-NOV-1997 (Rev. 35; Created)
DI 01-NOV-1997 (Rev. 35; Last sequence update)
DI 01-NOV-1997 (Rev. 35; Last annotation update)
DE Cytochrome c oxidase polypeptide Vie-2 (EC 1.9.3.1) (Fragments)
OS Thynnus obesus (Bigeye tuna).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygia; Teleostei; Euteleostei;
CC Acanthopterygia; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CC Scombridae; Thunnus
CX NCBI_TaxID:8243;
RN SEQUENCE.
RP TISSUE:Heart;
RX MEDLINE-9745429; PubMed:9310466;
RA Arnold S, Lee L, Kim M, Sosa E, Linder D, Lottspeich F,
RA Kadenbach H.
RI "The subunit structure of cytochrome c oxidase from tuna heart and
RI liver".
RL Eur. J. Biochem. 248:59-63(1997).
CC -1 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -2 CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
CC -3 SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CR PIR: S77967; S77967.
KW oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_CONS 8 9
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1696 MW: 44309667/440294 CRC64;

Query Match 27.4% Score 3; BB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1 98-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 7 AKK 9

RESULT 15
EFIA_MENP
ID EFIA_MENP STANDARD; PRI: 15 AA.
AC P81267;
DI 15-JUL-1998 (Rev. 36; Created)
DI 15-JUL-1998 (Rev. 36; Last sequence update)
DI 15-DEC-1998 (Rev. 37; Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (fragment).
OS Microplitis croceipes.
CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
CC Braconidae; Microgasterinae; Microplitis.
CX NCBI_TaxID:72115;
RN SEQUENCE.
RP MEDLINE 99034459; PubMed:9816671;
RA Stuart M K.
RI "An antibody diagnostic for hymenopteran parasitism is specific for a
RI homologue of elongation factor-1 alpha."
RL Arch. Insect Biochem. Physiol. 39:1-8(1998).
CC -1 FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS (BY SIMILARITY).
CC -2 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -3 SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-1U/EF-1A SUBFAMILY.
CR InterPro: IPR000795; EF_51Pbind.

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IP PROSTETIN PS00401: EFATOR GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT N_K_TER 15
SQ SEQUENCE 15 AA: 1670 MW: 167060.600-251 1670-4;
      27.34; Score 3; DB 1; Length 15;
Query Match: 27.34; Score 3; DB 1; Length 15;
Best Local Similarity: 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 5
DE 111
2 KKK 4

RESULT 19
UP02_METAN STANDARD; PRT: 15 AA.
AC B83439;
DT 28-FEB-2003 (Rel. 41; Created)
DE 28-FEB-2003 (Rel. 41; Last sequence update)
DE Unknown 70 kDa protein (Fragment).
OS Metathizium anisopliae.
GC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;
OC Mitosporic Clavicipitaceae; Metarhizium.
OX NCBI_TaxID 5530;
RN [1]
RP SEQUENCE
RC STRAIN:5AA-1b;
RX MEDLINE:22341006; PubMed:12455610;
KT Ramp A.M.; Bidochka M.J.;
RT "Protein analysis in a pleomorphic, deteriorated strain of the
RL insect pathogenic fungus Metarhizium anisopliae."
RL Can. J. Microbiol. 48:787-792(2002).
SQ 1: MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
protein is 70 kDa.
FT N_K_TER 15
SQ SEQUENCE 15 AA: 148; MW: 20147407060153 CRC64;
      27.34; Score 3; DB 1; Length 15;
Query Match: 27.34; Score 3; DB 1; Length 15;
Best Local Similarity: 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PND 1;
DE 111
8 PND 10

RESULT 19
FAR1_PANRE STANDARD; PRT: 8 AA.
AC P41872;
DT 01-NOV-1995 (Rel. 32; Created)
DE 01-NOV-1995 (Rel. 32; Last sequence update)
DE 01-NOV-1995 (Rel. 32; Last annotation update)
DE PNFamide-like neuropeptide PFI (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;

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86 Query Match: 18.2%; Score 2; DB 1; Length 8;  
 87 Best Local Similarity: 100.0%; Pred. No. 1.3e-05;  
 88 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
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95 Blatta orientalis (Oriental cockroach).  
 96 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 97 Neoptera; Orthoptera; Dictyoptera; Blattaria; Blattodea;  
 98 Blattellidae; Periplaneta.  
 99 NCBI\_TaxID: 5978, 7539, 6976;  
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GenCore version 3.1.6  
Copyright (c) 1994 - 2003 Computer 1.1.1

OR protein protein search, using SW mode

sub on September 09, 2003, 10:07 4 - Search for 1,000,000 sequences  
(with limit 1,000,000) in  
protein database

title: US 09-787-443-17

perfect score: 11 AKKPKKNG 11

Sequence: 1 AKKPKKNG 11

Search method: BLAST

Gapop: 60.0 / Gapext: 60.0

Source: 83,525 seqs, 258,052,001 res. base

Word size: 0

Total number of hits satisfying chosen parameters: 439

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: testing first 500 similarities

Database: SPTREMBL-23.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_humani.\*

5: sp\_invertebrate.\*

6: sp\_mammali.\*

7: sp\_mari.\*

8: sp\_ornanello.\*

9: sp\_planti.\*

10: sp\_planti.\*

11: sp\_planti.\*

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Q94401 homo sapien  
Q8CJ33 mus musculus  
Q67446 equine inte  
Q8X415 escherichia  
Q56750 western x p  
Q46291 canadian pe  
Q43905 azospirillu  
Q15222 homo sapien  
Q9QW75 mus sp. hom  
P82831 tata inteiv  
Q47612 escherichia  
Q9UBK0 homo sapien  
Q9UC07 homo sapien  
Q9UCN2 homo sapien  
Q81ZQ0 homo sapien  
Q9WQ2 tachypleus  
Q91W04 crithidia f  
Q9AT15 lycopersico  
Q9SQ16 oryza sativ  
Q97T22 escherichia  
Q9AQP4 athrobacte  
Q49534 mycoplasma  
Q93SR0 staphylococ  
Q56429 thermus the  
Q9R9E0 bacillus su  
Q9R5R0 shigella dy  
Q85406 coxiella bu  
Q9UB9 saccharomyc  
Q15888 homo sapien  
Q9UCN4 homo sapien  
Q9UCN3 homo sapien  
Q9UCN5 toxoplasma  
Q9LX88 bos taurus  
Q18854 canis famil  
Q95M23 sus scrofa  
Q35792 saccharomyc  
Q46982 nicotiana p  
Q94PX5 telis silve  
Q94PX7 telis silve  
Q94PX6 telis silve  
Q8SB10 bacterioph  
Q819K1 bacterioph  
Q9C615 mus musculu  
Q9C295 tulica leuc  
Q91310 borrelia a  
Q917E8 escherichia  
Q47556 escherichia  
Q95111 shigella dy  
Q45852 elostiridium  
Q9JN16 streptococ  
Q49687 lactococci  
Q41363 borrelia ga  
Q93718 escherichia  
Q48686 lactococci  
Q937H9 enterobacte  
Q97792 borrelia bu  
Q93E20 streptococ  
Q9UR18 scierotium  
Q47151 homo sapien  
Q9X14 homo sapien  
Q9RS0 mycobacter  
Q9T210 spinacia ol  
Q9T211 spinacia ol  
Q11653 anser caeru  
Q99M03 mus musculu  
Q9C919 rattus norv  
Q8CJ13 mus musculu  
Q8QRR6 transmissib  
Q82622 avian infec  
Q67605 squash leaf  
Q92766 equine dist  
Q67606 squash leaf  
Q8QRR6 transmissib

GenCore version 5.1.4 Copyright (c) 1993-2003 Computer 111	
W protein	protein search, using sw mode
Run on	September 09, 2005, 10:02:34, Search time: 0.0001 sec (1000



[illegible]





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Query Match: 36.48; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 5
ID 7 KKK 10

RESULT 2
Q9R735 PRELIMINARY: PRT: 8 AA.
ID Q9R735
AC Q9R735
DT 01-MAY-2000 (EMBLrel. 13, Created)
DT 01-MAY-2000 (EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)
DE FKBP-12 (Fragment)
GN FKBP1
OS Mus musculus (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Euprimates; Hominoidea;
OC Hominidae;
OX NCBI_TaxID:9606;
EN 11
RP SEQUENCE FROM N.A.
RX MEDLINE:9215747; PubMed:1014676;
RA White G.R.M., Varley J.M., Holgway J.,
RI "Genomic structure and expression profile of a novel gene
RI variably expressed in breast cancer cell lines."
RI Br J Cancer. 1999;81:1491-1492(240).
DR EMBL: A244569; CAB60204.1;
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 1025 MW: 4559076344AABAB GR64;

Query Match: 27.3%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NKP 9
ID 11
ID 4 NKP 6

RESULT 3
Q9R735 PRELIMINARY: PRT: 8 AA.
ID Q9R735
AC Q9R735
DT 01-JUN-1998 (EMBLrel. 96, Created)
DT 01-JUN-1998 (EMBLrel. 96, Last sequence update)
DT 01-NOV-1999 (EMBLrel. 12, Last annotation update)
DE Apoptoprotein A-II (APO-AII) (Fragment)
GN APCA2
OS Mus musculus (Western wild mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10096;
EN 11
RP SEQUENCE FROM N.A.
RX STRAIN:Strk7/El.
RA Ko M.S., Wang X., Horton J.H., Hager M.L., Takahashi N., Maczaki Y.,
RA Nardau J.H.,
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
RL Mamm. Genome 5:349-355(1994).

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Query Match: 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 6
ID 11
ID 5 EXP 5

RESULT 4
Q9EZ14 PRELIMINARY: PRT: 9 AA.
ID Q9EZ14
AC Q9EZ14
DT 01-MAR-2001 (EMBLrel. 16, Created)
DT 01-MAR-2001 (EMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)
DE SPAS (Fragment)
GN SPAS
OS Sodalis glossinidius
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis
OX NCBI_TaxID:63612;
EN 11
RP SEQUENCE FROM N.A.
RX STRAIN:MI;
RX MEDLINE:2117142; PubMed:11172045;
RA Dale C., Young S.A., Haydon D.T., Welburn S.C.,
RI "The insect endosymbiont Sodalis glossinidius utilizes a type III
RI secretion system for cell invasion."
RI Proc. Natl. Acad. Sci. U.S.A. 98:1883-1888(2001).
DR EMBL: AF106650; AAG48607.1;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA: 1035 MW: 8185633801A33455 GR64;

Query Match: 27.3%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 6
ID 11
ID 5 EXP 6

RESULT 5
Q9R735 PRELIMINARY: PRT: 9 AA.
ID Q9R735
AC Q9R735
DT 01-MAY-2000 (EMBLrel. 13, Created)
DT 01-MAY-2000 (EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)
DE FKBA protein (Fragment)
GN FKBA
OS Streptomyces chrysomallus
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces
OX NCBI_TaxID:1899;
EN 11
RP SEQUENCE FROM N.A.
RX MEDLINE:94341259; PubMed:8062824;
RA Pahl A., Keller U.;
RI "Streptomyces chrysomallus FKBP-13 is a novel immunophilin consisting
RI of two FK506-binding domains with its gene transcriptionally coupled
RI to the FKBP-12 gene."
RL EMBO J. 13:472-3480(1994).
DR EMBL: Z44523; CAA84282.1;

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[illegible]



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ID Q66746 PRELIMINARY: PRT: 13 AA.
AC Q66746
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Analogue of IN-2B (Fragment).
GN Analogue of IN-2B.
OS Insect softens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Hominoidea; Hominidae;
OC Homo;
OC NCBI_TaxID: 9606;
RN 1;
RP SEQUENCE FROM N.A.
RA MEDLINE: 20422911; PubMed: 10904117;
RA Mezquita J., Mezquita P., Montserrat P., Moripada R., Planasde V.,
RA Villarasa X., Mezquita C.
RA "Genomic structure and alternative splicing of chicken anti-hepatitis
RA 2B".
RL Barcelona, Biophys. Res. Commun. 275:643-651(2000).
DB EMBL: A284780; CAC08179.1;
FT NON_TER 13
SQ SEQUENCE 13 AA: 1548 MW: 334196A16F93602 CRR64;

Query Match: 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKP 4
DB 1
2 KKE 4

RESULT 18
Q66746
ID Q66746 PRELIMINARY: PRT: 13 AA.
AC Q66746
DT 01-MAR-2001 (TrEMBLrel. 24, Created)
DT 01-MAR-2001 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 24, Last annotation update)
DE Myosin in (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Soricimorpha; Muridae; Mus;
OC NCBI_TaxID: 10090;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN BALB/c; TISSUE-Kidney;
RA Rieger M., Porin J.P., Seddiq N., Gaudin N., Gaudin A., Marlet M.,
RA Rieger F., Alliel P.M.;
RA "The human and mouse myosin in breast cancer and fibrosarcoma: SE-29
RA variants, chromosomal mapping and functional assays".
RA Submitted (Jun-2002) to the EMBL/Genbank/TrEMBL databases.
DB EMBL: AF536454; AAN28707.1;
FT NON_TER 13
SQ SEQUENCE 13 AA: 1445 MW: 3096186A1PCE CRR64;

Query Match: 27.3%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 4 KKP 6
DB 1
1 KKP 6

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RESULT 19
Q66746
ID Q66746 PRELIMINARY: PRT: 13 AA.
AC Q66746
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Polynuclear (Fragment).
OS Equine infectious anemia virus
OS Viruses; Retroviruses; Retroviridae; Lentivirus.
OC NCBI_TaxID: 11655;
RN 1;
RP SEQUENCE FROM N.A.
RA MEDLINE: 90204701; PubMed: 21570647;
RA Naiman S., Yaniv A., Sherman L., Ironack S.R., Gariz A.;
RA "Pattern of transcription of the genome of equine infectious anemia
RA virus".
RL J. Virol. 64:1819-1843(1990).
DB EMBL: M33845; AAG6411.1;
FT NON_TER 13
SQ SEQUENCE 13 AA: 1493 MW: 97303905A92321 CRR64;

Query Match: 27.4%; Score 3; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KPN 7
DB 11
11 KPN 13

RESULT 20
Q66746
ID Q66746 PRELIMINARY: PRT: 13 AA.
AC Q66746
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein 25883.
OS Escherichia coli 0157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia
OC NCBI_TaxID: 83344;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN 0157:H7 / HUS-55 / A937-75(927);
RA MEDLINE: 21074945; PubMed: 11201517;
RA Perna N.J., Plunkett G., III, Hsland V., Mau R., Glasner J.B.,
RA Rose G.J., Mayhew G.E., Evans P.S., Gregor J., Kirkpatrick B.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.F., Potamoudis K.,
RA Apodaca J., Anantharaman I.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7".
RL Nature 409:529-533(2001).
DB EMBL: AE005659; AAG59469.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 13 AA: 1526 MW: 4145922739041877 CRR64;

Query Match: 27.4%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 6
6 AKK 10

RESULT 21
Q66750

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ID Q56750 PRELIMINARY: FRG: 14 AA
AC Q56750
CT 01-NOV-1996 (TREMBLER: 01, Created)
DT 01-NOV-1996 (TREMBLER: 01, Last sequence update)
DI 01-DEC-2001 (TREMBLER: 19, Last annotation update)
DE Ribosome; protein S19 (Fragment)
OS Mammalia; Chordata; Mollusca; Atherinomorpha
OC Actinopterygii; Clupeiformes; Clupeidae; Atherinidae
OX NCBI_TaxID: 17704
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE: 94355892; PubMed: 9071194
RA Gundersen L.E., Lee L.M., Rohrer S.A., Knust A.J. 1994
RT *Phylogeny of mycoplasma-like organisms (MPLs) as basis for
RT their classification.*
PL J. Bacteriol. 176:5244-5254 (1994)
DR EMBL: 127247; AAA83948.1
FT N N TER
SQ SEQUENCE: 14 AA; 1712 MW; 403476ER8FFP4A-02.64;

Query Match: 27.3%, Score 3; DB 2; Length 14;
Best Local Similarity: 100.0%; Prev. No. 1, 1e+04;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
LD 11
DD 6 KKK 10

RESULT 24
Q15222 PRELIMINARY: FRG: 14 AA
AC Q15222
CT 01-JAN-1998 (TREMBLER: 05, Created)
DT 01-JAN-1998 (TREMBLER: 05, Last sequence update)
DI 01-DEC-2001 (TREMBLER: 19, Last annotation update)
DE HOS9 protein (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
OX NCBI_TaxID: 9606
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE: 98019011; PubMed: 9557979
RA Fladelle B., Gibaud A., Dutrillaux B., Pouyon M.F., Maitoy B.
RT "Distinct patterns of all-trans retinoic acid dependent expression of
RT the HOX and HOSX homeoboxes in human embryonal and small-cell lung
RT carcinoma cell lines."
PL FEBS Lett. 415:264-267 (1997)
DR EMBL: X99622; AAA67998.1
FT N N TER
SQ SEQUENCE: 14 AA; 1725 MW; 40507272C5499A3B CRC64;

Query Match: 27.3%, Score 3; DB 4; Length 14;
Best Local Similarity: 100.0%; Prev. No. 1, 1e+04;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
LD 11
DD 6 KKK 6

RESULT 25
Q50W75 PRELIMINARY: FRG: 14 AA
AC Q50W75
CT 01-MAY-2000 (TREMBLER: 13, Created)
DT 01-MAY-2000 (TREMBLER: 13, Last sequence update)
DI 01-JUN-2002 (TREMBLER: 21, Last annotation update)
DE Homeobox GSH-4 (Fragment)
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID: 10095
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE: 94073066; PubMed: 1083707
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,

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RA Cooperand N.G., Potter S.S.:
RT "Identification of 10 murine homeobox genes."
RC Proc. Natl. Acad. Sci. U.S.A. 86:13766-13770(1989).
DR Int. Data: IPSC01456; Homeobox.
ER Pfam: PF00046; Homeobox.
FR PROSITE: PS00071; HOMEBOX_2; 1.
FT NON TER 1 1
FT NON TER 14 14
SQ SEQUENCE 14 AA: 1859 MW: 76186000 9AD0C4 (RefSeq)

Query Match: 27.4%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEK 5
DB 1
3 KEK 1;

RESULT 26
PRELIMINARY: PRT: 14 AA.
ID PF2831
AC PF2831
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Temporalin-1b.
OS Rana temporaria.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Nothobatrachia; Ranidae; Rana;
OX NCBI_TaxID:5817;
RN [1]
SQ SEQUENCE FUNCTION, AND MASS SPECTROMETRY.
RX MEDLINE:2217793; PubMed:10651828;
RA Sazaya J., Wang Y., Li Z., Griffiths R., Knapp J., Pless J.E.,
RA Gauthier J.M.
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana intermedia,
RT Rana berlandieri, and Rana pipiens."
RL Exp. Appl. Biochem. 267:894-900(2000).
FR FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST GRAM POSITIVE BACTERIOR
FR S. AUREUS. WEAK ACTIVITY AGAINST GRAM NEGATIVE BACTERIUM ESCHL AND
FR THE YEAST C. ALBICANS.
CV 1 MASS SPECTROMETRY: MW:1576; METHOD: ELECTRIC SPRAY
CV 1 SIMILARITY: BELONGS TO THE SEVININ/ESULENTIN/GABDIN/RN/SN
CV FAMILY.
KW Antimicrobial; Acidation; Fungicide.
FT NON TER 14 14
FT NON TER 14 14
SQ SEQUENCE 14 AA: 1576 MW: 15476000 9AD0C4 (RefSeq)

Query Match: 27.4%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 1
10 AKK 1;

RESULT 27
PRELIMINARY: PRT: 15 AA.
ID Q9UCG7
AC Q9UCG7
DT 01-MAY-2000 (TrEMBLrel. 15, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Midline (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
SQ SEQUENCE.
RX MEDLINE:94059921; PubMed:8241100;
RA Novotny W.F., Matti T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midline and pleiotrophin, in human postheparin plasma."
RC Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA: 1527 MW: 63486978 78474AC CRC64;
NCBI_TaxID:562;

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RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN-K-12;
RX MEDLINE:85267249; PubMed:4894885;
RA Schrier J., Iscono S., Cumberledge A.G., Iscono K.;
RT "Unstable mutations caused by regional tandem multiplications in the
RT gene for ribosomal protein S4 show thermosensitivity in Escherichia
RT coli."
RL Mol. Gen. Genet. 199:265-276(1985).
DR EMBL: M25824; AAA24594.1;
FT NON TER 1 1
FT NON TER 15 AA: 1545 MW: 74561554 4A8EU0C5 CRC64;
SQ SEQUENCE 15 AA: 1545 MW: 74561554 4A8EU0C5 CRC64;

Query Match: 27.4%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 1
3 AKK 5;

RESULT 28
PRELIMINARY: PRT: 15 AA.
ID Q9UBK0
AC Q9UBK0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Retal tissue-specific alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
SQ SEQUENCE.
RX MEDLINE:94092415; PubMed:14585452;
RA Nishihara Y., Hayashi Y., Adachi I., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney."
RL Clin. Chem. 38:2539-2542(1992).
SQ SEQUENCE 15 AA: 1931 MW: 9A28FDE13F01F716 CRC64;

Query Match: 27.4%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEK 5
DB 1
5 KEK 7;

RESULT 29
PRELIMINARY: PRT: 15 AA.
ID Q9UCG7
AC Q9UCG7
DT 01-MAY-2000 (TrEMBLrel. 15, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Midline (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
SQ SEQUENCE.
RX MEDLINE:94059921; PubMed:8241100;
RA Novotny W.F., Matti T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midline and pleiotrophin, in human postheparin plasma."
RC Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA: 1527 MW: 63486978 78474AC CRC64;
NCBI_TaxID:562;

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Query Match 27.3% Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 2 AKK 4

## RESULT 40

Q9U0N2 ID Q9U0N2 PRELIMINARY; PRT: 15 AA  
 AC Q9U0N2  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 15, Last annotation update)  
 DE Fructose-1,6-bisphosphate aldolase A (EC 4.1.2.13) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CN Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE:92453128; PubMed:1359685;  
 RA Lee K.N., Maxwell M.D., Patterson M.K. et al., Borextashler P.O., Conway E.J.  
 RT "Identification of transaminase substrates in HT29 colon cancer cells: use of 5-(biotamido)pentylamine as a transaminase-specific probe."  
 RT Biochim. Biophys. Acta 1136:12-16(1992).  
 DR HSSP: P04075; ZALD.  
 SQ SEQUENCE 15 AA; 1805 MW; 8D07546D4FC04E6; CRC64;

Query Match 27.3% Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4  
 DB 12 KKE 14

## RESULT 41

Q81ZQ0 ID Q81ZQ0 PRELIMINARY; PRT: 15 AA  
 AC Q81ZQ0  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Protein kinase A catalytic subunit beta (Fragment).  
 GN PKA-B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CN Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wu K.-J., Mattioli M., Morse H.C., Dalla-Favera R.  
 RT "c-MYC activates protein kinase A (PKA) by direct transcriptional activation of the PKA catalytic subunit beta (PKA-Cb) gene."  
 RT Oncogene 0:0 (2002).  
 DR EMBL: AF538872; AAN16454.1; ...  
 KW Kinase.  
 FT NON\_CTR 15 15  
 SQ SEQUENCE 15 AA; 1480 MW; 52FE5695C19870A; CRC64;

Query Match 27.3% Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 111

Db 7 AKK 9

## RESULT 32

Q9TWQ2 ID Q9TWQ2 PRELIMINARY; PRT: 15 AA  
 AC Q9TWQ2  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE Small granule S6 (Fragment).  
 OS Tachyplesus tridentatus (Japanese horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 CN Limulidae; Tachyplesus.  
 OX NCBI\_TaxID:6853;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE:94110249; PubMed:8482718;  
 RA Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Ito A., Iwanaga S.  
 RL J. Biochem. 114:307-315(1993).  
 SQ SEQUENCE 15 AA; 1697 MW; 0E847408C59C8245; CRC64;

Query Match 27.3% Score 3; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EKP 6  
 DB 1 EKP 3

## RESULT 33

Q9TWU4 ID Q9TWU4 PRELIMINARY; PRT: 15 AA  
 AC Q9TWU4  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE KENA-binding protein (Fragment).  
 OS Crithidia fasciculata.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.  
 OX NCBI\_TaxID:5656;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE:93245912; PubMed:8432355;  
 RA Tittawella J.  
 RT "Identification of DNA-binding proteins in the parasitic protozoan Crithidia fasciculata and evidence for their association with the mitochondrial genome."  
 RT mitochondrial genome.";  
 RL Exp. Cell Res. 206:143-151(1993).  
 SQ SEQUENCE 15 AA; 1453 MW; 7C737E529D9D8270; CRC64;

Query Match 27.3% Score 3; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 13 AKK 15

## RESULT 34

Q9AT15 ID Q9AT15 PRELIMINARY; PRT: 15 AA  
 AC Q9AT15  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Plasma membrane H<sup>+</sup>-ATPase (Fragment).  
 GN LHA1.  
 OS Lycopodium obscurum (Lomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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DT Streptophyta: Magnoliophyta: eudicotyledons: euro eudicots:
DE Asteridiales: Solanales: Solanaceae: Solanum
OX NCBI_taxid:4081;
GN 1;
SP SEQUENCE FROM N.A.
RC STRAIN:cv. VENT Cherry;
RA Binda N.N., Wermers L.E., Meyer L.J., Chetelat N.J., Boudett A.B.;
RT "Molecular cloning of tomato plasma membrane H+-ATPase";
RL Life Sci. Adv. Plant Physiol. 94:11-14 (1991);
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN:cv. VENT Cherry;
RA Binda N.N., Boudett A.B.;
RT "Assessment of the number and expression of P-type H+-ATPase genes
in tomato";
RL Life Sci. Adv. Plant Physiol. 106:547-557 (1994);
RN 13;
RP SEQUENCE FROM N.A.
RC STRAIN:cv. VENT Cherry;
RA Bahmani Z., Binda N.N.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF355103; AAK31206.1;
FT NON_TER 15
SQ SEQUENCE 15 AA: 1673 MW: 55704775.20858096 P1:64;

Query Match 27.3% Score 4 DB 10 Length 15;
Best Local Similarity 100.0% Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 5
DB 3 EXP 5

RESULT 35
Q5AGP4 PRELIMINARY: PRT: 15 AA
ID Q5AGP4
AC Q5AGP4
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
ET 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
FE Translation elongation factor (Fragment);
OS Glyza sativa (rice);
OC Eukaryota: Viridiplantae: Streptophyta: Eudicotyledons:
OC Eukaryota: Magnoliophyta: Eudicotyledons: Eurosid:
OC Eukaryota: Magnoliophyta: Eudicotyledons: Eurosid:
OC Eukaryota: Magnoliophyta: Eudicotyledons: Eurosid:
OC NCBI_taxid:4530;
GN 1;
RP SEQUENCE FROM N.A.
RC STRAIN:cv. Chen Sui;
RT "Predictable expression of translation elongation factor 1A gene in rice
seedlings in response to environmental stresses";
RA Acta Bot Sin. 41:800-806 (1999);
DR EMBL: AF067175; AAC79991.1;
FT Elongation factor;
KW Elongation factor;
FT NON_TER 1;
SQ SEQUENCE 15 AA: 1514 MW: 9255456.096975 P1:61;

Query Match 27.4% Score 4 DB 10 Length 15;
Best Local Similarity 100.0% Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 5
DB 12 AKK 14

RESULT 36
Q5G712 PRELIMINARY: PRT: 8 AA
ID Q5G712
AC Q5G712
DT 01-MAY-2003 (TrEMBLrel. 13, Created)

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DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical: 1.0 kDa protein (Fragment);
GN YCFG;
OS Escherichia coli;
OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales;
OC Enterobacteriaceae: Escherichia;
OX NCBI_taxid:562;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN K12;
RX MEDLINE:97061202; PubMed:8755242;
RA Oshata T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Ikada T., Itoh T., Kajiura M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiechi T.;
RT "A 718-kD DNA sequence of Escherichia coli K-12 Genome Corresponding
to the 12.7-26.0 min Region on the Linkage Map";
RL DNA Res. 3:137-155 (1996);
DR EMBL: D90705; BAA3510.1;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA: 964 MW: 261335BD0048476A CRC64;

Query Match 18.2% Score 2 DB 2 Length 8;
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
DB 7 KE 8

RESULT 37
Q5AGP4 PRELIMINARY: PRT: 8 AA
ID Q5AGP4
AC Q5AGP4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
ET 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serine hydroxymethyltransferase (Fragment);
GN GlyA;
OC Archaea: Crenarchaeota: Thermococcales: Thermococcus;
OC Bacteria: Actinobacteriales: Actinomycetales;
OC Micrococcineae: Micrococcaceae: Arthrobacter;
OX NCBI_taxid:153502;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN:LIN;
RA Meskys R., Battis R., Caselle V., Bosian J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
L-sarcosine degradation in Arthrobacter spp.: implications for glycine
betaine catabolism";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF22478; AAK36466.1;
KW Methyltransferase; Transferrase;
FT NON_TER 1
SQ SEQUENCE 8 AA: 806 MW: 651870533372457 CRC64;

Query Match 18.2% Score 2 DB 2 Length 8;
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
DB 4 KK 5

RESULT 38
Q5G5G4 PRELIMINARY: PRT: 8 AA
ID Q5G5G4
AC Q5G5G4
DT 01-MAY-2003 (TrEMBLrel. 13, Created)

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AC Q49544:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P120 (Fragment).
GN P120.
OS Mycoplasma hominis
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatidae; Mycoplasma
OX NCBI_TaxID:2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-V2785;
RA Nyvold G., Hixseland S., Christensen G.
RT "The Mycoplasma hominis p120 membrane protein forms a 100 base
RI pair hypervariable domain."
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL:U22025; AAA67455.1;
FT NON-TER
SQ SEQUENCE 8 AA: 859 MW: 91445.945082550 CRC64:
      Query Match      18.2%  Score 2: DB 2: Length 8:
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

Q7 6 KK 7
DB 5 KK 7

RESULT 49
Q9R9EC
ID Q9R9EC PRELIMINARY: PRI: 8 AA
AC Q9R9EC
DI 01-MAY-2000 (TrEMBLrel. 19, Created)
DI 01-MAY-2000 (TrEMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1424;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 168;
RA Henricques A.G., de Lencastre H., Plagiot P.J.;
RT "A bacillus subtilis morphotype cluster that includes spore is
RI homologous to the rsa region of Escherichia coli."
RL Biochimie 74:735-748(1992).
DR EMBL: X64258; CAA45556.1;
FT NON-TER
SQ SEQUENCE 8 AA: 893 MW: EE75A1A33321B1A6 CRC64:
      Query Match      18.2%  Score 2: DB 2: Length 8:
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

QY 2 KK 3
DB 4 KK 5

RESULT 42
Q9R5K0
ID Q9R5K0 PRELIMINARY: PRI: 8 AA
AC Q9R5K0
DI 01-MAY-2000 (TrEMBLrel. 19, Created)
DI 01-MAY-2000 (TrEMBLrel. 19, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11-500 DA product of ORFA (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID:622;
RN [1]
RP SEQUENCE.
RA MEDLINE:92085268; PubMed:1660923;
RA Polard P., Pierre M.F., Chaudier M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUG codon

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OC Thermaus.
OX NCBI_TaxID 274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BB-8;
RX MEDLINE:89025722; PubMed:4952437;
RA Bowen D., Littlechild J.A., Forthright J.E., Watson H.C., Hall J.;
RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
RI extreme thermophile, Thermus thermophilus."
RL Biochem. J. 254:539-547(1988).
DR EMBL: X12464; CAA1105.1;
FT NON-TER
SQ SEQUENCE 8 AA: 845 MW: 30e7333332572B CRC64:
      Query Match      18.4%  Score 2: DB 2: Length 8:
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

QY 2 KK 3
DB 5 KK 5

RESULT 41
Q9R9EC
ID Q9R9EC PRELIMINARY: PRI: 8 AA
AC Q9R9EC
DI 01-MAY-2000 (TrEMBLrel. 19, Created)
DI 01-MAY-2000 (TrEMBLrel. 19, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 19, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1424;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 168;
RA Henricques A.G., de Lencastre H., Plagiot P.J.;
RT "A bacillus subtilis morphotype cluster that includes spore is
RI homologous to the rsa region of Escherichia coli."
RL Biochimie 74:735-748(1992).
DR EMBL: X64258; CAA45556.1;
FT NON-TER
SQ SEQUENCE 8 AA: 893 MW: EE75A1A33321B1A6 CRC64:
      Query Match      18.2%  Score 2: DB 2: Length 8:
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0:

QY 2 KK 3
DB 4 KK 5

RESULT 42
Q9R5K0
ID Q9R5K0 PRELIMINARY: PRI: 8 AA
AC Q9R5K0
DI 01-MAY-2000 (TrEMBLrel. 19, Created)
DI 01-MAY-2000 (TrEMBLrel. 19, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11-500 DA product of ORFA (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID:622;
RN [1]
RP SEQUENCE.
RA MEDLINE:92085268; PubMed:1660923;
RA Polard P., Pierre M.F., Chaudier M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUG codon

```

57 10 gene expression of bacterial insertion sequence 15911.1;  
 FI J. Mol. Biol. 222:465-477(1991).  
 FT N-TER 8  
 SQ SEQUENCE 8 AA: 935 MW: 94559C45AF4346 CR664;

Query Match 18.2% Score 2: 05 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3  
 DB 2 KK 3

RESULT 44  
 Q90BN9  
 ID Q90BN9 PRELIMINARY: PRT: 8 AA  
 AC Q90BN9  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DE Hypothetical 1.0 kDa protein (Fragment).  
 DE Hypothetical 1.0 kDa protein (Fragment).  
 OS Coxiella burnetii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Coxiellaceae; Coxiella.  
 CX NCBI\_TaxID:777;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: Nite Mile Phase 1;  
 RX MEDLINE 96348442; PubMed-9683477;  
 RA Williams H., Jaeger C., Baljer G.  
 RT "Physical and genetic map of the obligate intracellular bacterium  
 Coxiella burnetii."  
 RC J. Bacteriol. 180:3816-3822(1998).  
 DR EMBL: AF064961; AAD9947.1;  
 KW Hypothetical protein.  
 FT N-TER 1  
 SQ SEQUENCE 8 AA: 933 MW: 94559AAM5472227 CR664;

Query Match 18.2% Score 2: 05 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ND 11  
 DB 1 ND 6

RESULT 44  
 Q90BN9  
 ID Q90BN9 PRELIMINARY: PRT: 8 AA  
 AC Q90BN9  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Aminopeptidase B (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.  
 CX NCBI\_TaxID:4942;  
 RN 1;  
 RP SEQUENCE  
 RX MEDLINE-92088139; PubMed-1750699;  
 RA Kassel D.B., Williams K.P., Musselman B.B., Smith A.J.  
 RT "Optimization of the fragmentation in a first fast atom bombardment ion  
 source for the sequencing of peptides at the picomole level."  
 RL Anal. Chem. 64:1578-1583(1991).  
 FT N-TER 1  
 SQ SEQUENCE 8 AA: 772 MW: 7830DAAC2074208 CR664;

Query Match 18.2% Score 2: 05 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AK 2  
 DB 7 AK 8

## RESULT 45

Q15888  
 ID Q15888 PRELIMINARY: PRT: 8 AA  
 AC Q15888  
 DT 01-NOV-1995 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1995 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Clone XPI548A) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID:9606;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: Placenta;  
 RA Lee C.-C., Yazdani A., Weinert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.L., Chinault C.A., Baldwin A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome specific genes by reciprocal probing of  
 arrayed cDNAs and cosmid libraries."  
 RC Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL: L32059; AAA74878.1;  
 FT N-TER 1  
 SQ SEQUENCE 8 AA: 1568 MW: 0315A47EAB580763 CR664;

Query Match 18.2% Score 2: 05 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KP 6  
 DB 1 KP 2

## RESULT 46

Q90CN4  
 ID Q90CN4 PRELIMINARY: PRT: 8 AA  
 AC Q90CN4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Cell-surface heparin/HEPARANSULFATE-binding protein peptide 3  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID:9606;  
 RN 1;  
 RP SEQUENCE  
 RX MEDLINE-92291065; PubMed-1601862;  
 RA Raboudi N., Julien J., Rohde L.H., Carson D.D.;  
 RT "Identification of cell-surface heparin/heparan sulfate-binding  
 proteins of a human uterine epithelial cell line (RL95)."  
 RL J. Biol. Chem. 267:11910-11919(1992).  
 SQ SEQUENCE 8 AA: 689 MW: 808733DD33DD87D CR664;

Query Match 18.2% Score 2: 05 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AK 2  
 DB 3 AK 4

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RESULT 47
Q9H4D3      PRELIMINARY:      PRT:      8 AA.
AC Q9H4D3;
DT 01-MAR-2003 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LIM domain only 1 protein (Fragment).
GN LIM
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC ISSUe-Blood;
RA Bruckmann T., Winterpacht A., Hankeln T., Schmidt E.R., Zuber H.C.,
RT "Human PAC clone RCIP704K03781 (p63 781K)", sequenced in DHGP project
RT (Comparative Sequencing of a 1 Mb Region in Man (Chromosome 11p15), and
RT Mouse (Chromosome 7))";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ277661; CAC14573.1;
FT NON_TER 8
SQ SEQUENCE 8 AA: 980 MW: F3AB133AA32C696 CRC64;

Query Match      18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
DB 6 KE 7

RESULT 48
Q9NM5      PRELIMINARY:      PRT:      8 AA.
AC Q9NM5;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE Dihydrofolate reductase thymidylate synthase (Fragment).
GN F011
OS Tokoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystoidea;
OC Tokoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH, COUGAR TC751G34, SEA OFFER T82861, HIG BEVERLEY;
RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.,
RT "Strain Typing of Tokoplasma gondii: Comparison of Antigen Coding and
RT Housekeeping Genes.";
RL J. Parasitol. 0:0-0(2000).
DR EMBL: AF249695; AAF79153.1;
DR EMBL: AF249692; AAF79150.1;
DR EMBL: AF249693; AAF79151.1;
DR EMBL: AF249694; AAF79152.1;
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 1035 MW: 33CAAAA35B33644 CRC64;

Query Match      18.2%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
DB 3 KE 4

RESULT 49
Q9TRX8      PRELIMINARY:      PRT:      8 AA.
AC Q9TRX8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE;
RC MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Kramdieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity.";
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 920 MW: 05DAFAF76322D767 CRC64;

Query Match      18.2%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KP 6
DB 4 KP 5

RESULT 50
C18854      PRELIMINARY:      PRT:      8 AA.
AC C18854;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE CD19 antigen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu P.-C., Shibuya H., Katz M.L., Johnson G.S.;
RT "A BsmFI PCR/RELP in the canine CD19 antigen gene.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF024717; AAB81967.1;
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 812 MW: 6735A1ADDB1325A7 CRC64;

Query Match      18.2%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
DB 3 KE 4

Search completed: September 30, 2003, 10:18:00
Job time : 60.6667 secs

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OM proteins - protein search, using sw model

Run on: September 30, 2003, 10:07:05 / Search time 11:53.3 Seconds  
(without alignments)  
39.331 Million cell updates/sec

Title: US-09-787-443-17

Perfect score: 11

Sequence: AKKEKPNKND 11

Scoring table: MEMO

Gapop 60.0 / Gapext 60.0

Searched: 328717 seqs, 42310558 residues

Word size: 0

Total number of hits satisfying chosen parameters: 78454

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database: Issued\_Patents\_AA:\*

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3: /cgn2.6/protdata/1/iaa/6A\_GUMB.pep:\*

4: /cgn2.6/protdata/1/iaa/6B\_GUMB.pep:\*

5: /cgn2.6/protdata/1/iaa/PCUS\_GUMB.pep:\*

6: /cgn2.6/protdata/1/iaa/back:iles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	5	45.5	12	3	US-08-464-841A : Sequence 1, Appl
2	4	36.4	8	2	US-08-459-568-85 Sequence 85, Appl
3	4	36.4	8	2	US-08-499-411-85 Sequence 85, Appl
4	4	36.4	9	2	US-08-534-242-24 Sequence 24, Appl
5	4	36.4	8	2	US-08-534-412-24 Sequence 24, Appl
6	4	36.4	8	2	US-09-257-611-24 Sequence 24, Appl
7	4	36.4	8	2	US-08-532-815-24 Sequence 24, Appl
8	4	36.4	8	2	US-08-413-859A-85 Sequence 2, Appl
9	4	36.4	8	3	US-08-515-859A-85 Sequence 85, Appl
10	4	36.4	8	3	US-09-231-797-24 Sequence 24, Appl
11	4	36.4	8	3	US-08-534-224-24 Sequence 24, Appl
12	4	36.4	8	3	US-08-533-843-24 Sequence 24, Appl
13	4	36.4	8	3	US-08-534-223-24 Sequence 24, Appl
14	4	36.4	8	3	US-09-413-492-24 Sequence 24, Appl
15	4	36.4	8	4	US-09-586-472-85 Sequence 85, Appl
16	4	36.4	8	4	US-08-197-484-19 Sequence 19, Appl
17	4	36.4	8	4	US-09-526-706-85 Sequence 85, Appl
18	4	36.4	8	5	PCI-US95-021211-19 Sequence 11, Appl
19	4	36.4	9	2	US-08-407-458-11 Sequence 45, Appl
20	4	36.4	9	2	US-08-318-859A-45 Sequence 58, Appl
21	4	36.4	10	1	US-07-789-184-50 Sequence 50, Appl
22	4	36.4	10	1	US-07-789-184-50 Sequence 50, Appl
23	4	36.4	10	1	US-07-789-184-50 Sequence 50, Appl
24	4	36.4	10	1	US-07-789-184-50 Sequence 50, Appl
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26	4	36.4	10	1	US-07-789-184-50 Sequence 50, Appl
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32	4	36.4	10	1	US-08-475-263-65 Sequence 65, Appl
33	4	36.4	10	1	US-08-475-263-66 Sequence 66, Appl
34	4	36.4	10	1	US-08-475-263-67 Sequence 67, Appl
35	4	36.4	10	1	US-08-475-263-203 Sequence 203, App
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47	4	36.4	10	2	US-08-477-362-66 Sequence 66, Appl
48	4	36.4	10	2	US-08-477-362-67 Sequence 67, Appl
49	4	36.4	10	2	US-08-477-362-203 Sequence 203, App
50	4	36.4	10	2	US-08-477-134-45 Sequence 45, Appl
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53	4	36.4	10	2	US-08-477-134-65 Sequence 65, Appl
54	4	36.4	10	2	US-08-477-134-66 Sequence 66, Appl
55	4	36.4	10	2	US-08-477-134-67 Sequence 67, Appl
56	4	36.4	10	2	US-08-477-134-203 Sequence 203, App
57	4	36.4	10	3	US-08-473-489A-45 Sequence 45, Appl
58	4	36.4	10	3	US-08-473-489A-50 Sequence 50, Appl
59	4	36.4	10	3	US-08-473-489A-60 Sequence 60, Appl
60	4	36.4	10	3	US-08-473-489A-65 Sequence 65, Appl
61	4	36.4	10	3	US-08-473-489A-66 Sequence 66, Appl
62	4	36.4	10	3	US-08-473-489A-67 Sequence 67, Appl
63	4	36.4	10	3	US-08-473-489A-203 Sequence 203, App
64	4	36.4	10	3	US-08-485-695-45 Sequence 45, Appl
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66	4	36.4	10	3	US-08-485-695-60 Sequence 60, Appl
67	4	36.4	10	3	US-08-485-695-65 Sequence 65, Appl
68	4	36.4	10	3	US-08-485-695-66 Sequence 66, Appl
69	4	36.4	10	3	US-08-485-695-67 Sequence 67, Appl
70	4	36.4	10	3	US-08-485-695-203 Sequence 203, App
71	4	36.4	10	3	US-08-018-760-45 Sequence 45, Appl
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76	4	36.4	10	3	US-08-018-760-67 Sequence 67, Appl
77	4	36.4	10	3	US-08-018-760-203 Sequence 203, App
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80	4	36.4	11	3	US-09-100-930A-10 Sequence 10, Appl
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82	4	36.4	12	3	US-08-407-207A-4 Sequence 4, Appl
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84	4	36.4	13	3	US-09-098-244-24 Sequence 24, Appl
85	4	36.4	13	3	US-09-208-059-27 Sequence 27, Appl
86	4	36.4	13	3	US-08-842-306B-41 Sequence 41, Appl
87	4	36.4	13	3	US-08-842-306B-42 Sequence 42, Appl
88	4	36.4	13	3	US-08-838-973B-41 Sequence 41, Appl
89	4	36.4	13	3	US-08-838-973B-42 Sequence 42, Appl
90	4	36.4	13	4	US-09-375-314-24 Sequence 24, Appl
91	4	36.4	13	4	US-08-771-212A-37 Sequence 37, Appl
92	4	36.4	13	4	US-08-771-212A-38 Sequence 38, Appl
93	4	36.4	13	4	US-09-767-395-24 Sequence 24, Appl
94	4	36.4	15	1	US-08-080-073-19 Sequence 19, Appl
95	4	36.4	15	1	US-08-080-073-21 Sequence 21, Appl
96	4	36.4	15	1	US-08-080-073-27 Sequence 27, Appl
97	4	36.4	15	3	US-08-976-255-21 Sequence 21, Appl
98	4	36.4	15	4	US-09-009-953-216 Sequence 216, App
99	3	27.3	8	1	US-07-666-719-4 Sequence 4, Appl
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164	3	27.3	8	1	US-08-469-563-15	Sequence 15, Appl	177	3	27.3	8	5	PCT-US96-00310-7	Sequence 7, Appl
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166	3	27.3	8	1	US-08-240-514-39	Sequence 49, Appl	179	3	27.3	8	6	5179037-11	Patent No. 5179037
167	3	27.3	8	1	US-08-249-381-2	Sequence 2, Appl	180	3	27.3	8	6	5258287-41	Patent No. 5258287
168	3	27.3	8	1	US-08-249-324A-15	Sequence 15, Appl	181	3	27.3	9	1	US-07-657-769B-9	Sequence 9, Appl
169	3	27.3	8	1	US-08-461-507-8	Sequence 8, Appl	182	3	27.3	9	1	US-07-657-769B-49	Sequence 49, Appl
170	3	27.3	8	1	US-08-043-548-20	Sequence 20, Appl	183	3	27.3	9	1	US-08-116-733-45	Sequence 45, Appl
171	3	27.3	8	1	US-08-456-343-20	Sequence 20, Appl	184	3	27.3	9	1	US-08-178-570-39	Sequence 39, Appl
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173	3	27.3	8	1	US-08-622-362A-49	Sequence 49, Appl	186	3	27.3	9	1	US-07-789-184-30	Sequence 40, Appl
174	3	27.3	8	2	US-08-467-593-6	Sequence 6, Appl	187	3	27.3	9	1	US-07-789-184-41	Sequence 41, Appl
175	3	27.3	8	2	US-08-473-190-43	Sequence 43, Appl	188	3	27.3	9	1	US-07-789-184-56	Sequence 56, Appl
176	3	27.3	8	2	US-08-784-594A-18	Sequence 18, Appl	189	3	27.3	9	1	US-07-789-184-204	Sequence 204, Appl
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182	3	27.3	8	2	US-08-466-793-6	Sequence 6, Appl	195	3	27.3	9	1	US-08-485-886-30	Sequence 30, Appl
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187	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	200	3	27.3	9	2	US-08-477-362-41	Sequence 41, Appl
188	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	201	3	27.3	9	2	US-08-477-362-56	Sequence 56, Appl
189	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	202	3	27.3	9	2	US-08-477-362-204	Sequence 204, Appl
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191	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	204	3	27.3	9	2	US-08-477-134-30	Sequence 30, Appl
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201	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	214	3	27.3	9	2	US-08-874-678-29	Sequence 29, Appl
202	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	215	3	27.3	9	2	US-08-318-856A-7	Sequence 7, Appl
203	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	216	3	27.3	9	2	US-08-318-856A-19	Sequence 19, Appl
204	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	217	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
205	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	218	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
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214	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	227	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
215	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	228	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
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218	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	231	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
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222	3	27.3	8	2	US-08-434-861A-6	Sequence 6, Appl	235	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
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262	3	27.3	9	4	US-09-424-3836-41	Sequence 36, Appl	335	10	1	US-08-485-886-55	Sequence 55, Appl
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267	3	27.3	9	4	US-09-424-3836-41	Sequence 36, Appl	340	10	1	US-08-485-886-112	Sequence 112, App
268	3	27.3	9	4	US-09-424-3836-41	Sequence 36, Appl	341	10	1	US-08-485-886-138	Sequence 138, App
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270	3	27.3	9	5	PCT-US92/09454A-6	Sequence 39, Appl	343	10	1	US-08-485-886-197	Sequence 197, App
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274	3	27.3	10	1	US-07-657-7698-8	Sequence 8, Appl	347	10	2	US-08-477-362-29	Sequence 29, Appl
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465 3 US-08-485-695-64 Sequence 64, Appl.

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## ALIGNMENTS

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RESULT 1
US-08-464-841A-1
Sequence 1, Application US/0844-841A
Patent No. 619889
GENERAL INFORMATION
APPLICANT: HARRIS, DENISE GURRY, JOSE
APPLICANT: HARRIS, DENISE GURRY, JOSE
TITLE OF INVENTION: HARP FAMILY GROWTH FACTORS, PREPARATION
TITLE OF INVENTION: HARP FAMILY GROWTH FACTORS, PREPARATION
NUMBER OF SEQUENCES: 8
REFERENCE ADDRESS
ADDRESS: BUCKMAN & MUSEGGAN
STREET: 609 TREMAY AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER RESEARCH FORM
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA
APPLICATION NUMBER: US-08-464-841A
FILING DATE: 23 AUGUST 1995
CLASSIFICATION: 532
PRIORITY APPLICATION DATA
APPLICATION NUMBER: PCT/EP94/00219
FILING DATE:
ATTORNEY/AGENT: INDIANAPOLIS
NAME: CHARLES A. MUSEGGAN
REGISTRATION NUMBER: 10,664
REFERENCE/WORK NUMBER: 104,165

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TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 661-8000  
 TELEFAX: (212) 661-8002  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12  
 TYPE: Amino Acid  
 STRANDEDNESS: Unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-464-84:A-1

Query Match 45.5% Score 5.0 DB 2 Length 12  
 Best Local Similarity 100.0% Pred. No. 18  
 Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEP 6  
 DB 5 KKEP 9

## RESULT 2

US-08-459-568-85  
 Sequence 85, Application US/08459568

PATENT NO. 581104  
 GENERAL INFORMATION:  
 APPLICANT: Huang, Shi  
 TITLE OF INVENTION: Retinoblastoma Protein Interacting  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 NUMBER OF SEQUENCES: 93  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/459,568  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/399,411  
 FILING DATE: 06-MAR-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-459-568-85

Query Match 36.4% Score 4.0 DB 2 Length 8  
 Best Local Similarity 100.0% Pred. No. 25  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11  
 DB 2 KPND 5

## RESULT 3

US-08-399-411-85  
 Sequence 85, Application US/08399411  
 Patent No. 5811008  
 GENERAL INFORMATION:  
 APPLICANT: Huang, Shi  
 TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 NUMBER OF SEQUENCES: 93  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/399,411  
 FILING DATE: 06-MAR-1995  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-399-411-85

Query Match 36.4% Score 4.0 DB 2 Length 8  
 Best Local Similarity 100.0% Pred. No. 25  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11  
 DB 2 KPND 5

## RESULT 4

US-08-934-222-24  
 Sequence 24, Application US/08934222

PATENT NO. 5928896  
 GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include Conformation-  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 3000 K Street NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20007

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/934,222  
 FILING DATE: 19-SEP-1997

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 08/532,818
3 FILING DATE: 03-MAY-1996
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: U.S. 08/143,364
6 FILING DATE: 29-OCT-1993
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: U.S. 08/051,741
9 FILING DATE: 23-APR-1993
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Isacson, John P.
12 REGISTRATION NUMBER: 33,751
13 REFERENCE/DOCKET NUMBER: 040433/0148
14 INFORMATION FOR SEQ ID NO: 24:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 8 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19
20 US-08-944 222-24
21
22 Query Match 36.4% Score 4: DB 2: Length 8:
23 Best Local Similarity 100.0% Pred. No. 2.5e+05;
24 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
25
26 QY 3 KEKP 6
27 DB 4 KEKP 7
28
29 RESULT 5
30 US-08-944 402-24
31 Sequence 24, Application US/08/94402
32 Patent No. 5948887
33 GENERAL INFORMATION:
34 APPLICANT: EVANS, Herbert J.
35 APPLICANT: KINI, R. Manjunatha
36 TITLE OF INVENTION: Polypeptides That Include Conformation:
37 TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
38 NUMBER OF SEQUENCES: 153
39 CORRESPONDENCE ADDRESS:
40 ADDRESSEE: Foley & Lardner
41 STREET: Suite 500, 3000 K Street NW
42 CITY: Washington
43 STATE: DC
44 ZIP: 20007
45 COUNTRY: USA
46 COMPUTER READABLE FORM:
47 MEDIUM TYPE: Floppy disk
48 COMPUTER: IBM PC compatible
49 OPERATING SYSTEM: PC-DOS/MS-DOS
50 SOFTWARE: Patent In Release #1.0, Version #1.25
51 CURRENT APPLICATION DATA:
52 APPLICATION NUMBER: US/09/207,621
53 FILING DATE:
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: 08/532,818
56 FILING DATE: 03-MAY-1996
57 APPLICATION NUMBER: PCT/US94/04294
58 FILING DATE: 21-APR-1994
59 PRIOR APPLICATION DATA:
60 APPLICATION NUMBER: U.S. 08/143,364
61 FILING DATE: 29-OCT-1993
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: U.S. 08/051,741
64 FILING DATE: 23-APR-1993
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Isacson, John P.
67 REGISTRATION NUMBER: 33,751
68 REFERENCE/DOCKET NUMBER: 040433/0148
69 INFORMATION FOR SEQ ID NO: 24:
70 SEQUENCE CHARACTERISTICS:
71 LENGTH: 8 amino acids
72 TYPE: amino acid
73 TOPOLOGY: linear
74
75 US-09-207-621-24
76
77 Query Match 36.4% Score 4: DB 2: Length 8:
78 Best Local Similarity 100.0% Pred. No. 2.5e+05;
79 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
80
81 QY 3 KEKP 6
82 DB 4 KEKP 7
83
84 RESULT 7
85 US-08-532-818-24
86 Sequence 24, Application US/08/532818
87 Patent No. 5965698
88 GENERAL INFORMATION:
89 APPLICANT: EVANS, Herbert J.

```

```

1 APPLICANT: KINI, R. Manjunatha
2 TITLE OF INVENTION: Polypeptides That Include Conformation-
3 TITLE OF INVENTION: Constraining Groups Which Flank A Protein Protein Interaction
4 TITLE OF INVENTION: Site
5 NUMBER OF SEQUENCES: 153
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Foley & Lardner
8 STREET: Suite 500, 3000 K Street NW
9 CITY: Washington
10 STATE: DC
11 COUNTRY: USA
12 ZIP: 20007
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/532,814
22 FILING DATE: 03-MAY-1996
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: PCT/US94/04294
25 FILING DATE: 21-APR-1994
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: U.S. 08/144,464
28 FILING DATE: 29-OCT-1994
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: U.S. 08/065,741
31 FILING DATE: 23-APR-1993
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Jackson, John P.
34 REGISTRATION NUMBER: 33,751
35 REFERENCE/DOCKET NUMBER: 04043/0148
36 INFORMATION FOR SEQ ID NO: 24:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 8 amino acids
39 TYPE: amino acid
40 TOPOLOGY: linear
41
42 US 08-532-818-24
43
44 Query Match 36.4% Score 4; DB 2; Length 8;
45 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
46 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
47
48 QY 3 KEKP 6
49 DB 4 KEKP 7
50
51 RESULT 8
52 US-08-516-856A-2
53 Sequence 2, Application US/08/48956A
54 Patent No. 5972351
55 GENERAL INFORMATION:
56 APPLICANT: Adrian V.S. Hill, et al.
57 TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHF CLASS 17
58 TITLE OF INVENTION: RESTRICTED CELL LINES DERIVED FROM PRE-ERYTHROCYTIC STAGE
59 TITLE OF INVENTION: ANTIGENS (AS AMEN-HEL)
60 NUMBER OF SEQUENCES: 86
61 CORRESPONDENCE ADDRESS:
62 ADDRESSEE: Wenderoth, Lind & Parnack, LLP
63 STREET: 2033 K Street, N.W., Suite 800
64 CITY: Washington
65 STATE: D.C.
66 COUNTRY: U.S.A.
67 ZIP: 20006
68
69 COMPUTER READABLE FORM:
70 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
71 COMPUTER: IBM PC compatible
72 OPERATING SYSTEM: PC-DOS/MS-DOS
73 SOFTWARE: WordPerfect 5.1+
74 CURRENT APPLICATION DATA:
75 APPLICATION NUMBER: US/08/318,854A

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1 FILING DATE: October 3, 1994
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: GB 92 08 068.8
4 FILING DATE: April 3, 1992
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: GB 92 17 704.7
7 FILING DATE: August 20, 1992
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: WO 87T/GB93/00711
10 FILING DATE: April 5, 1993
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Lee Cheng
13 REGISTRATION NUMBER: 40,949
14 REFERENCE/DOCKET NUMBER: 263-PP1R15770US
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (202) 721-8200
17 TELEFAX: (202) 721-8250
18 INFORMATION FOR SEQ ID NO: 2:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 8 amino acid residues
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 ORIGINAL SOURCE:
26 ORGANISM: Plasmodium falciparum
27
28 US-08-318-856A-2
29
30 Query Match 36.4% Score 4; DB 2; Length 8;
31 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
32 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
33
34 QY 8 KPND 11
35 DB 1 KPND 4
36
37 RESULT 9
38 US-08-516-859A-R5
39 Sequence 85, Application US/08/16859A
40 Patent No. 6069231
41 GENERAL INFORMATION:
42 APPLICANT: Huang, Shi
43 TITLE OF INVENTION: Retinoblastoma Protein - Interacting
44 TITLE OF INVENTION: Zinc Finger Proteins
45 NUMBER OF SEQUENCES: 106
46 CORRESPONDENCE ADDRESS:
47 ADDRESSEE: Campbell & Flores LLP
48 STREET: 4370 La Jolla Village Drive, Suite 700
49 CITY: San Diego
50 STATE: California
51 COUNTRY: USA
52 ZIP: 92122
53
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: Floppy disk
56 COMPUTER: IBM PC compatible
57 OPERATING SYSTEM: PC-DOS/MS-DOS
58 SOFTWARE: PatentIn Release #1.0, Version #1.25
59 CURRENT APPLICATION DATA:
60 APPLICATION NUMBER: US/08/516,859A
61 FILING DATE: 18-AUG-1995
62 CLASSIFICATION: 514
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: US 08/399,411
65 FILING DATE: 06-MAR-1995
66 PRIOR APPLICATION DATA:
67 APPLICATION NUMBER: US 08/292,683
68 FILING DATE: 18-AUG-1994
69 ATTORNEY/AGENT INFORMATION:
70 NAME: Campbell, Cathryn A.
71 REGISTRATION NUMBER: 31,815
72 REFERENCE/DOCKET NUMBER: P-LJ 1776
73 TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (619) 535-9501  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US 08 934-224 R5

Query Match 36.4% Score 41.00 40.00 40.00 40.00  
 Best Local Similarity 100.0% Ident. No. 2 Gaps 0  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KEK 11  
 11  
 2 KND 5

RESULT 11  
 US-08-934-224-24  
 Sequence 24, Application US/08934224  
 Patent No. 6100044  
 GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include Conformation-  
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interac  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 4000 K Street NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20007  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/934,224  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/532,818  
 FILING DATE: 03-MAY 1996  
 APPLICATION NUMBER: PCT/US94/04294  
 FILING DATE: 21-APR 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/143,464  
 FILING DATE: 29-OCT-1993  
 APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/051,741  
 FILING DATE: 23-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isaacson, John P.  
 REGISTRATION NUMBER: 33,751  
 REFERENCE FOR SEQ ID NO: 24:  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-09-787-443-17-24

QY 8 KEK 6  
 11  
 4 KEK 7

RESULT 22  
 US-08-934-224-24  
 Sequence 24, Application US/08934224  
 Patent No. 6100044  
 GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include Conformation-  
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interac  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 4000 K Street NW  
 CITY: Washington  
 QY 8 KEK 6  
 11  
 4 KEK 7

Query Match 36.4% Score 41.00 40.00 40.00 40.00  
 Best Local Similarity 100.0% Ident. No. 2 Gaps 0  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KEK 6  
 11  
 4 KEK 7

Query Match 36.4% Score 41.00 40.00 40.00 40.00  
 Best Local Similarity 100.0% Ident. No. 2 Gaps 0  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KEK 6  
 11  
 4 KEK 7

RESULT 22  
 US-08-934-224-24  
 Sequence 24, Application US/08934224  
 Patent No. 6100044  
 GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include Conformation-  
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interac  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 4000 K Street NW  
 CITY: Washington

STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/543,615  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,819  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,064  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
US-08-533-843-24

Query Match 36.48; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEKP 6  
DB 4 KEKP 7

RESULT 14  
US-08-543-223-24  
Sequence 24, Application US/08/543,615  
Patent No. 6147189  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
Title of Invention: Constraining Groups Which Flank A Protein-Protein Interac-  
TION  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/543,615  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/542,819  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/543,615  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
US-08-543-223-24

FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
US-08-534-223-24

Query Match 36.48; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEKP 6  
DB 4 KEKP 7

RESULT 14  
US-09-413-492-24  
Sequence 24, Application US/09413492  
Patent No. 6258550  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
Title of Invention: Constraining Groups Which Flank A Protein-Protein Interac-  
TION  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09413492  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/542,819  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/543,615  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
US-09-413-492-24

Query Match 36.48; Score 4; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEXP 6

ID 4 KEXP 7

# RESULT 15

US-09-586-472-85  
Sequence 85, Application: US/09586472  
Patent No. 642335

## GENERAL INFORMATION:

APPLICANT: Huang, Shi  
TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
Zinc Finger Proteins

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09586472

FILING DATE: 01-Jun-2000

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/586 700

FILING DATE: 17 MAR 2002

APPLICATION NUMBER: US 08/518 999

FILING DATE: 18-AUG-1995

APPLICATION NUMBER: US 08/499 411

FILING DATE: 06-MAR-1995

APPLICATION NUMBER: US 08/292 193

FILING DATE: 18-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,813

REFERENCE/DOCKET NUMBER: P 11 413

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9401

TELEFAX: (619) 535-8949

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 85

US-09-586-472-85

## Query Match

Best Local Similarity 36.4%; Score 4; ID 4; Length 8;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KPNB 11

ID 2 KPNB 5

# RESULT 16

US 08 197-484-19

Sequence 19, Application US/08197484

Patent No. 641931

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.

ADDRESSEE: CHESTNUT, Robert W.

APPLICANT: SEITZ, Alessandro D.  
APPLICANT: CELIS, Esteban  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crow  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105 1434

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197.484

FILING DATE: 16-FER-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/535,811

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/149,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 423-6793

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-197 484-19

## Query Match

Best Local Similarity 36.4%; Score 4; ID 4; Length 8;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KPNB 11

ID 1 KPNB 4

# RESULT 17

US-09 528-706-85

Sequence 85, Application US/09528706

Patent No. 646985

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

```

: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/528,706
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/516,859
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/292,683
: FILING DATE: 18-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-LJ 1776
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 85:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-09-528-706-85

Query Match: 36.4%, Score 4; DB 4; Length 8;
Best Local Similarity 100.0%, Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPND 11
Db 2 KPND 5

RESULT 18
PCT US95 02121-19
: SQUENCE IN: Application PC/TUS9502121
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
: TITLE OF INVENTION: CTL IMMUNITY
: NUMBER OF SEQUENCES: 154
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/02121
: FILING DATE: 16-FEB-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/197,494
: FILING DATE: 16-FEB-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/335,611
: FILING DATE: 26-AUG-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/874,491
: FILING DATE: 27-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/827,682
: FILING DATE: 29-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/749,568
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:

```

```

: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 14137-26-4PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 467-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: PCT-US95-02121-19

Query Match: 36.4%, Score 4; DB 5; Length 8;
Best Local Similarity 100.0%, Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPND 11
Db 1 KPND 4

RESULT 19
US-08-407-468-11
: Sequence 11, Application US/08407468
: Patent No. 5866681
: GENERAL INFORMATION:
: APPLICANT: Scarborough, Robert M.
: TITLE OF INVENTION: Thrombin Receptor Antagonists
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/407,468
: FILING DATE: 20-MAR-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/080,788
: FILING DATE: 28-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/922,340
: FILING DATE: 30-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Heines, M. Henry
: REGISTRATION NUMBER: 28,219
: REFERENCE/DOCKET NUMBER: 012418-002020US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /product- "OTHER"
: OTHER INFORMATION: /note- "Xaa = Phe N-substituted with various R groups"

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: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 2
: OTHER INFORMATION: /product: "OTHER"
: OTHER INFORMATION: /note: "Xaa - cyclohexylalanine"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /product: "OTHER"
: OTHER INFORMATION: /note: "Xaa - cyclohexylalanine"
: FEATURE:
: NAME/KEY: Modified site
: LOCATION: 9
: OTHER INFORMATION: /product: "OTHER"
: OTHER INFORMATION: /note: "Xaa - lysine"
: US 08 437-468-11
:
: Query Match 36.4% Score 4; DB 2; Length 9;
: Best Local Similarity 100.0% Pred. No. 2.5e+05;
: Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 8 KPND 11
: DB 5 KPND 8
:
: RESULT 20
: US 08-418-596A-45
: Sequence 45, Application US/08318856A
: Patent No. 5972351
: GENERAL INFORMATION:
: APPLICANT: Adrian V.S. BULL, et al.
: TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I
: TITLE OF INVENTION: RESTRICTED CD8 EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
: NUMBER OF SEQUENCES: 86
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wenderoth, Lind & Ponder, L.L.P.
: STREET: 2033 K Street, N.W., Suite 800
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20006
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/418,866A
: FILING DATE: October 3, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 92 08 066,8
: FILING DATE: April 3, 1994
: APPLICATION NUMBER: GB 92 17 704,7
: FILING DATE: August 20, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/GB93/00371
: FILING DATE: April 5, 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee Cheng
: REGISTRATION NUMBER: 40,949
: REFERENCE/DOCKET NUMBER: 263-PPI-157705
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 721-8200
: TELEFAX: (202) 721-8250
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acid residues
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear

```

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: MOLECULE TYPE: peptide
: US-08-318-856A-45
:
: Query Match 36.4% Score 4; DB 2; Length 9;
: Best Local Similarity 100.0% Pred. No. 2.5e+05;
: Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 8 KPND 11
: DB 1 KPND 4
:
: RESULT 21
: US-08-986-234-66
: Sequence 68, Application US/08986234
: Patent No. 5981786
: GENERAL INFORMATION:
: APPLICANT: Wallen, et al.
: TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
: FILE REFERENCE: UNNE-00081
: CURRENT APPLICATION NUMBER: US/08/986,234
: CURRENT FILING DATE: 1997-12-05
: NUMBER OF SEQ ID NOS: 114
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 68
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus
: US-08-986-234-68
:
: Query Match 36.4% Score 4; DB 2; Length 9;
: Best Local Similarity 100.0% Pred. No. 2.5e+05;
: Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 2 KKEK 5
: DB 3 KKEK 6
:
: RESULT 22
: US-07-789-184-45
: Sequence 45, Application US/07789184
: Patent No. 5688768
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/789,184
: FILING DATE: 19911107
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154

```

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note- "This position is Mpr."

OTHER INFORMATION: S-Mpr or Mba."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 3

OTHER INFORMATION: /note- "This position is Cha."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /note- "This position is Cha."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 10

OTHER INFORMATION: /note- "This position is K NH2."

US-07-789-184-45

Query Match

Best Local Similarity 36.4%; Score 4; DB 1; Length 10;

Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11

DB 6 KPND 9

RESULT 23

US-07-789-184-50

Sequence 50, Application US/07789184

Patent No. 5688768

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.

APPLICANT: SCARBOROUGH, ROBERT M.

TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

RELATED PHARMACEUTICALS

NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/07789184

FILING DATE: 19911107

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20502-20

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 44-0154

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

OTHER INFORMATION: /note- "This position is Mpr."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

TOPOLOGY: linear

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note- "This position is Mpr,

OTHER INFORMATION: S-Mpr or Mba."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 3

OTHER INFORMATION: /note- "This position is Cha."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /note- "This position is Cha."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 10

OTHER INFORMATION: /note- "This position is A-NH2."

US-07-789-184-50

Query Match

Best Local Similarity 36.4%; Score 4; DB 1; Length 10;

Mismatches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11

DB 6 KPND 9

RESULT 24

US-07-789-184-60

Sequence 60, Application US/07789184

Patent No. 5688768

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.

APPLICANT: SCARBOROUGH, ROBERT M.

TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

RELATED PHARMACEUTICALS

NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07789184

FILING DATE: 19911107

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20502-20

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 44-0154

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note- "This position is Mpr."

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1 FEATURE:
2 NAME/KEY: Modified-site
3 LOCATION: 4
4 OTHER INFORMATION: /note- "This position is Cha."
5 FEATURE:
6 NAME/KEY: Modified-site
7 LOCATION: 4
8 OTHER INFORMATION: /note- "This position is Cha."
9 FEATURE:
10 NAME/KEY: Modified-site
11 LOCATION: 10
12 OTHER INFORMATION: /note "This position is A-NH2."
13 US-07 789-184-65
14
15 Query Match: 36.4% Score 4: DP 1: Length 10:
16 Best Local Similarity: 100.0% Pred. No. 1: 0:
17 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
18
19 CY 8 KIND 11
20
21 DL 6 KIND 9
22
23 RESULT 25
24 US-07 789-184 65
25 Sequence 65: Application US/07789184
26 Patent No. 5648766
27 GENERAL INFORMATION:
28 APPLICANT: COUGHLIN, SHAWN R.
29 APPLICANT: SCARBOROUGH, ROBERT M.
30 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
31 TITLE OF INVENTION: RELATED PHARMACEUTICALS
32 NUMBER OF SEQUENCES: 223
33 CORRESPONDENCE ADDRESS:
34 ADDRESSEE: MORRISON & FORSTER
35 STREET: 735 Page Mill Road
36 CITY: Palo Alto
37 STATE: California
38 COUNTRY: USA
39 ZIP: 94304-1018
40 COMPUTER READABLE FORM:
41 MEDIUM TYPE: Floppy disk
42 COMPUTER: IBM PC compatible
43 OPERATING SYSTEM: PC-DOS/MS-DOS
44 SOFTWARE: Patent In Release #1.0, Version #1.25
45 CURRENT APPLICATION DATA:
46 APPLICATION NUMBER: US/07/789,184
47 FILING DATE: 19911107
48 CLASSIFICATION: 514
49 ATTORNEY/AGENT INFORMATION:
50 NAME: MURASHIGE, KATE H.
51 REGISTRATION NUMBER: 29,959
52 REFERENCE/DOCKET NUMBER: 22000-20502.20
53 TELEPHONE: (415) 813-5600
54 TELEFAX: (415) 494-0792
55 TELEX: 44-0154
56 INFORMATION FOR SEQ ID NO: 65:
57 SEQUENCE CHARACTERISTICS:
58 LENGTH: 10 amino acids
59 TYPE: AMINO ACID
60 STRANDEDNESS: single
61 TOPOLOGY: linear
62 FEATURE:
63 NAME/KEY: Modified-site
64 LOCATION: 1
65 OTHER INFORMATION: /note- "This position is Cha."
66 FEATURE:
67 NAME/KEY: Modified-site
68 LOCATION: 3
69 OTHER INFORMATION: /note "This position is Cha."
70 FEATURE:
71 NAME/KEY: Modified-site
72 LOCATION: 10
73 OTHER INFORMATION: /note "This position is K-NH2."

```

```

1 FEATURE:
2 NAME/KEY: Modified-site
3 LOCATION: 4
4 OTHER INFORMATION: /note- "This position is Cha."
5 FEATURE:
6 NAME/KEY: Modified-site
7 LOCATION: 10
8 OTHER INFORMATION: /note "This position is A-NH2."
9 US-07 789-184-65
10
11 Query Match: 36.4% Score 4: DP 1: Length 10:
12 Best Local Similarity: 100.0% Pred. No. 1: 0:
13 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
14
15 CY 8 KIND 11
16
17 DL 6 KIND 9
18
19 RESULT 26
20 US-07 789-184 66
21 Sequence 66: Application US/07789184
22 Patent No. 5688768
23 GENERAL INFORMATION:
24 APPLICANT: COUGHLIN, SHAWN R.
25 APPLICANT: SCARBOROUGH, ROBERT M.
26 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
27 TITLE OF INVENTION: RELATED PHARMACEUTICALS
28 NUMBER OF SEQUENCES: 223
29 CORRESPONDENCE ADDRESS:
30 ADDRESSEE: MORRISON & FORSTER
31 STREET: 735 Page Mill Road
32 CITY: Palo Alto
33 STATE: California
34 COUNTRY: USA
35 ZIP: 94304-1018
36 COMPUTER READABLE FORM:
37 MEDIUM TYPE: Floppy disk
38 COMPUTER: IBM PC compatible
39 OPERATING SYSTEM: PC-DOS/MS-DOS
40 SOFTWARE: Patent In Release #1.0, Version #1.25
41 CURRENT APPLICATION DATA:
42 APPLICATION NUMBER: US/07/789,184
43 FILING DATE: 19911107
44 CLASSIFICATION: 514
45 ATTORNEY/AGENT INFORMATION:
46 NAME: MURASHIGE, KATE H.
47 REGISTRATION NUMBER: 29,959
48 REFERENCE/DOCKET NUMBER: 22000-20502.20
49 TELEPHONE: (415) 813-5600
50 TELEFAX: (415) 494-0792
51 TELEX: 44-0154
52 INFORMATION FOR SEQ ID NO: 66:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 10 amino acids
55 TYPE: AMINO ACID
56 STRANDEDNESS: single
57 TOPOLOGY: linear
58 FEATURE:
59 NAME/KEY: Modified-site
60 LOCATION: 1
61 OTHER INFORMATION: /note- "This position is Mba."
62 FEATURE:
63 NAME/KEY: Modified-site
64 LOCATION: 4
65 OTHER INFORMATION: /note- "This position is Cha."
66 FEATURE:
67 NAME/KEY: Modified-site
68 LOCATION: 4
69 OTHER INFORMATION: /note- "This position is Cha."
70 FEATURE:
71 NAME/KEY: Modified-site
72 LOCATION: 10
73 OTHER INFORMATION: /note "This position is K-NH2."

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US-07-789-184-66

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

RESULT 27

US-07-789-184-67  
Sequence 67, Application US/07789184  
Patent No. 5688769  
GENERAL INFORMATION:  
APPLICANT: CUGHILIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent It Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07789-184  
FILING DATE: 19911107  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34 0154  
INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "This position is  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note- "This position is Cha."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note- "This position is Cha."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note- "This position is K-NH2."  
US-07-789-184-67

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

RESULT 28

US-07-789-184-203  
Sequence 203, Application US/07789184  
Patent No. 5688769  
GENERAL INFORMATION:  
APPLICANT: CUGHILIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent It Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07789-184  
FILING DATE: 19911107  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34 0154  
INFORMATION FOR SEQ ID NO: 203:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "This position is (2-Mba)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note- "This position is (Cha)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note- "This position is (Cha)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note- "This position is K-NH2."  
US-07-789-184-203

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

RESULT 28

US-07-789-184-203  
Sequence 203, Application US/07789184  
Patent No. 5688769  
GENERAL INFORMATION:  
APPLICANT: CUGHILIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent It Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07789-184  
FILING DATE: 19911107  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34 0154  
INFORMATION FOR SEQ ID NO: 203:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "This position is (2-Mba)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note- "This position is (Cha)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note- "This position is (Cha)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note- "This position is K-NH2."  
US-07-789-184-203

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

Matches 4; Conservative 0; Mismatches 0; Indels 0;

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RESULT 29
US-08-475-263-45
: Sequence 45, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note= "This position is Mpr."
: OTHER INFORMATION: S-Me Mpr. or Mba."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note= "This position is A-NH2."
US-08-475-263-50
Query Match 36.4%, Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB 6 KPND 9

RESULT 31
US-08-475-263-60
: Sequence 60, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note= "This position is Mpr."
: OTHER INFORMATION: S-Me Mpr. or Mba."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note= "This position is A-NH2."
US-08-475-263-45
Query Match 36.4%, Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB 6 KPND 9

RESULT 30
US-08-475-263-50
: Sequence 50, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:

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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DCKET NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "This position is Mpr."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "This position is A-NH2."
US-08 475 263-66

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Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

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QY 8 KPND 11
DB 6 KPND 9

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RESULT 32
US-08-475-263-66
: Sequence 65, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA

```

```

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DCKET NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "This position is Mpr."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "This position is A-NH2."
US-08-475-263-65

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Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

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QY 8 KPND 11
DB 6 KPND 9

```

```

RESULT 33
US-08-475-263-66
: Sequence 66, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note- "This position is Pla."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note- "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note- "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note- "This position is Cha."
NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /note- "This position is K NH2."
US-08-475-263-66

Query Match 36.4% Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPNQ 11
DB 6 KPNQ 9

RESULT 34
US-08-475-263-67
Sequence 67, Application US/08/475,263
Patent No. 575994
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note "This position is
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note- "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note- "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note- "This position is K-NH2."
US-08-475-263-67

Query Match 36.4% Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPNQ 11
DB 6 KPNQ 9

RESULT 35
US-08-475-263-203
Sequence 203, Application US/08/475,263
Patent No. 575994
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

```

```

1  TELEX: 90-4030
2  INFORMATION FOR SEQ ID NO: 203:
3  SEQUENCE CHARACTERISTICS:
4  LENGTH: 10 amino acids
5  TYPE: amino acid
6  STRANDEDNESS: single
7  TOPOLOGY: linear
8  FEATURE:
9  NAME/KEY: Modified-site
10 LOCATION: 1
11 OTHER INFORMATION: /note= "This position is (Cha)."
12 FEATURE:
13 NAME/KEY: Modified-site
14 LOCATION: 3
15 OTHER INFORMATION: /note= "This position is (Cha)."
16 FEATURE:
17 NAME/KEY: Modified-site
18 LOCATION: 4
19 OTHER INFORMATION: /note= "This position is (Cha)."
20 FEATURE:
21 NAME/KEY: Modified-site
22 LOCATION: 10
23 OTHER INFORMATION: /note= "This position is K-NH2."
24 US 08 475-263-203

```

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Query Match: 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 KPN0 11
DB 6 KPN0 9

```

```

RESULT 36
US-08-485-886-45
: Sequence 45, Application US/08485886
: Patent No. 5798248
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485.886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5660
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:

```

```

1  LENGTH: 10 amino acids
2  TYPE: amino acid
3  STRANDEDNESS: single
4  TOPOLOGY: linear
5  FEATURE:
6  NAME/KEY: Modified-site
7  LOCATION: 1
8  OTHER INFORMATION: /note= "This position is Mpr,
9  OTHER INFORMATION: S Me Mpr or Mba."
10 FEATURE:
11 NAME/KEY: Modified-site
12 LOCATION: 4
13 OTHER INFORMATION: /note= "This position is Cha."
14 FEATURE:
15 NAME/KEY: Modified-site
16 LOCATION: 4
17 OTHER INFORMATION: /note= "This position is Cha."
18 FEATURE:
19 NAME/KEY: Modified-site
20 LOCATION: 10
21 OTHER INFORMATION: /note= "This position is K-NH2."
22 US-08-485-886-45

```

```

Query Match: 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 KPN0 11
DB 6 KPN0 9

```

```

RESULT 37
US-08-485-886-50
: Sequence 50, Application US/08485886
: Patent No. 5798248
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485.886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid

```





```

: OTHER INFORMATION: /note- "This position is Mpr."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is A NH2."
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-65

Query Match          36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB 1111
6 KPND 9

RESULT 40
US-08-485-886-66
: Sequence 66, Application US/08485886
: Patent No. 5798248
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is Mpr."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."

```

```

: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-66

Query Match          36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB 1111
6 KPND 9

RESULT 41
US-08-485-886-67
: Sequence 67, Application US/08485886
: Patent No. 5798248
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is
: OTHER INFORMATION: Smpw."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."

```

```

: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-57
Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPN0 1;
DB 1;
6 KPN0 9

RESULT 42
US-08-485-886-203
: Sequence 203; Application US/08485886
: Patent No. 5798246
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 203:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is (x-MLe).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is (Cha).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4

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: OTHER INFORMATION: /note- "This position is (Cha).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-203
Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPN0 1;
DB 1;
6 KPN0 9

RESULT 43
US-08-477-362-45
: Sequence 45; Application US/08477362
: Patent No. 5849507
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,362
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is Mpr,
: OTHER INFORMATION: S-Me Mpr or Mba."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:

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1 NAME/KEY: Modified-site
2 LOCATION: 10
3 OTHER INFORMATION: /note- "This position is K NH2."
4 US-08-477 362-45
5
6 Query Match 36.4% Score 4; DB 2; Length 10;
7 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
8 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9
10 QY 8 KPND 11
11      ||||
12 Db 6 KPND 9
13
14 RESULT 44
15 US-08-477-362-50
16 Sequence 50, Application US/08477362
17 Patent No. 5849507
18 GENERAL INFORMATION:
19 APPLICANT: COUGHLIN, SHAUN R.
20 APPLICANT: SCARBOROUGH, ROBERT M.
21 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
22 TITLE OF INVENTION: RELATED PHARMACEUTICALS
23 NUMBER OF SEQUENCES: 223
24 CORRESPONDENCE ADDRESS:
25 ADDRESSEE: MORRISON & FOERSTER
26 STREET: 755 Page Mill Road
27 CITY: Palo Alto
28 STATE: California
29 COUNTRY: USA
30 ZIP: 94304-1018
31 COMPUTER READABLE FORM:
32 MEDIUM TYPE: Floppy disk
33 COMPUTER: IBM PC compatible
34 OPERATING SYSTEM: PC-DOS/MS-DOS
35 SOFTWARE: Patent In Release #1.0, Version #1.25
36 CURRENT APPLICATION DATA:
37 APPLICATION NUMBER: US/08/477,362
38 FILING DATE: 07-JUN-1995
39 CLASSIFICATION: 435
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 07/789,184
42 FILING DATE: 07-NOV-1991
43 ATTORNEY/AGENT INFORMATION:
44 NAME: MURASHIGE, KATE H.
45 REGISTRATION NUMBER: 29,959
46 REFERENCE/DCKET NUMBER: 22000-20502.20
47 TELECOMMUNICATION INFORMATION:
48 TELEPHONE: (415) 813-5600
49 TELEFAX: (415) 494-0792
50 TELEX: 34-0154
51 INFORMATION FOR SEQ ID NO: 50:
52 SEQUENCE CHARACTERISTICS:
53 LENGTH: 10 amino acids
54 TYPE: amino acid
55 STRANDEDNESS: single
56 TOPOLOGY: linear
57 FEATURE:
58 NAME/KEY: Modified-site
59 LOCATION: 1
60 OTHER INFORMATION: /note- "This position is Mpr."
61 OTHER INFORMATION: S-Me Mpr G: MPr."
62 FEATURE:
63 NAME/KEY: Modified-site
64 LOCATION: 3
65 OTHER INFORMATION: /note- "This position is Cha."
66 FEATURE:
67 NAME/KEY: Modified-site
68 LOCATION: 4
69 OTHER INFORMATION: /note- "This position is Cha."
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71 NAME/KEY: Modified-site
72 LOCATION: 10
73 US-08-477 362-60

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1 OTHER INFORMATION: /note- "This position is A-NH2."
2 US-08-477-362-50
3
4 Query Match 36.4% Score 4; DB 2; Length 10;
5 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
6 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
7
8 QY 8 KPND 11
9      ||||
10 Db 6 KPND 9
11
12 RESULT 45
13 US-08-477-362-60
14 Sequence 60, Application US/08477362
15 Patent No. 5849507
16 GENERAL INFORMATION:
17 APPLICANT: COUGHLIN, SHAUN R.
18 APPLICANT: SCARBOROUGH, ROBERT M.
19 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
20 TITLE OF INVENTION: RELATED PHARMACEUTICALS
21 NUMBER OF SEQUENCES: 223
22 CORRESPONDENCE ADDRESS:
23 ADDRESSEE: MORRISON & FOERSTER
24 STREET: 755 Page Mill Road
25 CITY: Palo Alto
26 STATE: California
27 COUNTRY: USA
28 ZIP: 94304-1018
29 COMPUTER READABLE FORM:
30 MEDIUM TYPE: Floppy disk
31 COMPUTER: IBM PC compatible
32 OPERATING SYSTEM: PC-DOS/MS-DOS
33 SOFTWARE: Patent In Release #1.0, Version #1.25
34 CURRENT APPLICATION DATA:
35 APPLICATION NUMBER: US/08/477,362
36 FILING DATE: 07-JUN-1995
37 CLASSIFICATION: 435
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 07/789,184
40 FILING DATE: 07-NOV-1991
41 ATTORNEY/AGENT INFORMATION:
42 NAME: MURASHIGE, KATE H.
43 REGISTRATION NUMBER: 29,959
44 REFERENCE/DCKET NUMBER: 22000-20502.20
45 TELECOMMUNICATION INFORMATION:
46 TELEPHONE: (415) 813-5600
47 TELEFAX: (415) 494-0792
48 TELEX: 34-0154
49 INFORMATION FOR SEQ ID NO: 60:
50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 10 amino acids
52 TYPE: amino acid
53 STRANDEDNESS: single
54 TOPOLOGY: linear
55 FEATURE:
56 NAME/KEY: Modified-site
57 LOCATION: 1
58 OTHER INFORMATION: /note- "This position is Mpr."
59 FEATURE:
60 NAME/KEY: Modified-site
61 LOCATION: 3
62 OTHER INFORMATION: /note- "This position is Cha."
63 FEATURE:
64 NAME/KEY: Modified-site
65 LOCATION: 4
66 OTHER INFORMATION: /note- "This position is Cha."
67 FEATURE:
68 NAME/KEY: Modified-site
69 LOCATION: 10
70 OTHER INFORMATION: /note- "This position is K-NH2."
71 US-08-477 362-60

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Query Match	36.4%	Score 4	28	Length 100
Best Local Similarity	100.0%	pred. No.	1,700,000	
Matches	47	Conservative	67	Mismatches 67
				Labels

Q27 8 KING 11  
1111  
Q28 6 KING 9

RESULT 46  
US-08-477-362 65  
Sequence 65, Application: US/08477362

RESULT 47  
OS-08-477-362-66  
: Sequence 66, Application OS/08477362

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—

( )

DB 6 KPN0 9

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RESULT 48
US-08-477-362-67
: Sequence 203, Application US/08477362
: Patent No. 5849507
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FERNSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,362
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION NUMBER:
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note= "This position is"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note= "This position is K-NH2."
: US-08-477-362-67

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Query Match 36.4%, Score 4; DB 2; Length 10;
Best local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 KPN0 11
DB 6 KPN0 9

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RESULT 50
US-08-477-362-203

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RESULT 49
US-08-477-362-203
: Sequence 203, Application US/08477362
: Patent No. 5849507
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FERNSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,362
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION NUMBER:
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 203:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note= "This position is (2-Mba).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note= "This position is (Cha).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note= "This position is (Cha).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note= "This position is K-NH2."
: US-08-477-362-203

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Query Match 36.4%, Score 4; DB 2; Length 10;
Best local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 KPN0 11
DB 6 KPN0 9

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Sequence 45, Application US/98477144  
Patent No. 5856448  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT TETRAMIN PEPTIDES AND  
TITLE OF INVENTION: RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORBES  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304 1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,144  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/789,144  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 45,959  
REFERENCE/DOCKET NUMBER: 22000-296.2.20  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-3600  
TELEFAX: (415) 494-0792  
TELEX: 34 0154  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRAND/NESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "this position is Met  
OTHER INFORMATION: S-Met of Mod."  
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LOCATION: 3  
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LOCATION: 4  
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FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note- "this position is K Met."  
US 08-477-144-45

Query Match 36.48; Score 43; PP 20; E 0.015; 200  
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Matches 4; Conservative 0; Mismatches 3; Gaps 0

QY 8 KPN1 11  
1.11  
DB 6 KPN3 9

Search completed: September 30, 2003, 11:28:53  
Job time: 13.9167 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:10:03 : Search time 21.5 seconds  
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77.413 Million cell updates/sec

Title: US-09-787-443-17

Perfect score: 11

Sequence: 1 AKKEPNKPNQ 11

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Minimum DB seq length: 8

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# SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	5	45.5	14	15	US-10-116-91	Sequence 1, Appl
2	4	36.4	8	12	US-10-079-167	Sequence 2, Appl
3	4	36.4	8	15	US-10-128-71	Sequence 19, Appl
4	4	36.4	8	15	US-10-143-210	Sequence 181, App
5	4	36.4	9	9	US-09-010-74	Sequence 1, Appl
6	4	36.4	9	10	US-09-984-056	Sequence 10, Appl
7	4	36.4	9	10	US-09-994-057	Sequence 10, Appl
8	4	36.4	9	12	US-10-077-109	Sequence 13, Appl
9	4	36.4	9	12	US-10-077-109	Sequence 15, Appl
10	4	36.4	9	15	US-10-211-207	Sequence 13, Appl
11	4	36.4	9	15	US-10-211-207	Sequence 15, Appl
12	4	36.4	9	15	US-10-143-210	Sequence 58, Appl
13	4	36.4	9	15	US-10-211-088	Sequence 271, Appl
14	4	36.4	10	9	US-09-010-714	Sequence 4, Appl
15	4	36.4	10	10	US-09-984-056	Sequence 91, App

16	4	36.4	10	11	US-09-876-904A-572	Sequence 572, App
17	4	36.4	10	11	US-09-572-404B-1774	Sequence 1774, App
18	4	36.4	10	12	US-10-155-693-26	Sequence 26, Appl
19	4	36.4	10	12	US-10-239-313A-458	Sequence 458, App
20	4	36.4	10	15	US-10-133-210-31	Sequence 31, Appl
21	4	36.4	10	15	US-10-133-210-92	Sequence 92, Appl
22	4	36.4	10	15	US-10-072-602B-503	Sequence 503, App
23	4	36.4	11	9	US-09-879-936-10	Sequence 10, Appl
24	4	36.4	11	11	US-09-876-904A-237	Sequence 237, App
25	4	36.4	11	11	US-09-876-904A-354	Sequence 354, App
26	4	36.4	13	9	US-09-767-395-24	Sequence 24, Appl
27	4	36.4	13	9	US-09-873-676-27	Sequence 27, Appl
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29	4	36.4	13	10	US-09-359-325A-19	Sequence 19, Appl
30	4	36.4	13	10	US-09-945-249-24	Sequence 24, Appl
31	4	36.4	13	10	US-09-945-249-29	Sequence 29, Appl
32	4	36.4	13	11	US-09-820-053A-88	Sequence 88, Appl
33	4	36.4	13	15	US-10-211-088-232	Sequence 232, App
34	4	36.4	13	15	US-10-109-171-88	Sequence 88, Appl
35	4	36.4	14	9	US-09-010-714-2	Sequence 2, Appl
36	4	36.4	14	11	US-09-966-782A-43	Sequence 43, Appl
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43	3	27.3	8	9	US-09-358-423-11	Sequence 11, Appl
44	3	27.3	8	9	US-09-358-423-12	Sequence 12, Appl
45	3	27.3	8	9	US-09-804-733A-19	Sequence 19, Appl
46	3	27.3	8	9	US-09-813-653-5	Sequence 5, Appl
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48	3	27.3	8	10	US-09-966-955A-7	Sequence 7, Appl
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50	3	27.3	8	11	US-09-876-904A-57	Sequence 57, Appl
51	3	27.3	8	11	US-09-876-904A-352	Sequence 352, App
52	3	27.3	8	11	US-09-876-904A-393	Sequence 393, App
53	3	27.3	8	11	US-09-876-904A-394	Sequence 394, App
54	3	27.3	8	11	US-09-876-904A-439	Sequence 439, App
55	3	27.3	8	11	US-09-876-904A-493	Sequence 493, App
56	3	27.3	8	11	US-09-876-904A-502	Sequence 502, App
57	3	27.3	8	11	US-09-876-904A-505	Sequence 505, App
58	3	27.3	8	11	US-09-876-904A-515	Sequence 515, App
59	3	27.3	8	11	US-09-876-904A-518	Sequence 518, App
60	3	27.3	8	11	US-09-876-904A-536	Sequence 536, App
61	3	27.3	8	11	US-09-876-904A-537	Sequence 537, App
62	3	27.3	8	11	US-09-876-904A-595	Sequence 595, App
63	3	27.3	8	11	US-09-876-904A-599	Sequence 599, App
64	3	27.3	8	12	US-10-039-183A-13	Sequence 13, Appl
65	3	27.3	8	12	US-10-073-333A-28	Sequence 28, Appl
66	3	27.3	8	12	US-10-079-167-60	Sequence 60, Appl
67	3	27.3	8	12	US-10-014-322A-62	Sequence 62, Appl
68	3	27.3	8	12	US-10-293-580-41	Sequence 41, Appl
69	3	27.3	8	12	US-10-239-313A-93	Sequence 93, Appl
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73	3	27.3	8	14	US-10-057-503-7	Sequence 7, Appl
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81	3	27.3	8	15	US-10-140-164-29	Sequence 29, Appl
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83	3	27.3	8	15	US-10-052-942-71	Sequence 71, Appl
84	3	27.3	8	15	US-10-173-138A-20	Sequence 52, Appl
85	3	27.3	8	15	US-10-168-843A-52	Sequence 20, Appl
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87	3	27.3	9	7	US-08-344-824-166	Sequence 166, App
88	3	27.3	9	8	US-08-831-310-12	Sequence 12, Appl



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91	3	27.3	9	9	US-09-879-936-24	Sequence 24, Appl	164	3	27.3	9	11	US-09-820-053A-123	Sequence 123, App
92	3	27.3	9	9	US-09-829-549A-19	Sequence 19, Appl	165	3	27.3	9	11	US-09-820-053A-135	Sequence 135, App
93	3	27.3	9	9	US-09-192-854-25	Sequence 25, Appl	166	3	27.3	9	11	US-09-820-053A-136	Sequence 136, App
94	3	27.3	9	9	US-09-142-854-44	Sequence 44, Appl	167	3	27.3	9	11	US-09-029-479-3	Sequence 3, Appl1
95	3	27.3	9	9	US-09-981-063-76	Sequence 176, App	168	3	27.3	9	11	US-09-557-823-6	Sequence 6, Appl1
96	3	27.3	9	9	US-09-879-063-93	Sequence 3, Appl1	169	3	27.3	9	12	US-09-932-165-226	Sequence 226, App
97	3	27.3	9	10	US-09-740-533-58	Sequence 58, App	170	3	27.3	9	12	US-09-932-165-244	Sequence 244, App
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109	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	182	3	27.3	9	12	US-10-291-250-10	Sequence 10, Appl
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113	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	186	3	27.3	9	12	US-09-968-744A-66	Sequence 66, Appl
114	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	187	3	27.3	9	12	US-09-315-355-3	Sequence 3, Appl1
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116	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	189	3	27.3	9	12	US-10-050-200-20	Sequence 20, Appl
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123	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	196	3	27.3	9	12	US-09-942-052-140	Sequence 140, App
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137	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	210	3	27.3	9	12	US-10-357-175-76	Sequence 76, Appl
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151	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	224	3	27.3	9	15	US-10-125-635A-184	Sequence 184, App
152	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	225	3	27.3	9	15	US-10-125-635A-207	Sequence 207, App
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155	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	228	3	27.3	9	15	US-10-125-635A-277	Sequence 277, App
156	3	27.3	9	10	US-09-956-056-31	Sequence 46, App	229	3	27.3	9	15	US-10-084-813-987	Sequence 987, App
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384	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	457	3	27.3	US-09-876-904A-78	Sequence 280, App
385	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	458	3	27.3	US-09-876-904A-78	Sequence 414, App
386	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	459	3	27.3	US-09-876-904A-78	Sequence 445, App
387	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	460	3	27.3	US-09-876-904A-78	Sequence 607, App
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408	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	481	3	27.3	US-09-876-904A-78	Sequence 51, Appl
409	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	482	3	27.3	US-09-876-904A-78	Sequence 127, App
410	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	483	3	27.3	US-09-876-904A-78	Sequence 524, App
411	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	484	3	27.3	US-09-876-904A-78	Sequence 3, Appl
412	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	485	3	27.3	US-09-876-904A-78	Sequence 25, Appl
413	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	486	3	27.3	US-09-876-904A-78	Sequence 7, Appl
414	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	487	3	27.3	US-09-876-904A-78	Sequence 23, Appl
415	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	488	3	27.3	US-09-876-904A-78	Sequence 41, Appl
416	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	489	3	27.3	US-09-876-904A-78	Sequence 1033, Ap
417	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	490	3	27.3	US-09-876-904A-78	Sequence 1035, Ap
418	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	491	3	27.3	US-09-876-904A-78	Sequence 1036, Ap
419	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	492	3	27.3	US-09-876-904A-78	Sequence 1037, Ap
420	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	493	3	27.3	US-09-876-904A-78	Sequence 1038, Ap
421	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	494	3	27.3	US-09-876-904A-78	Sequence 1039, Ap
422	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	495	3	27.3	US-09-876-904A-78	Sequence 1040, Ap
423	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	496	3	27.3	US-09-876-904A-78	Sequence 1041, Ap
424	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	497	3	27.3	US-09-876-904A-78	Sequence 1042, Ap
425	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	498	3	27.3	US-09-876-904A-78	Sequence 139, App
426	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	499	3	27.3	US-09-876-904A-78	
427	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl	500	3	27.3	US-09-876-904A-78	
428	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
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430	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
431	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
432	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
433	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
434	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
435	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
436	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
437	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
438	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
439	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
440	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
441	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
442	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
443	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
444	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
445	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
446	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
447	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
448	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
449	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
450	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
451	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
452	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					
453	3	27.3	10	15	US-09-876-904A-78	Sequence 11, Appl					

## ALIGNMENTS

## RESULT 1

US-10-116-391-1  
 : Sequence 1, Application: US/10116391  
 : Publication No. US20030087255A1  
 : GENERAL INFORMATION:  
 : APPLICANT: BARRITAU, DENIS  
 : APPLICANT: AGUR, JOSE  
 : APPLICANT: AGUR, JOSE  
 : TITLE OF INVENTION: PEPTIDES WHICH STIMULATE THE IMMUNE RESPONSE AND TISSUE  
 : TITLE OF INVENTION: REGENERATION  
 : FILE REFERENCE: 1081-C2  
 : CURRENT APPLICATION NUMBER: US/10/116,391  
 : CURRENT FILING DATE: 2002-04-04  
 : PRIOR APPLICATION NUMBER: PCT/FR00/02786  
 : PRIOR FILING DATE: 2000-10-06  
 : PRIOR APPLICATION NUMBER: FR 99/12714  
 : PRIOR FILING DATE: 1999-10-12  
 : NUMBER OF SEQ. ID NOS: 22  
 : SOFTWARE: Patent In Ver. 2.1  
 : SEQ. ID NO: 1  
 : LENGTH: 14

? TYPE: PRT  
 ? ORGANISM: Unknown Organism  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Unknown Organism. HARP peptide fragment  
 US 10-116-391-1

Query Match: 45.5%; Score 5; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 KKEKP 6  
 DB 2 KKEKP 6

RESULT 2  
 US-10-079-167-2  
 ? Sequence 2: Application US/10079167  
 ? Publication No. US20030138454A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Hill, Adrian V.S.  
 ? APPLICANT: McShane, Helen  
 ? APPLICANT: Gilbert, Sarah C.  
 ? APPLICANT: Reese, William  
 ? APPLICANT: Schneider, Joerg  
 ? TITLE OF INVENTION: Vaccination Method  
 ? FILE REFERENCE: 2907.1006-001  
 ? CURRENT APPLICATION NUMBER: US/10-079-167  
 ? PRIOR FILING DATE: 2002-02-19  
 ? PRIOR APPLICATION NUMBER: US 09/454,204  
 ? PRIOR FILING DATE: 1999-12-09  
 ? PRIOR APPLICATION NUMBER: PCT/US98/01681  
 ? PRIOR FILING DATE: 1998-06-09  
 ? PRIOR APPLICATION NUMBER: GB 97 11957.2  
 ? PRIOR FILING DATE: 1997-05-09  
 ? PRIOR APPLICATION NUMBER: PCT/US96/04116  
 ? PRIOR FILING DATE: 2001-09-13  
 ? PRIOR APPLICATION NUMBER: GB 00 23204.3  
 ? PRIOR FILING DATE: 2001-09-21  
 ? NUMBER OF SEQ ID NOS: 99  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 2  
 ? LENGTH: 6  
 ? TYPE: PRT  
 ? ORGANISM: Unknown  
 ? FEATURE:  
 ? OTHER INFORMATION: CTL Epitope of the Major Histocompatibility Complex

Query Match: 36.4%; Score 1; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KPNQ 11  
 DB 1 KPNQ 4

RESULT 3  
 US-10-128-711-19  
 ? Sequence 19: Application US/10128711  
 ? Publication No. US20030099634A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: VITIELLO, Maria A.  
 ? CHESTNUT, Robert W.  
 ? SETTE, Alessandro D.  
 ? CELIS, Esteban  
 ? GRAY, Howard  
 ? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
 ? CTL IMMUNITY  
 ? NUMBER OF SEQUENCES: 153  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Townsend and Townsend Klepper and Fiew

? STREET: Stuart Street Tower, One Market Plaza  
 ? CITY: San Francisco  
 ? STATE: California  
 ? COUNTRY: US  
 ? ZIP: 94105-1493  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC Compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/10/128-711  
 ? FILING DATE: 22-Apr-2002  
 ? CLASSIFICATION: <Unknown>  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/197,484  
 ? FILING DATE: 16-FEB-1994  
 ? APPLICATION NUMBER: US 07/935,811  
 ? FILING DATE: 26-AUG-1992  
 ? APPLICATION NUMBER: US 07/874,491  
 ? FILING DATE: 27-APR-1992  
 ? APPLICATION NUMBER: US 07/827,682  
 ? FILING DATE: 29 JAN-1992  
 ? APPLICATION NUMBER: US 07/749,568  
 ? FILING DATE: 26-AUG-1991  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Parmelee, Steven W.  
 ? REGISTRATION NUMBER: 31,990  
 ? REFERENCE/DOCKET NUMBER: 14137-26-4  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (206) 467-9600  
 ? TELEFAX: (206) 623-6793  
 ? INFORMATION FOR SEQ ID NO: 19:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 8 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: unknown  
 ? TOPOLOGY: unknown  
 ? MOLECULE TYPE: peptide  
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 US-10-128-711-19

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KPNQ 11  
 DB 1 KPNQ 4

RESULT 4  
 US-10-133-210-181  
 ? Sequence 181: Application US/10133210  
 ? Publication No. US20030103964A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Delisi, Charles  
 ? APPLICANT: Herzofsky, Jay  
 ? APPLICANT: Gulukota, Kamalakara  
 ? APPLICANT: Vaccaro, Dennis  
 ? APPLICANT: Weng, Zhiping  
 ? APPLICANT: Zhang, Chao  
 ? TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
 ? FILE REFERENCE: BU-035AX  
 ? CURRENT APPLICATION NUMBER: US/10/133,210  
 ? CURRENT FILING DATE: 2002-04-26  
 ? NUMBER OF SEQ ID NOS: 281  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 181  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-10-133-210-181

Query Match 36.4%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 ||||  
 DB 2 KKEK 5

## RESULT 5

US-09-010-714-1  
 : Sequence 1, Application US/09010714  
 : Patent No. US20020012942A1  
 : GENERAL INFORMATION:  
 : APPLICANT: McCarthy, James B.  
 : APPLICANT: Furcht, Leo T.  
 : APPLICANT: Iida, Joti  
 : TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED  
 : TITLE OF INVENTION: ACTIVITY  
 : FILE REFERENCE: 600.3320S01  
 : CURRENT APPLICATION NUMBER: US/09/010-714  
 : CURRENT FILING DATE: 1998-01-22  
 : NUMBER OF SEQ ID NOS: 11  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1:  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-09-010-714-1

Query Match 36.4%; Score 4; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 ||||  
 DB 1 KKEK 4

## RESULT 6

US-09-984-056-10  
 : Sequence 10, Application US/090984056  
 : Patent No. US20020120106A1  
 : GENERAL INFORMATION:  
 : APPLICANT: HOGGCH, ELENORE S.  
 : TITLE OF INVENTION: ANTHRAX AND SMALL Pox PATHOGENS AND METHODS OF USE  
 : FILE REFERENCE: 09425-46903  
 : CURRENT APPLICATION NUMBER: US/09/984-056  
 : CURRENT FILING DATE: 2001-10-26  
 : PRIOR APPLICATION NUMBER: 60/303,396  
 : PRIOR FILING DATE: 2001-07-09  
 : PRIOR APPLICATION NUMBER: 60/278,761  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 09/146,755  
 : PRIOR FILING DATE: 1998-09-04  
 : PRIOR APPLICATION NUMBER: 09/817,144  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 08/158,139  
 : PRIOR FILING DATE: 1994-02-17  
 : NUMBER OF SEQ ID NOS: 103  
 : SOFTWARE: PatentIn 2.1  
 : SEQ ID NO 10  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Staphylococcus aureus  
 US-09-984-056-10

Query Match 36.4%; Score 4; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 ||||  
 DB 1 KKEK 4

## RESULT 7

US-09-984-057-10  
 : Sequence 10, Application US/09984057  
 : Patent No. US20020151677A1  
 : GENERAL INFORMATION:  
 : APPLICANT: BOGACH, SAMUEL  
 : APPLICANT: HOGGCH, ELENORE S.  
 : TITLE OF INVENTION: REPLIKINS AND METHODS OF IDENTIFYING  
 : TITLE OF INVENTION: REPLIKIN-CONTAINING SEQUENCES  
 : FILE REFERENCE: 09425-46902  
 : CURRENT APPLICATION NUMBER: US/09/984,057  
 : CURRENT FILING DATE: 2001-10-26  
 : PRIOR APPLICATION NUMBER: 60/303,396  
 : PRIOR FILING DATE: 2001-07-09  
 : PRIOR APPLICATION NUMBER: 60/278,761  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 09/146,755  
 : PRIOR FILING DATE: 1998-09-04  
 : PRIOR APPLICATION NUMBER: 09/817,144  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 08/198,139  
 : PRIOR FILING DATE: 1994-02-17  
 : NUMBER OF SEQ ID NOS: 90  
 : SOFTWARE: PatentIn 2.1  
 : SEQ ID NO 10  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Staphylococcus aureus  
 US-09-984-057-10

Query Match 36.4%; Score 4; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 ||||  
 DB 1 KKEK 4

## RESULT 8

US-10-077-106-13  
 : Sequence 13, Application US/10077106  
 : Publication No. US20030166531A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cgillins, Mary  
 : APPLICANT: Madrenas, Joaquin  
 : APPLICANT: Cairneo, Beatriz  
 : APPLICANT: Kuchroo, Vijay  
 : TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 : TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND  
 : FILE REFERENCE: GNN-027  
 : CURRENT APPLICATION NUMBER: US/10/077,106  
 : CURRENT FILING DATE: 2002-02-15  
 : PRIOR APPLICATION NUMBER: 60/269,757  
 : PRIOR FILING DATE: 2001-02-16  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 13  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-077-106-13

Query Match 36.4%; Score 4; DB 12; Length 9;

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best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 9
US-10-077-106-15
; Sequence 15, Application US/100/7106
; Publication No. US20030166541A;
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/077,106
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-077-106-15

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 10
US-10-211-207-13
; Sequence 14, Application US/10211207
; Publication No. US2003004113A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/211,207
; PRIOR FILING DATE: 2002-08-02
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-207-13

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 11
US-10-211-207-15
; Sequence 15, Application US/10211207
; Publication No. US2003004113A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/211,207
; PRIOR FILING DATE: 2002-08-02
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-211-207-15

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 12
US-10-133-210-58
; Sequence 58, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-58

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 4 KKEK 7

RESULT 13

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US-09-211-088-271
: Sequence 271, Application US/09211-088
: Publication No. US20030104479A1
: GENERAL INFORMATION:
: APPLICANT: Bright, Gary R.
: APPLICANT: Prekumar, D. David
: APPLICANT: Chen, Yih-Tai
: TITLE OF INVENTION: NO. US20030104479A1: Fast to Proteins And Assays For Molecular Bi
: FILE REFERENCE: 01-1022-US
: CURRENT APPLICATION NUMBER: US/09-211-088
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/395,395
: PRIOR FILING DATE: 2001-08-01
: PRIOR APPLICATION NUMBER: 60/341,589
: PRIOR FILING DATE: 2001-12-13
: NUMBER OF SEQ ID NOS: 366
: SOFTWARE: Patent in version 3.1
: SEQ ID NO 271
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Artificial sequence
: OTHER INFORMATION: Nuclear localization signal
US-09-211-088 271

Query Match 36.4%, Score 4; DB 1b; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
DB 1111
: KKEK 4

RESULT 14
US-09-010-714-4
: Sequence 4, Application US/09010-714
: Patent No. US20020012942A1
: GENERAL INFORMATION:
: APPLICANT: McCarthy, James B.
: APPLICANT: Furcht, Leo T.
: APPLICANT: Lida, Joel
: TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 1 INTEGRIN SIGNAL RELATED
: TITLE OF INVENTION: ACTIVITY
: FILE REFERENCE: 600,332US01
: CURRENT APPLICATION NUMBER: US/09-010-714
: CURRENT FILING DATE: 1998-01-22
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: Patent in Ver. 2.0
: SEQ ID NO 4
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-010-714-4

Query Match 36.4%, Score 4; DB 09; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
DB 1111
: KKEK 4

RESULT 15
US-09-984-056-91
: Sequence 91, Application US/09984-056
: Patent No. US20020120106A1
: GENERAL INFORMATION:
: APPLICANT: BOGOCH, SAMUEL
: APPLICANT: BOGOCH, ELENOR S.
: TITLE OF INVENTION: ANTHRAX AND SMALL POX RECEPTORS AND METHODS OF USE
: FILE REFERENCE: 09425-46903

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: CURRENT APPLICATION NUMBER: US/09/984,056
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 65/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 69/146,745
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,149
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 103
: SOFTWARE: Patent in 2.1
: SEQ ID NO 91
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Bacillus anthracis
US-09-984-056-91

```

```

Query Match 36.4%, Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 KKEK 5
DB 1111
: KKEK 6

```

```

RESULT 16
US-09-876-904A-572
: Sequence 572, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: FILE REFERENCE: TB-2002-00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: Patent in Ver. 2.1
: SEQ ID NO 572
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
: FEATURE:
: OTHER INFORMATION: Yeast GBF5p.
US-09-876-904A-572

```

```

Query Match 36.4%, Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 KKEK 5
DB 1111
: KKEK 4

```

```

RESULT 17
US-09-572-404B 1774
: Sequence 1774, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203

```

SOFTWARE: ProtPatent version 1.0

SEQ ID NO: 1774

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: Sequence located in MAPLE at 55442 and may interact with Sequen

US-09-572-404B 1774

Query Match 36.4% Score 4; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 4; le-02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKEK 6

III

DB 1 KKEK 4

RESULT 18

US-10-155-693-26

Sequence 26, Application US/10155693

Publication No. US20030175876A1

GENERAL INFORMATION:

APPLICANT: FOX, GARY M.

APPLICANT: KING, SHUOLAN

APPLICANT: KEN, GUANZHI

TITLE OF INVENTION: GLIAL CELL LINE DERIVED NEUR TROPHIC FACTOR RECEPTOR

FILE REFERENCE: A-401C

CURRENT APPLICATION NUMBER: US/10/155-693

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: US/08/07,199

PRIOR FILING DATE: 1997-04-14

PRIOR APPLICATION NUMBER: US 60/6-15,907

PRIOR FILING DATE: 1996-04-22

PRIOR APPLICATION NUMBER: US 60/7-17,421

PRIOR FILING DATE: 1996-05-09

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 10

TYPE: PRT

ORGANISM: HUMAN

US-10-155-693-26

Query Match:

Best Local Similarity 36.4%; Score 4; DB 10; Length 10;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKEK 5

III

DB 5 KKEK 9

RESULT 19

US-10-239-313A-459

Sequence 459, Application US/1023933A

Publication No. US20030175285A1

GENERAL INFORMATION:

APPLICANT: KLINGNER - HAMOUR, Christine

APPLICANT: CORVAIA, Nathalie

APPLICANT: BECK, Alain

APPLICANT: GOETSCH, Liliane

TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS

TITLE OF INVENTION: N-TERMINAL A GLUTAMINYL AMIDE OF A GLUTAMINE IN THE FORM

FILE REFERENCE: OF A PHYSIOLOGICALLY ACCEPTABLE SWEET ACID

FILE REFERENCE: 343 727 - US

CURRENT APPLICATION NUMBER: US/10/239-313A

CURRENT FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: FR 00/6411

PRIOR FILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: PCT 01/30772

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 697

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 458

LENGTH: 10

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-10-239-313A-458

Query Match:

Best Local Similarity 46.4%; Score 4; DB 12; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5

III

DB 4 KKEK 7

RESULT 20

US-10-133-210-31

Sequence 31, Application US/10133210

Publication No. US20030103964A1

GENERAL INFORMATION:

APPLICANT: Delisi, Charles

APPLICANT: Berzofsky, Jay

APPLICANT: Gulakota, Kamalakar

APPLICANT: Vaccaro, Dennis

APPLICANT: Weng, Zhiping

APPLICANT: Zhang, Chao

TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND

FILE REFERENCE: RU 035AX

CURRENT APPLICATION NUMBER: US/10/133-210

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 281

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 31

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-133-210-31

Query Match:

Best Local Similarity 46.4%; Score 4; DB 15; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5

III

DB 4 KKEK 7

RESULT 21

US-10-134-210-92

Sequence 92, Application US/10133210

Publication No. US20030103964A1

GENERAL INFORMATION:

APPLICANT: Delisi, Charles

APPLICANT: Berzofsky, Jay

APPLICANT: Gulakota, Kamalakar

APPLICANT: Vaccaro, Dennis

APPLICANT: Weng, Zhiping

APPLICANT: Zhang, Chao

TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND

FILE REFERENCE: RU 035AX

CURRENT APPLICATION NUMBER: US/10/133-210

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 281

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 92

LENGTH: 10

TYPE: PRT



1 ORGANISM: Artificial Sequence  
2 FEATURE:  
3 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
4 US-10-072-602B-503

Query Match: 36.4%, Score 4; DB 12; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 4.5e+02;  
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
DB 7 KKEK 10

RESULT 22

1 Sequence 503, Application US/10-72628  
2 Publication No. US2003019470A1  
3 GENERAL INFORMATION:

4 APPLICANT: University of Utah Research Foundation

5 APPLICANT: Cognetix, Inc.

6 APPLICANT: Olivera, Baldomero M.

7 APPLICANT: McIntosh, C. Michael

8 APPLICANT: Watkins, Marion

9 APPLICANT: Garrett, James E.

10 APPLICANT: Gray, Lourdes C.

11 APPLICANT: Grilley, Michelle

12 APPLICANT: Schoenfeld, Robert M.

13 APPLICANT: Walker, Craig

14 APPLICANT: Shetty, Reshma

15 APPLICANT: Jones, Robert M.

16 TITLE OF INVENTION: Cone Scall Peptides

17 FILE REFERENCE: 2314 249

18 CURRENT APPLICATION NUMBER: US/10-072-602B

19 PRIOR FILING DATE: 2002-02-11

20 PRIOR APPLICATION NUMBER: US 63/267,408

21 PRIOR FILING DATE: 2001-02-09

22 NUMBER OF SEQ ID NOS: 638

23 SOFTWARE: Patent in version 3.0

24 SEQ ID NO 503

25 LENGTH: 10

26 TYPE: PRT

27 ORGANISM: Various characteristics

28 US-10-072-602B-503

Query Match: 36.4%, Score 4; DB 12; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 4.5e+02;  
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ENKI 7  
DB 6 ENKI 7

RESULT 23

1 Sequence 504, Application US/09874904

2 Patent No. US20030045564A1

3 GENERAL INFORMATION:

4 APPLICANT: Van Eyk, Jennifer E.

5 APPLICANT: Max, Alan S.

6 APPLICANT: Cole, Graham P.

7 TITLE OF INVENTION: Methods of Modulating Ras in Cytototoxic

8 FILE REFERENCE: 1997-021-0308

9 CURRENT APPLICATION NUMBER: US/09874904

10 CURRENT FILING DATE: 2001-06-14

11 PRIOR APPLICATION NUMBER: 60/050,476

12 PRIOR FILING DATE: 1997-06-23

13 PRIOR APPLICATION NUMBER: 60/089,505

14 PRIOR FILING DATE: 1998-06-16

15 NUMBER OF SEQ ID NOS: 26

16 SOFTWARE: Patent in Ver. 2.1

17 SEQ ID NO 10

1 LENGTH: 11  
2 TYPE: PRT  
3 ORGANISM: Unknown  
4 FEATURE:  
5 NAME/KEY: PEPTIDE  
6 LOCATION: (1)-(11)  
7 OTHER INFORMATION: Residues 424 to 433 of chicken gizzard caldesmon  
8 NAME/KEY: PEPTIDE  
9 LOCATION: (11)  
10 OTHER INFORMATION: Targeted Ser phospho-amino acid  
11 US-09-879-936-10

Query Match: 36.4%, Score 4; DB 9; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 4.5e+02;  
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKE 4  
DB 7 AKKE 10

RESULT 24

1 Sequence 237, Application US/09874904

2 Publication No. US2003007274A1

3 GENERAL INFORMATION:

4 APPLICANT: HOGLIKAS, TENI

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES

8 FILE REFERENCE: TB-2002-00

9 CURRENT APPLICATION NUMBER: US/09/876,904A

10 CURRENT FILING DATE: 2001-06-08

11 PRIOR APPLICATION NUMBER: US 60/210,925

12 PRIOR FILING DATE: 2000-09-09

13 NUMBER OF SEQ ID NOS: 629

14 SOFTWARE: Patent in Ver. 2.1

15 SEQ ID NO 237

16 LENGTH: 11

17 TYPE: PRT

18 ORGANISM: Unknown Sequence

19 FEATURE:

20 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein

21 US-09-876,904A-237

Query Match: 36.4%, Score 4; DB 11; Length 11;  
Best Local Similarity: 100.0%; Pred. No. 4.5e+02;  
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
DB 7 KKEK 10

RESULT 25

1 Sequence 354, Application US/09874904

2 Publication No. US2003007274A1

3 GENERAL INFORMATION:

4 APPLICANT: HOGLIKAS, TENI

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES

8 FILE REFERENCE: TB-2002-00

9 CURRENT APPLICATION NUMBER: US/09/876,904A

10 CURRENT FILING DATE: 2001-06-08

11 PRIOR APPLICATION NUMBER: US 60/210,925

12 PRIOR FILING DATE: 2000-06-09

13 NUMBER OF SEQ ID NOS: 629

14 SOFTWARE: Patent in Ver. 2.1

15 SEQ ID NO 354

16 LENGTH: 11

17 TYPE: PRT

ORGANISM: Homo sapiens  
OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)  
US-09-876-904A-354

Query Match 36.4% Score 4 DB 11 Length 13  
Best Local Similarity 100.0% Pred. No. 5.1e+02  
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KKEK 5  
DB 7 KKEK 10

## RESULT 26

US-09-767-395-24  
Sequence 24 Application US/09767395  
Patent No. US2002004215A1  
GENERAL INFORMATION:

APPLICANT: Osbourn, Jane K  
Betbyshire, Elaine J  
McCafferty, John G  
Vaughan, Kristan J  
Johnson, Kevin S

TITLE OF INVENTION: Labelling and selection of molecules

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESS: Marshall, G'Toole, Gerstein, Murray & Boruh  
STREET: 6300 Sears Tower, 243 South Wacker Drive  
CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Vers.00, #1.25 (EPC)

CURRENT APPLICATION DATA: US/09/767,395

FILING DATE: 23-Jan-2001

C:ASSIGNATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/098,244

FILING DATE: <Unknown>

APPLICATION NUMBER: PCT/US97/01455

FILING DATE: 08-JUL-1997

APPLICATION NUMBER: GB 9714292.4

FILING DATE: 08-JUL-1997

APPLICATION NUMBER: GB 972484.2

FILING DATE: 29-NOV-1996

APPLICATION NUMBER: GB 9712618.5

FILING DATE: 18-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/4800

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-767-395-24

Query Match 36.4% Score 4 DB 9 Length 13  
Best Local Similarity 100.0% Pred. No. 5.1e+02  
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 NKPN 10  
DB : NKPN 4

## RESULT 27

US-09-873-676-27

Sequence 27 Application US/09873676

Patent No. US20020077289A1

GENERAL INFORMATION:

APPLICANT: Macdonald, Nicholas J.

APPLICANT: Sim, Kim L.

TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use

FILE REFERENCE: 05213-0378 (43170-259333)

CURRENT APPLICATION NUMBER: US/09/873,676

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: US 60/209,065

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: US 60/289,387

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 123

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic binding peptide

US-09-873-676-27

Query Match 36.4% Score 4 DB 9 Length 13

Best Local Similarity 100.0% Pred. No. 5.1e+02

Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 3 KKEP 6

DB 3 KKEP 5

## RESULT 28

US-09-359-325A-18

Sequence 18 Application US/09359325A

Patent No. US20020107226A1

GENERAL INFORMATION:

APPLICANT: Berlin, Vivian

Levin, David

Ohya, Yoshikazu

TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATED THERETO

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & FLEOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordpad

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/359,325A

FILING DATE: 22-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/631,319

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-074.08

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

```

1  LENGTH: 13 amino acids
2  TYPE: amino acid
3  STRANDEDNESS: <unknown>
4  TOPOLOGY: linear
5  MOLECULE TYPE: protein
6  SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-459-425A-18

Query Match
Best Local Similarity 36.4%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 29
US-09-459-425A-19
1  Sequence 29, Application US/09359425A
2  Patent No. US20020107226A1
3  GENERAL INFORMATION:
4  APPLICANT: Berlin, Vivian
5  Levin, David
6  Ohya, Yoshikazu
7  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING
8  ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
9  NUMBER OF SEQUENCES: 31
10  CORRESPONDENCE ADDRESS:
11  ADDRESSEE: FOLEY, HOAG & ERIC LLP
12  STREET: One Post Office Square
13  CITY: Boston
14  STATE: MA
15  COUNTRY: USA
16  ZIP: 02109-2170
17  COMPUTER READABLE FORM:
18  MEDIUM TYPE: Floppy disk
19  COMPUTER: IBM PC compatible
20  OPERATING SYSTEM: PC-DOS/MS-DOS
21  SOFTWARE: Wordpad
22  CURRENT APPLICATION DATA:
23  APPLICATION NUMBER: US/09/459,425A
24  FILING DATE: 22-Jul-1999
25  PRIOR APPLICATION NUMBER: US 08/641,419
26  FILING DATE: 11-Apr-1996
27  ATTORNEY/AGENT INFORMATION:
28  NAME: Vincent, Matthew J.
29  REGISTRATION NUMBER: 36,797
30  REFERENCE/DOC# NUMBER: MIV-074-06
31  TELECOMMUNICATION INFORMATION:
32  TELEPHONE: 617-832-1300
33  TELEFAX: 617-832-7000
34  INFORMATION FOR SEQ ID NO: 19:
35  SEQUENCE CHARACTERISTICS:
36  LENGTH: 13 amino acids
37  TYPE: amino acid
38  STRANDEDNESS: <unknown>
39  TOPOLOGY: linear
40  MOLECULE TYPE: protein
41  SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-459-425A-19

Query Match
Best Local Similarity 36.4%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 30
US-09-459-425A-19
1  Sequence 30, Application US/09455249
2  Patent No. US20020168748A1
3  GENERAL INFORMATION:
4  APPLICANT: BERLIN, VIVIAN
5  APPLICANT: DAMAGNEZ, VERONIQUE
6  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
7  AND USES RELATED THERETO
8  FILE REFERENCE: MIV-074-06
9  CURRENT FILING DATE: 2001-08-31
10  PRIOR APPLICATION NUMBER: US/09/945,249
11  PRIOR FILING DATE: 2001-01-13
12  PRIOR APPLICATION NUMBER: 08/771,212
13  PRIOR FILING DATE: 1996-12-20
14  PRIOR APPLICATION NUMBER: 08/631,319
15  PRIOR FILING DATE: 1996-04-11
16  NUMBER OF SEQ ID NOS: 89
17  SOFTWARE: PatentIn Ver. 2.1
18  SEQ ID NO 24
19  LENGTH: 13
20  TYPE: PRT
21  ORGANISM: Homo sapiens
22  US-09-945-249-29

Query Match
Best Local Similarity 100.0%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 31
US-09-945-249-29
1  Sequence 29, Application US/09455249
2  Patent No. US20020168748A1
3  GENERAL INFORMATION:
4  APPLICANT: BERLIN, VIVIAN
5  APPLICANT: DAMAGNEZ, VERONIQUE
6  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
7  AND USES RELATED THERETO
8  FILE REFERENCE: MIV-074-06
9  CURRENT APPLICATION NUMBER: US/09/945,249
10  CURRENT FILING DATE: 2001-08-31
11  PRIOR APPLICATION NUMBER: 09/041,990
12  PRIOR FILING DATE: 2001-01-13
13  PRIOR APPLICATION NUMBER: 08/771,212
14  PRIOR FILING DATE: 1996-12-20
15  PRIOR APPLICATION NUMBER: 08/631,319
16  PRIOR FILING DATE: 1996-04-11
17  NUMBER OF SEQ ID NOS: 89
18  SOFTWARE: PatentIn Ver. 2.1
19  SEQ ID NO 29
20  LENGTH: 13
21  TYPE: PRT
22  ORGANISM: Homo sapiens
23  US-09-945-249-29

Query Match
Best Local Similarity 100.0%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 32
US-09-820-051A-98
```

Sequence 88, Application US/09820053A  
Publication No. US20030083243A1  
GENERAL INFORMATION:  
APPLICANT: Owen, Donald R.  
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES  
FILE REFERENCE: HELX027  
CURRENT APPLICATION NUMBER: US/09/820,053A  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 88  
LENGTH: 13  
TYPE: PRT  
ORGANISM: ARTIFICIAL SEQUENCE  
FEATURE:  
OTHER INFORMATION: SYNTHETIC SEQUENCE  
NAME/KEY: MOD\_RES  
LOCATION: (13)  
OTHER INFORMATION: AMIDATION  
US-09-820-053A-88

Query Match 36.4% Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKE 4  
DB 9 AKKE 12

## RESULT 35

US-10-211-088-232  
Sequence 232, Application US/10211088  
Publication No. US20030104479A1  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David  
APPLICANT: Chen, Yih-Tai  
TITLE OF INVENTION: NO US20030104479A1, Fusion Proteins And Assays For Molecular Biology  
FILE REFERENCE: 01-1022-US  
CURRENT APPLICATION NUMBER: US/10/211,088  
PRIORITY FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/409,495  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/441,589  
PRIOR FILING DATE: 2003-12-13  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 232  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Nuclear localization signal.  
US-10-211-088-232

Query Match 36.4% Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
DB 3 KKEK 6

## RESULT 34

US-10-109-171-88  
Sequence 88, Application US/10109171  
Publication No. US20030109452A1  
GENERAL INFORMATION:  
APPLICANT: Owen, Donald R.  
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE  
FILE REFERENCE: HELX028

CURRENT APPLICATION NUMBER: US/10/109,171  
CURRENT FILING DATE: 2002-03-28  
NUMBER OF SEQ ID NOS: 165  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 88  
LENGTH: 13  
TYPE: PRT  
ORGANISM: ARTIFICIAL SEQUENCE  
FEATURE:  
OTHER INFORMATION: SYNTHETIC SEQUENCE  
NAME/KEY: MOD\_RES  
LOCATION: (13)  
OTHER INFORMATION: AMIDATION  
US-10-109-171-88

Query Match 36.4% Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKKE 4  
DB 9 AKKE 12

## RESULT 35

US-09-010-714-2  
Sequence 2, Application US/09010714  
Patent No. US20020912942A1  
GENERAL INFORMATION:  
APPLICANT: McCarthy, James H.  
APPLICANT: Furcht, Leo T.  
APPLICANT: Iida, Joji  
TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED  
FILE REFERENCE: 560,332US01  
CURRENT APPLICATION NUMBER: US/09/010,714  
CURRENT FILING DATE: 1998-01-22  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-010-714-2

Query Match 36.4% Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
DB 4 KKEK 7

## RESULT 36

US-09-966-782A-43  
Sequence 43, Application US/09966782A  
Publication No. US20030022183A1  
GENERAL INFORMATION:  
APPLICANT: Battaglini, P.  
APPLICANT: Feder, J. N.  
APPLICANT: Mintier, G.  
APPLICANT: Ramanathan, C. S.  
APPLICANT: Westphal, R.  
APPLICANT: Hawken, D. R.  
APPLICANT: Cacace, A.  
APPLICANT: Barber, L.  
APPLICANT: Kornacker, M. G.  
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM7,  
FILE REFERENCE: 00044NP  
CURRENT APPLICATION NUMBER: US/09/966,782A  
CURRENT FILING DATE: 2001-09-26

1 PRIOR APPLICATION NUMBER: 60/245,249  
 2 PRIOR FILING DATE: 2000-09-27  
 3 PRIOR APPLICATION NUMBER: 60/268,590  
 4 PRIOR FILING DATE: 2001-02-14  
 5 PRIOR APPLICATION NUMBER: 60/115,421  
 6 PRIOR FILING DATE: 2001-08-28  
 7 NUMBER OF SEQ ID NOS: 64  
 8 SOFTWARE: PatentIn Ver. 2.1  
 9 SEQ ID NO 43  
 10 LENGTH: 14  
 11 TYPE: PRT  
 12 ORGANISM: Artificial Sequence  
 13 FEATURE:  
 14 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 15 OTHER INFORMATION: Polypeptide  
 16 US-09 945-249-43

Query Match 36.4% Score 4; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 6

DB 10 KKK 13

#### RESULT 47

US-09-945-249-60

1 Sequence 80; Application US/09945249

2 Patent No. US20020168748A1

3 GENERAL INFORMATION:

4 APPLICANT: BERLIN, VIVIAN

5 APPLICANT: DAMAGNEZ, VERONIQUE

6 APPLICANT: SMITH, SUSAN E.

7 TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS.

8 FILE REFERENCE: M/V-074.06

9 CURRENT APPLICATION NUMBER: US/09/945,249

10 PRIOR FILING DATE: 2001-08-31

11 PRIOR APPLICATION NUMBER: 09/041,990

12 PRIOR FILING DATE: 2001-01-15

13 PRIOR APPLICATION NUMBER: 08/771,212

14 PRIOR FILING DATE: 1996-12-20

15 PRIOR APPLICATION NUMBER: 08/631,319

16 PRIOR FILING DATE: 1996-04-11

17 NUMBER OF SEQ ID NOS: 89

18 SOFTWARE: PatentIn Ver. 2.1

19 SEQ ID NO 80

20 LENGTH: 15

21 TYPE: PRT

22 ORGANISM: Artificial Sequence

23 OTHER INFORMATION: Description of Artificial Sequence: Peptide that

24 OTHER INFORMATION: corresponds to the C-termini of F1ase of G1ase

25 OTHER INFORMATION: substrates

US-09 945-249-60

Query Match

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 5

DB 5 KKK 8

#### RESULT 48

US-09 945-249-80

1 Sequence 81; Application US/09945249

2 Patent No. US20020168748A1

3 GENERAL INFORMATION:

4 APPLICANT: BERLIN, VIVIAN

5 APPLICANT: DAMAGNEZ, VERONIQUE

6 APPLICANT: SMITH, SUSAN E.

7 TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS.

8 FILE REFERENCE: M/V-074.06

9 CURRENT APPLICATION NUMBER: US/09/945,249

10 PRIOR FILING DATE: 2001-08-31

11 PRIOR APPLICATION NUMBER: 09/041,990

12 PRIOR FILING DATE: 2001-01-15

13 PRIOR APPLICATION NUMBER: 08/771,212

14 PRIOR FILING DATE: 1996-12-20

15 PRIOR APPLICATION NUMBER: 08/631,319

16 PRIOR FILING DATE: 1996-04-11

17 NUMBER OF SEQ ID NOS: 89

18 SOFTWARE: PatentIn Ver. 2.1

19 SEQ ID NO 81

20 LENGTH: 15

21 TYPE: PRT

22 ORGANISM: Artificial Sequence

23 OTHER INFORMATION: Description of Artificial Sequence: Peptide that

24 OTHER INFORMATION: corresponds to the C-termini of F1ase of G1ase

25 OTHER INFORMATION: substrates

US-09 945-249-80

Query Match

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 5

DB 5 KKK 8

APPLICANT: SMITH, SUSAN E.

TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,

FILE REFERENCE: M/V-074.06

CURRENT APPLICATION NUMBER: 09/041,990

PRIOR FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 08/771,212

PRIOR FILING DATE: 1996-12-20

PRIOR APPLICATION NUMBER: 08/631,319

PRIOR FILING DATE: 1996-04-11

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 81

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide that

OTHER INFORMATION: corresponds to the C-termini of F1ase of G1ase

OTHER INFORMATION: substrates

US-09-945-249-80

Query Match

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 5

DB 5 KKK 8

#### RESULT 49

US-10-293-983-15

1 Sequence 16; Application US/10293983

2 Publication No. US20030145998A1

3 GENERAL INFORMATION:

4 APPLICANT: Wyeth

5 APPLICANT: Blatchford, Maria

6 APPLICANT: Paulsen, Janet

7 APPLICANT: Bates, Brian G

8 TITLE OF INVENTION: Genes Encoding G Protein Coupled Receptors and Uses Thereof

9 FILE REFERENCE: AM190476

10 CURRENT APPLICATION NUMBER: 09/10/293,983

11 PRIOR FILING DATE: 2002-11-13

12 NUMBER OF SEQ ID NOS: 25

13 SOFTWARE: PatentIn Ver. 2.1

14 SEQ ID NO 15

15 LENGTH: 15

16 TYPE: PRT

17 ORGANISM: Homo sapiens

18 US-10-293-983-15

Query Match

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 4

DB 9 KKK 12

#### RESULT 40

US-08-431-310-13

1 Sequence 13; Application US/0884310

2 Publication No. US2002026045A1

3 GENERAL INFORMATION:

4 APPLICANT: Kluwe, Louis, Harold et al.

5 TITLE OF INVENTION: Polypeptides and Corresponding Polynucleotides

6 FILE REFERENCE: M/V-074.06

7 CURRENT APPLICATION NUMBER: 08/041,990

8 PRIOR FILING DATE: 2001-08-31

9 NUMBER OF SEQ ID NOS: 12

10 SOFTWARE: PatentIn Ver. 2.1

11 SEQ ID NO 13

12 LENGTH: 15

13 TYPE: PRT

14 ORGANISM: Homo sapiens

15 US-10-293-983-15

Query Match

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 4

DB 9 KKK 12

ADDRESSEE: Clark & Ebling LLP  
 STREET: 176 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/641,671  
 FILING DATE: 01-APR-1997

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,175  
 REFERENCE/DOCKET NUMBER: 06142/347001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-428-0200  
 TELEFAX: 617-428-7045  
 TELEX:

INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US 08-641-310-13

Query Match 27.4% Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 AKK 3  
 III  
 DB 3 AKK 5

RESULT 41  
 US-05-981-824-32  
 : Sequence 12, Application US/08941824  
 : Publication No. US20020114816A1  
 : GENERAL INFORMATION:  
 : APPLICANT: ENDEL, Josef  
 : APPLICANT: STAHL, Peter  
 : APPLICANT: ALBERT, Manfred  
 : APPLICANT: SCHNEBEL, Georges  
 : APPLICANT: BOUTARD, Christian  
 : APPLICANT: VAN ENDELT, Peter  
 : APPLICANT: JUNG, Gunther-Gerhard  
 : TITLE OF INVENTION: AUTOREGULATIVE PEPTIDES FROM HUMAN GLUCAMIC ACID  
 : FILE REFERENCE: 554-7029  
 : CURRENT APPLICATION NUMBER: US/08/981,824  
 : CURRENT FILING DATE: 1998-09-18  
 : EARLIER APPLICATION NUMBER: PCT/EP95/05064  
 : EARLIER FILING DATE: 1996-07-15  
 : EARLIER APPLICATION NUMBER: DE/195 25 744.7  
 : EARLIER FILING DATE: 1995-07-14  
 : NUMBER OF SEQ ID NOS: 47  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 42  
 : LENGTH: 8  
 : TYPE: PKI  
 : ORGANISM: Homo sapiens  
 US 08-981-824-32

Query Match 27.4% Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 KEK 5  
 III  
 DB 5 KEK 7

RESULT 42  
 US-09-374-671-6  
 : Sequence 6, Application US/09374671  
 : Patent No. US20020012963A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Morquenstern, Jay P  
 : APPLICANT: Karlovczy, Andriey  
 : APPLICANT: Bizidaukas, Christine B.  
 : APPLICANT: Brauer, Andrew W.  
 : TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 : NUMBER OF SEQUENCES: 104  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 : STREET: 28 State Street  
 : CITY: Boston  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII-text  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/374,671  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/491,861  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Mandragorian, Amy E  
 : REGISTRATION NUMBER: 15,207  
 : REFERENCE/DOCKET NUMBER: IM1-026CP(IPC-048CP)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 227-7400  
 : TELEFAX: (617) 742-4214  
 : INFORMATION FOR SEQ ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: Peptide  
 : FRAGMENT TYPE: Internal  
 : US-09-374-671-6

Query Match 27.4% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 EXP 6  
 III  
 DB 6 EXP 8

RESULT 43  
 US-09-358-423-11  
 : Sequence 11, Application US/09358423  
 : Patent No. US20020951790A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arian W. Clippes  
 : APPLICANT: Robert L. Clancy  
 : APPLICANT: Louis McShane  
 : APPLICANT: Christopher J. Smith  
 : APPLICANT: David R. Tyreman  
 : APPLICANT: Row Ho

? TITLE OF INVENTION: H. PYLORI ANTIGENS  
 ? FILE REFERENCE: 064727.0106  
 ? CURRENT APPLICATION NUMBER: US/09/458,423  
 ? PRIOR FILING DATE: 1999-07-22  
 ? PRIOR APPLICATION NUMBER: GB 9701487.2  
 ? PRIOR FILING DATE: 1997-01-24  
 ? PRIOR APPLICATION NUMBER: GB 9710629.8  
 ? PRIOR FILING DATE: 1997-05-22  
 ? PRIOR APPLICATION NUMBER: PCT/GB98/00226  
 ? PRIOR FILING DATE: 1998-01-26  
 ? NUMBER OF SEQ ID NOS: 41  
 ? SOFTWARE: FASTSEQ for Windows Version 3.0  
 ? SEQ ID NO 1:  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: H. pylori  
 US 09-358 423-11

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKE 5  
 DB 111  
 5 KKE 5

RESULT 44  
 US-09-458 423-12  
 ? Sequence 12, Application US/09/58424  
 ? Patent No. US2002005170A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Allan W. Cripps  
 ? APPLICANT: Robert L. Clancy  
 ? APPLICANT: Lois McShane  
 ? APPLICANT: Christopher J. Smith  
 ? APPLICANT: David R. Tyreman  
 ? APPLICANT: How Ho  
 ? TITLE OF INVENTION: H. PYLORI ANTIGENS  
 ? FILE REFERENCE: 064727.0106  
 ? CURRENT APPLICATION NUMBER: US/09/458,423  
 ? PRIOR FILING DATE: 1999-07-22  
 ? PRIOR APPLICATION NUMBER: GB 9701487.2  
 ? PRIOR FILING DATE: 1997-01-24  
 ? PRIOR APPLICATION NUMBER: GB 9710629.8  
 ? PRIOR FILING DATE: 1997-05-22  
 ? PRIOR APPLICATION NUMBER: PCT/GB98/00226  
 ? PRIOR FILING DATE: 1998-01-26  
 ? NUMBER OF SEQ ID NOS: 41  
 ? SOFTWARE: FASTSEQ for Windows Version 3.0  
 ? SEQ ID NO 12  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: H. pylori  
 US-09-458 423-12

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKE 5  
 DB 111  
 3 KKE 5

RESULT 45  
 US 09-804-733A 19  
 ? Sequence 19, Application US/09/804733A  
 ? Patent No. US20020059656A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Monsanto Company  
 ? TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING REPEATING UNITS  
 ? FILE REFERENCE: MTC6614.2

? CURRENT APPLICATION NUMBER: US/09/804,733A  
 ? CURRENT FILING DATE: 2001-03-13  
 ? PRIOR APPLICATION NUMBER: US 60/188,990  
 ? PRIOR FILING DATE: 2000-03-13  
 ? NUMBER OF SEQ ID NOS: 29  
 ? SOFTWARE: Patent in version 3.0  
 ? SEQ ID NO 19  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? NAME/KEY: VARIANT  
 ? LOCATION: (1)-(6)  
 ? OTHER INFORMATION: fusion protein  
 US 09-804-733A 19

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KPN 7  
 DB 111  
 5 KPN 7

RESULT 46  
 US-09-813-653 5  
 ? Sequence 5, Application US/09/813653  
 ? Patent No. US20020064770A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Nestor, John  
 ? APPLICANT: Wilson, Carol  
 ? APPLICANT: See, Raymond  
 ? APPLICANT: Tan, Hehir, Christina  
 ? TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compou  
 ? FILE REFERENCE: CNS-005  
 ? CURRENT APPLICATION NUMBER: US/09/813,653  
 ? CURRENT FILING DATE: 2001-03-20  
 ? PRIOR APPLICATION NUMBER: US 60/190,946  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: US 60/190,996  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: US 60/191,299  
 ? NUMBER OF SEQ ID NOS: 44  
 ? SOFTWARE: Patent in version 3.0  
 ? SEQ ID NO 5  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: preferred peptide for pdz binding domain  
 US-09-813-653-5

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKE 4  
 DB 111  
 3 KKE 5

RESULT 47  
 US-09-813-448-2  
 ? Sequence 2, Application US/09/813448  
 ? Patent No. US20020142346A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Nestor, John  
 ? APPLICANT: Wilson, Carol  
 ? TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou  
 ? FILE REFERENCE: CNS-006  
 ? CURRENT APPLICATION NUMBER: US/09/813,448

```

: CURRENT FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: US 60/190,946
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/150,996
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/141,293
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: preferred amino acids for PL2 binding domain
US-09-813 448-2

```

```

Query Match      27.3% Score 3: DB 11: Length 8:
Best Local Similarity 100.0%: Pred. No. 5e+05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

QY      2 KKE 4
      |||
DB      3 KKE 5

```

```

RESULT 48
US-09-966 955A-7
: Sequence 7: Application US/09966955A
: Patent No. US2002015563A1
: GENERAL INFORMATION:
: APPLICANT: Perez Villar, Juan J.
: APPLICANT: Chang, Han
: APPLICANT: Yang, Wen-Pin
: APPLICANT: Wu, Yuli
: APPLICANT: Whitney, Gena S.
: APPLICANT: Kanner, Steven B.
: TITLE OF INVENTION: Identification and cloning of a full length Human
: TITLE OF INVENTION: Cink-related gene, MSL (Muscle cell immunoreceptor)
: TITLE OF INVENTION: Signal transducer
: FILE REFERENCE: 3053-4113051
: CURRENT APPLICATION NUMBER: US/09/966,955A
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 60/237060
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 8
: TYPE: PRT
: ORGANISM: HUMAN
: FEATURE:
: OTHER INFORMATION: PHOSPHOPETIDE DERIVED FROM THE SEQUENCE OF HUMAN
: OTHER INFORMATION: SEP-75
: NAME/KEY: MOD_RES
: LOCATION: (3)
: OTHER INFORMATION: PHOSPHORYLATION: TYR IN POSITION 4 & 15
: OTHER INFORMATION: PHOSPHORYLATED.
US-09-966 955A-7

```

```

Query Match      27.3% Score 3: DB 10: Length 8:
Best Local Similarity 100.0%: Pred. No. 5e+05:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

QY      9 PND 11
      |||
DB      6 PND 8

```

```

RESULT 49
US-09-726-470A-67
: Sequence 67: Application US/09726470A

```

```

: Publication No. US20030036628A1
: GENERAL INFORMATION:
: APPLICANT: Zheleva, Daniela I
: APPLICANT: Fischer, Peter M
: APPLICANT: McInnes, Campbell
: APPLICANT: Andrews, Martin JI
: APPLICANT: Chao, Weng C
: APPLICANT: Atkinson, Gail E
: TITLE OF INVENTION: p21 Peptides
: FILE REFERENCE: C01-014
: CURRENT APPLICATION NUMBER: US/09/726,470A
: CURRENT FILING DATE: 2000-11-29
: PRIOR APPLICATION NUMBER: GB 9928333.6
: PRIOR FILING DATE: 1999-11-30
: NUMBER OF SEQ ID NOS: 275
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 67
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: p21 derived
: OTHER INFORMATION: peptide
: OTHER INFORMATION: Synthesised with free amino terminus and as the
: OTHER INFORMATION: C-terminal carboxamide
US-09-726-470A-67

```

```

Query Match      27.3% Score 3: DB 11: Length 8:
Best Local Similarity 100.0%: Pred. No. 5e+05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

QY      1 AKK 3
      |||
DB      2 AKK 4

```

```

RESULT 50
US-09-876-904A-57
: Sequence 57: Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSCENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 57
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Chicken Ets1
: OTHER INFORMATION: core NLS peptide
US-09-876-904A-57

```

```

Query Match      27.3% Score 3: DB 11: Length 8:
Best Local Similarity 100.0%: Pred. No. 5e+05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

QY      7 NKP 9
      |||
DB      5 NKP 7

```

```

Search completed: September 30, 2003, 10:33:04
Job time : 22.5 secs

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Gender version 5.1.5  
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OM protein - protein search, using SW model;

16:07:44 : 50412, 1100 42.0843 39.6543  
 (w, h) : (400, 128)  
 42.499 11.110 0.000000/0.000

Title: US-09-787-443-19

11 : 31.005 1301901

Sequencia: 1 AEGGKKKKKRA 11

Score: 0.00

Gapop 60.0 , Gapext: 60.0

Searched: 1107863 seqs. 15872573 reads. Index

word size :

Total: number of hits satisfying condition  $\text{parallel} = 27$  and  $\text{serial} = 27$ 

Minimum Up Size Limit: 8

Maximum DB Seq	length: 8
Maximum DB Seq	length: 15

Post-processing: Listing first 500 summed: 105

Database : A\_Geneseq\_19Jun03:\*

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2:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1181..EAT
3:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1182..EAT
4:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1183..EAT
5:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1184..EAT
6:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1185..EAT
7:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1186..EAT
8:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1187..EAT
9:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1188..EAT
10:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1189..EAT
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13:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1192..EAT
14:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1193..EAT
15:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1194..EAT
16:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1195..EAT
17:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1196..EAT
18:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1197..EAT
19:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1198..EAT
20:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1199..EAT
21:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1200..EAT
22:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1201..EAT
23:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1202..EAT
24:	/SIDSI/qcgdata/qeneseq/qeneseq	emb1/AA1203..EAT

PROD. No. is the number of results produced by the test; there may be a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res. #	Query	8			Description
		Score	Match	Length	
1	11	100.0	11	21	NCAM Iq1 binding p
2	11	100.0	11	23	Human neural cell
3	7	63.6	13	23	DNA repair protein
4	7	51.6	13	23	Nuclear protein hn
5	6	54.5	8	15	(2'-5'-oligoadenylate
6	6	54.5	8	15	poly(ADP-ribose) XL
7	9	54.5	9	15	Polysulfone linker A1A
8	6	54.5	10	15	Polysulfone linker A1X
9	6	54.5	10	15	Receptor kinase A1A

83	5	45.5	10	23	AA579941	MB1 class 1 molecu	156	5	45.5	15	21	AA531283	K4B-Ras protein de
84	5	45.5	10	23	AA579973	MHC class I molecu	157	5	45.5	15	21	AA52557	K4B-Ras protein de
85	5	45.5	10	23	AA579984	MHC class I molecu	158	5	45.5	15	21	AA558865	Membrane binding e
86	5	45.5	10	23	AA579992	9 Lysine peptide	159	5	45.5	15	21	AA568697	Ras peptide used t
87	5	45.5	10	24	AA580019	Human immunodefici	160	5	45.5	15	21	AA559299	Ras peptide derive
88	5	45.5	10	24	AA580077	Human immunodefici	161	5	45.5	15	21	AA569630	K4B-Ras-derived pe
89	5	45.5	10	24	AA580094	Human immunodefici	162	5	45.5	15	21	AA558603	Ras peptide used i
90	5	45.5	10	24	AA580098	Human immunodefici	163	5	45.5	15	21	AA558606	Ras peptide used i
91	5	45.5	10	24	AA580103	Human immunodefici	164	5	45.5	15	21	AA558637	K4B-Ras protein Ra
92	5	45.5	10	24	AA580121	Human immunodefici	165	5	45.5	15	22	AA585421	Ras peptide. Synt
93	5	45.5	11	22	AA581456	HIV A03 super moti	166	5	45.5	15	22	AA511766	Human K4B-Ras prot
94	5	45.5	11	22	AA581457	HIV A03 super moti	167	5	45.5	15	22	AA508707	Human Ras peptide
95	5	45.5	11	22	AA581458	HIV A03 super moti	168	5	45.5	15	22	AA508746	K4B-Ras protein de
96	5	45.5	11	22	AA581704	HIV B27 super moti	169	5	45.5	15	22	AA507265	Human K4B-Ras prot
97	5	45.5	11	22	AA581705	HIV B27 super moti	170	5	45.5	15	22	AA563809	Amino acid sequenc
98	5	45.5	11	22	AA581706	HIV B27 super moti	171	5	45.5	15	22	AA563842	Amino acid sequenc
99	5	45.5	11	22	AA582406	HIV A03 motif gag	172	5	45.5	15	22	AA563845	Ras derived peptid
100	5	45.5	11	22	AA582058	HIV A03 motif gag	173	5	45.5	15	22	AA583322	K4B-Ras protein de
101	5	45.5	11	22	AA582058	HIV A03 motif gag	174	5	45.5	15	22	AA574936	K4B-Ras protein de
102	5	45.5	11	22	AA582058	HIV A11 motif gag	175	5	45.5	15	22	AA572373	Ras peptide used i
103	5	45.5	11	22	AA582058	HIV A11 motif gag	176	5	45.5	15	22	AA560573	K4B-Ras geranylger
104	5	45.5	11	23	AA582458	Transcription fact	177	5	45.5	15	22	AA586574	Ras peptide. Und
105	5	45.5	11	23	AA582459	Transcription fact	178	5	45.5	15	22	AA559853	Ras peptide. Und
106	5	45.5	12	19	AA583406	Nuclear localisati	179	5	45.5	15	22	AA585913	K4B-Ras protein de
107	5	45.5	12	21	AA579943	Beta-amyloid hyperi	180	5	45.5	15	22	AA585915	K4B-Ras protein de
108	5	45.5	12	21	AA579943	Mortalin (p115) (SV	181	5	45.5	15	22	AA585917	K4B-Ras protein de
109	5	45.5	12	22	AA582065	Nuclear localisati	182	5	45.5	15	23	AA584480	Human K4B0-Ras pro
110	5	45.5	12	23	AA581704	Fluorescent timer	183	5	45.5	15	23	AA524538	Ras peptide used i
111	5	45.5	12	24	AA582407	Staple nuclear loc	184	5	45.5	15	23	AA597073	Ras peptide #3. S
112	5	45.5	12	24	AA582407	Staple nuclear loc	185	5	45.5	15	23	AA597073	Human Miller-Dieke
113	5	45.5	13	17	AA582407	Staple peptide 3, a b	186	5	45.5	15	23	AA593302	Granulocyte-colony
114	5	45.5	13	23	AA582407	Anti-death protect	187	5	45.5	15	24	AA576808	Human Ras peptide
115	5	45.5	13	24	AA582407	Amino acid sequenc	188	5	45.5	15	23	AA515866	Biotinylated Ras p
116	5	45.5	14	19	AA582407	Peptide membrane b	189	5	45.5	15	23	AA509694	Ras peptide derive
117	5	45.5	14	21	AA582407	Transmembrane b	190	5	45.5	15	24	AA596407	HIV-1 gag epitope
118	5	45.5	14	21	AA582407	Transmembrane b	191	5	45.5	15	24	AA533873	K4B-Ras peptide
119	5	45.5	14	22	AA582407	Ras peptide. Synt	192	5	45.5	15	24	AA526605	Amino acid pendant
120	5	45.5	14	23	AA582407	Protein kinase T	193	4	36.4	8	7	AA561397	Prenyl-protein tra
121	5	45.5	14	23	AA582407	Anti-infectious memb	194	4	36.4	8	18	AA532275	M. catarrhalis out
122	5	45.5	14	23	AA582407	Nucleophile linked	195	4	36.4	8	18	AA548862	Delivery peptide u
123	5	45.5	14	24	AA582407	Peptide used as p	196	4	36.4	8	18	AA538782	Delivery peptide u
124	5	45.5	14	24	AA582407	Peptide used as p	197	4	36.4	8	18	AA538819	Delivery peptide u
125	5	45.5	14	24	AA582407	Peptide used as p	198	4	36.4	8	18	AA559810	Chimeric adenoviru
126	5	45.5	14	24	AA582407	Peptide used as p	199	4	36.4	8	18	AA518640	Peptide resulting
127	5	45.5	15	10	AA582407	Peptide used as p	200	4	36.4	8	19	AA521080	Human p53 cellular
128	5	45.5	15	16	AA582407	Peptide used as p	201	4	36.4	8	19	AA520160	Human neurofilamen
129	5	45.5	15	19	AA582407	Peptide used as p	202	4	36.4	8	19	AA579168	Conserved sequence
130	5	45.5	15	20	AA582407	Peptide used as p	203	4	36.4	8	20	AA542244	Multivalent ligand
131	5	45.5	15	20	AA582407	Peptide used as p	204	4	36.4	8	20	AA543412	Multivalent ligand
132	5	45.5	15	20	AA582407	Peptide used as p	205	4	36.4	8	20	AA543412	Flase substrate Ca
133	5	45.5	15	20	AA582407	K4B-Ras peptide	206	4	36.4	8	21	AA521219	RTR tetramer. Syn
134	5	45.5	15	20	AA582407	K4B-Ras peptide	207	4	36.4	8	21	AA521220	ASA tetramer. Syn
135	5	45.5	15	20	AA582407	K4B-Ras peptide	208	4	36.4	8	21	AA521222	RTR tetramer conta
136	5	45.5	15	20	AA582407	K4B-Ras peptide	209	4	36.4	8	21	AA536033	Human beta3 subuni
137	5	45.5	15	20	AA582407	K4B-Ras peptide	210	4	36.4	8	21	AA508150	Peptide modulating
138	5	45.5	15	20	AA582407	Peptide fragment 1	211	4	36.4	8	21	AA508152	Peptide modulating
139	5	45.5	15	20	AA582407	Ras peptide derive	212	4	36.4	8	21	AA505544	Conus kappa-A cono
140	5	45.5	15	20	AA582407	Peptide derived 1	213	4	36.4	8	21	AA566383	HLA-B8-binding HIV
141	5	45.5	15	20	AA582407	Peptide derived 1	214	4	36.4	8	21	AA566384	HLA-B8-binding HIV
142	5	45.5	15	20	AA582407	Ras peptide SEQ 1	215	4	36.4	8	22	AA513143	HIV A02 super moti
143	5	45.5	15	20	AA582407	Ras peptide SEQ 1	216	4	36.4	8	22	AA514441	HIV A03 super moti
144	5	45.5	15	20	AA582407	Ras peptide SEQ 1	217	4	36.4	8	22	AA514644	HIV A03 super moti
145	5	45.5	15	20	AA582407	Ras peptide SEQ 1	218	4	36.4	8	22	AA516988	HIV B27 super moti
146	5	45.5	15	21	AA582407	Ras peptide. Synt	219	4	36.4	8	22	AA519387	HIV B62 super moti
147	5	45.5	15	21	AA582407	K4B-Ras-derived Ra	220	4	36.4	8	22	AA520815	HIV A03 motif gag
148	5	45.5	15	21	AA582407	K4B-Ras-derived Ra	221	4	36.4	8	22	AA521678	HIV A03 motif pol
149	5	45.5	15	21	AA582407	K4B-Ras-derived Ra	222	4	36.4	8	22	AA522925	HIV A11 motif gag
150	5	45.5	15	21	AA582407	K4B-Ras-derived Ra	223	4	36.4	8	22	AA523557	HIV A11 motif pol
151	5	45.5	15	21	AA582407	K4B-Ras-derived Ra	224	4	36.4	8	22	AA508714	Preferred peptide
152	5	45.5	15	21	AA582407	Human K4B-Ras deri	225	4	36.4	8	22	AA597316	HMG-1/2 box domain
153	5	45.5	15	21	AA582407	Human K4B-Ras deri	226	4	36.4	8	22	AA500704	Internal peptide o
154	5	45.5	15	21	AA582407	Human Ras trinitro	227	4	36.4	8	22	AA570276	Peptide #20. Und
155	5	45.5	15	21	AA582407	K4B-Ras peptide to	228	4	36.4	8	22	AA531765	Amino acid sequenc

229	4	36.4	8	23	AAE28473	NLS based peptide	302	4	36.4	9	24	ABR02934	Human cancer-relat
230	4	36.4	8	23	ABG95831	Adaptor domain pep	303	4	36.4	9	24	ABR02963	Human cancer-relat
231	4	36.4	8	23	ABP52588	CXC chemokine rece	304	4	36.4	9	24	ABR03099	Human cancer-relat
232	4	36.4	8	23	AAU78918	Cuprous latexin nuc	305	4	36.4	9	24	ABR03159	Human cancer-relat
233	4	36.4	8	23	AA013960	Cysteine-X-Cystein	306	4	36.4	9	24	ABR06474	Human cancer-relat
234	4	36.4	8	23	ABH05967	Monoclonal antibod	307	4	36.4	9	24	ABR06475	Human cancer-relat
235	4	36.4	8	23	AAU76376	Neureptin-like in	308	4	36.4	9	24	ABR06477	Human cancer-relat
236	4	36.4	8	23	AAAS2277	PL2 domain-binding	309	4	36.4	9	24	ABR06496	Human cancer-relat
237	4	36.4	8	23	ABB74249	Simple nuclear fac	310	4	36.4	9	24	ABR06689	Human cancer-relat
238	4	36.4	8	23	ABB74330	Transcription fact	311	4	36.4	9	24	ABR06691	Human cancer-relat
239	4	36.4	8	23	ABH74641	Transcription fact	312	4	36.4	9	24	ABR06694	Human cancer-relat
240	4	36.4	8	23	ABH74721	Transcription fact	313	4	36.4	9	24	ABR06707	Human cancer-relat
241	4	36.4	8	24	ABH08788	Lys-C digested Mor	314	4	36.4	9	24	ABR06719	Human cancer-relat
242	4	36.4	9	14	AAE23038	Gro-gamma cytokine	315	4	36.4	10	13	AAE30815	Bacteriophage fd r
243	4	36.4	9	15	AAK57514	Peptide (14) inhib	316	4	36.4	10	14	AAE323049	Leukocyte-binding
244	4	36.4	9	15	AAK57516	Peptide (16) inhib	317	4	36.4	10	15	AAE42527	Peptide inhibitor
245	4	36.4	9	15	AAK57517	Peptide (17) inhib	318	4	36.4	10	15	AAE56336	Antigenic fragment
246	4	36.4	9	15	AAK57538	Peptide (38) inhib	319	4	36.4	10	15	AAE46274	SV40 nuclear membr
247	4	36.4	9	15	AAK57539	Peptide (39) inhib	320	4	36.4	10	15	AAE48280	Peptide fragment (
248	4	36.4	9	15	AAE57540	Peptide (40) inhib	321	4	36.4	10	15	AAE61656	Bradykinin recepto
249	4	36.4	9	15	AAE57541	Peptide (41) inhib	322	4	36.4	10	15	AAE61380	Peptide neutralisi
250	4	36.4	9	15	AAE57542	Peptide (42) inhib	323	4	36.4	10	15	AAE61390	Peptide neutralisi
251	4	36.4	9	15	AAE57543	Peptide (43) inhib	324	4	36.4	10	16	AAE71774	Peptide neutralisi
252	4	36.4	9	15	AAE57548	Peptide (38) inhib	325	4	36.4	10	16	AAE71783	Peptide neutralisi
253	4	36.4	9	15	AAE57549	Peptide (39) inhib	326	4	36.4	10	16	AAE71790	Peptide neutralisi
254	4	36.4	9	15	AAE57546	Peptide (26) inhib	327	4	36.4	10	16	AAE83810	GAP-43 protein N-t
255	4	36.4	9	15	AAE57547	Peptide (27) inhib	328	4	36.4	10	18	AAE38864	Delivery peptide u
256	4	36.4	9	15	AAE57548	Peptide (28) inhib	329	4	36.4	10	18	AAE38784	Delivery peptide u
257	4	36.4	9	15	AAE57549	Peptide (29) inhib	330	4	36.4	10	18	AAE38821	Delivery peptide u
258	4	36.4	9	15	AAE57540	Peptide (30) inhib	331	4	36.4	10	18	AAE24435	K5, a nucleic acid
259	4	36.4	9	15	AAE57541	Peptide (31) inhib	332	4	36.4	10	18	AAE24436	Nucleic acid (NA)
260	4	36.4	9	18	AAE38864	Delivery peptide u	333	4	36.4	10	18	AAE24437	Nucleic acid (NA)
261	4	36.4	9	18	AAE38784	Delivery peptide u	334	4	36.4	10	18	AAE21630	Antibiotic potenti
262	4	36.4	9	18	AAE24434	K4, a nucleic acid	335	4	36.4	10	18	AAE21589	Antibiotic potenti
263	4	36.4	9	19	AAE42478	Protein kinase C p	336	4	36.4	10	18	AAE21600	Antibiotic potenti
264	4	36.4	9	20	AAE55548	HLA binding pla-1	337	4	36.4	10	18	AAE21607	Antibiotic potenti
265	4	36.4	9	20	AAE55549	HLA binding pla-1	338	4	36.4	10	18	AAE17698	Substrate #3 for m
266	4	36.4	9	20	AAE55544	HLA binding pla-1	339	4	36.4	10	19	AAE51430	Nuclear localisati
267	4	36.4	9	20	AAE55544	HLA binding pla-1	340	4	36.4	10	20	AAE45449	Immunogenic peptid
268	4	36.4	9	20	AAE55547	HLA binding pla-1	341	4	36.4	10	20	AAE25073	SV40 nuclear local
269	4	36.4	9	20	AAE55543	HLA binding pla-1	342	4	36.4	10	20	AAE24883	HIV-MA NLS peptide
270	4	36.4	9	20	AAE55544	HLA binding pla-1	343	4	36.4	10	20	AAE24898	Peptide HIV-MA NLS
271	4	36.4	9	20	AAE55546	HLA binding pla-1	344	4	36.4	10	20	AAE10271	T cell epitope/MHC
272	4	36.4	9	20	AAE55542	T cell epitope/MHC	345	4	36.4	10	20	AAE86733	Anticoagulant pept
273	4	36.4	9	21	AAE26642	Peptidic membrane	346	4	36.4	10	20	AAE84255	Antigenic peptide
274	4	36.4	9	21	AAE55543	Heparin sulphate f	347	4	36.4	10	20	AAE84232	Antigenic peptide
275	4	36.4	9	21	AAE55547	Human antithrombin	348	4	36.4	10	21	AAE29414	SV40 nuclear local
276	4	36.4	9	21	AAE55549	HLA-B27 binding H	349	4	36.4	10	21	AAE56901	Peptide contained
277	4	36.4	9	22	ABP13407	HIV B27 super moti	350	4	36.4	10	21	AAE56912	Peptide contained
278	4	36.4	9	22	ABP13406	HIV B27 super moti	351	4	36.4	10	21	AAE56919	Peptide contained
279	4	36.4	9	22	AAE55545	N terminus, Stenoz	352	4	36.4	10	21	AAE56942	Peptide contained
280	4	36.4	9	22	AAE55545	Formula for hepari	353	4	36.4	10	21	AAE51014	HLA-A2-binding HIV
281	4	36.4	9	23	ABG57445	HIV cytotoxic lymph	354	4	36.4	10	21	AAE66269	HIV A02 super moti
282	4	36.4	9	23	ABG57445	HIV cytotoxic lymph	355	4	36.4	10	22	ABP13589	HIV A02 super moti
283	4	36.4	9	23	ABG52827	PP2A-binding pep	356	4	36.4	10	22	ABP13590	HIV A03 super moti
284	4	36.4	9	23	ABG79944	MHC class I molecu	357	4	36.4	10	22	ABP14505	HIV A03 super moti
285	4	36.4	9	23	AAE24906	Nuclear localisati	358	4	36.4	10	22	ABP16269	HIV A04 super moti
286	4	36.4	9	23	AAE24906	Human MMP-2 pep pe	359	4	36.4	10	22	ABP16903	HIV B07 super moti
287	4	36.4	9	23	AAE55547	Oligolysine, K9	360	4	36.4	10	22	ABP17393	HIV B27 super moti
288	4	36.4	9	23	ABP05973	Monoclonal antibod	361	4	36.4	10	22	ABP17393	HIV B27 super moti
289	4	36.4	9	23	ABP05973	Monoclonal-like im	362	4	36.4	10	22	ABP19366	HIV B62 super moti
290	4	36.4	9	23	AAU73340	Human protective p	363	4	36.4	10	22	ABP20792	HIV A03 motif gag
291	4	36.4	9	23	ABH74507	DNA repair protein	364	4	36.4	10	22	ABP22917	HIV A11 motif gag
292	4	36.4	9	23	ABH74507	Transcription fact	365	4	36.4	10	22	ABP22917	Human peptide #158
293	4	36.4	9	23	ABH74507	Transcription fact	366	4	36.4	10	22	AAE98306	Human complementar
294	4	36.4	9	23	ABH74507	Transcription fact	367	4	36.4	10	22	AAE83562	Arabidopsis thalia
295	4	36.4	9	24	ABR01887	Human cancer-relat	368	4	36.4	10	22	AAE84121	Arabidopsis thalia
296	4	36.4	9	24	ABR01926	Human cancer-relat	369	4	36.4	10	22	AAE86185	Saccharomyces cere
297	4	36.4	9	24	ABR01948	Human cancer-relat	370	4	36.4	10	22	AAE86209	Saccharomyces cere
298	4	36.4	9	24	ABR02153	Human cancer-relat	371	4	36.4	10	22	AAE31762	Amino acid sequenc
299	4	36.4	9	24	ABR02153	Human cancer-relat	372	4	36.4	10	22	AAE31766	Amino acid sequenc
300	4	36.4	9	24	ABR02745	Human cancer-relat	373	4	36.4	10	22	AAE31771	Amino acid sequenc
301	4	36.4	9	24	ABR02920	Human cancer-relat	374	4	36.4	10	22	AAE31772	Amino acid sequenc

375	4	36.4	10	22	AAR70239	Polyionic peptide	448	4	36.4	12	15	AAR45681	Rabbit TFPI hepari
376	4	36.4	10	23	ABU57494	HIV cytotoxic lymph	449	4	36.4	12	15	AAR47667	Nerve growth facto
377	4	36.4	10	23	ABG79953	MHC class I molecu	450	4	36.4	12	15	AAR57401	Peptide for treati
378	4	36.4	10	23	ABP53304	Gene delivery rela	451	4	36.4	12	17	AAR96743	Hepatitis A virus
379	4	36.4	10	23	ABR00485	Peptide #1 used in	452	4	36.4	12	17	AAR94332	Anti-thrombogenic
380	4	36.4	10	23	AAU76375	Nociceptin-like im	453	4	36.4	12	17	AAR86961	Nuclear localisati
381	4	36.4	10	23	AAU76377	Nociceptin-like im	454	4	36.4	12	18	AAW27473	Human TSP homologu
382	4	36.4	10	23	AAU76114	Nociceptin-like pe	455	4	36.4	12	18	AAW27477	Human TSP homologu
383	4	36.4	10	23	ABH74326	Bipartite/split nu	456	4	36.4	12	18	AAW27471	Human TSP homologu
384	4	36.4	10	23	ABH74720	Transcription fact	457	4	36.4	12	18	AAW38866	Delivery peptide u
385	4	36.4	10	24	ASU66752	Human immunodefici	458	4	36.4	12	18	AAW38823	Delivery peptide u
386	4	36.4	10	24	ASU66795	Human immunodefici	459	4	36.4	12	18	AAW38786	Delivery peptide u
387	4	36.4	10	24	ASU66929	Human immunodefici	460	4	36.4	12	18	AAW19793	Compressing heptid
388	4	36.4	10	24	ABU65935	Human immunodefici	461	4	36.4	12	18	AAW25568	Synthetic heptati
389	4	36.4	10	24	ASU70742	Human immunodefici	462	4	36.4	12	18	AAW24439	Nucleic acid (NA)
390	4	36.4	10	24	ASU70741	Human cancer-relat	463	4	36.4	12	19	AAW4629	Amino acid sequenc
391	4	36.4	10	24	ABR03022	Human cancer-relat	464	4	36.4	12	19	AAW4630	Peptide branch
392	4	36.4	10	24	ABR02861	Human cancer-relat	465	4	36.4	12	19	AAW55555	Peptide prodrug co
393	4	36.4	10	24	ABR03032	Human cancer-relat	466	4	36.4	12	19	AAW51570	Human vascular per
394	4	36.4	10	24	ABR03042	Human cancer-relat	467	4	36.4	12	19	AAW55891	Human vascular per
395	4	36.4	10	24	ABR03053	Human cancer-relat	468	4	36.4	12	19	AAW55890	Human vascular per
396	4	36.4	10	24	ABR04233	Human cancer-relat	469	4	36.4	12	19	AAW53385	Vascular endotheli
397	4	36.4	10	24	ABR04255	Human cancer-relat	470	4	36.4	12	19	AAW53386	Vascular endotheli
398	4	36.4	10	24	ABR05570	Human cancer-relat	471	4	36.4	12	20	AAW31628	HIV-1 matrix prote
399	4	36.4	10	24	ABR05571	Human cancer-relat	472	4	36.4	12	20	AAW86737	Anticoagulant pept
400	4	36.4	10	24	ABR05574	Human cancer-relat	473	4	36.4	12	20	AAW86738	Anticoagulant pept
401	4	36.4	10	24	ABR05598	Human cancer-relat	474	4	36.4	12	20	AAW86739	Anticoagulant pept
402	4	36.4	10	24	ABR05627	Human cancer-relat	475	4	36.4	12	20	AAW95384	Antimicrobial pept
403	4	36.4	10	24	ABR05769	Human cancer-relat	476	4	36.4	12	21	AAW35821	T7 phage coat prot
404	4	36.4	10	24	ABR05780	Human cancer-relat	477	4	36.4	12	21	AAW57615	Human vascular end
405	4	36.4	10	24	ABR05782	Human cancer-relat	478	4	36.4	12	21	AAW57616	Human vascular end
406	4	36.4	10	24	ABR05785	Human cancer-relat	479	4	36.4	12	21	AAW58057	Vascular endotheli
407	4	36.4	10	24	ABR05792	Human cancer-relat	480	4	36.4	12	21	AAW58058	Vascular endotheli
408	4	36.4	10	24	ABR05821	Human cancer-relat	481	4	36.4	12	22	ABW51257	Human secreted pro
409	4	36.4	11	13	ABR06180	PP1 2-T12 N termin	482	4	36.4	12	22	AAW98676	Human peptide #195
410	4	36.4	11	15	ABR55163	Fragment of retino	483	4	36.4	12	22	AAW98676	Human peptide #195
411	4	36.4	11	16	AAW2301	Anti-HIV MBPc.3.	484	4	36.4	12	22	AAW979080	Human peptide which inhi
412	4	36.4	11	17	AAW23018	Human retinoid aci	485	4	36.4	12	22	AAW97834	Human VEGF/VPF pep
413	4	36.4	11	18	AAW38865	Delivery peptide u	486	4	36.4	12	22	AAW97835	Human VEGF/VPF pep
414	4	36.4	11	18	AAW38865	Delivery peptide u	487	4	36.4	12	22	AAW74507	VEGF VPF antagonis
415	4	36.4	11	18	AAW38765	Delivery peptide u	488	4	36.4	12	22	AAW74508	VEGF VPF antagonis
416	4	36.4	11	18	AAW16616	Phosphoinositide-3	489	4	36.4	12	23	ABG95828	Adaptor domain pep
417	4	36.4	11	18	AAW26574	M2 derivative of	490	4	36.4	12	23	AAW22420	Protease cleavage
418	4	36.4	11	18	AAW24436	Nucleic acid (NA)	491	4	36.4	12	23	ABW75882	Cyclodextrin glyco
419	4	36.4	11	20	AAW77457	Lipophilic binding	492	4	36.4	12	23	AAU76069	Nociceptin-like pe
420	4	36.4	11	20	AAW5735	Anticoagulant pept	493	4	36.4	12	23	AAU76070	Nociceptin-like pe
421	4	36.4	11	21	AAW5735	Peptide #12. Unid	494	4	36.4	12	23	AAU76071	Nociceptin-like pe
422	4	36.4	11	21	AAW5735	Transactivator of	495	4	36.4	12	23	AAU76099	Nociceptin-like pe
423	4	36.4	11	21	AAW5735	Transactivator of	496	4	36.4	12	23	AAU76100	Nociceptin-like pe
424	4	36.4	11	21	AAW5735	Transactivator of	497	4	36.4	12	23	AAU76102	Nociceptin-like pe
425	4	36.4	11	21	AAW5735	Transactivator of	498	4	36.4	12	23	AAU76103	Nociceptin-like pe
426	4	36.4	11	21	AAW5735	Transactivator of	499	4	36.4	12	23	AAU76104	Nociceptin-like pe
427	4	36.4	11	21	AAW5735	Transactivator of	500	4	36.4	12	23	AAU76105	Nociceptin-like pe
428	4	36.4	11	22	ABP13805	HIV AC2 super moti							
429	4	36.4	11	22	ABP13805	HIV AC2 super moti							
430	4	36.4	11	22	ABP13805	HIV AC2 super moti							
431	4	36.4	11	22	AAW42176	Human polypeptide							
432	4	36.4	11	22	AAW42176	Human polypeptide							
433	4	36.4	11	22	AAW50376	Amino acid sequenc							
434	4	36.4	11	22	ABG75612	Ask tyrosine kinas							
435	4	36.4	11	23	ABG75612	Asy111 il ser pep							
436	4	36.4	11	23	AAU94627	Human: Abp1 tryptic							
437	4	36.4	11	23	AAU94627	Molecular marker i							
438	4	36.4	11	23	AAU76079	Nociceptin-like pe							
439	4	36.4	11	23	ABH74327	Nociceptin-like pe							
440	4	36.4	11	23	ABH74327	Bipartite/split nu							
441	4	36.4	11	24	ABH74327	Transcription fact							
442	4	36.4	11	24	AAO27080	Fibrinogen E fragm							
443	4	36.4	11	24	AAO27080	Fibrinogen E fragm							
444	4	36.4	12	8	AAW71160	Peptide which inhi							
445	4	36.4	12	8	AAW71165	Peptide which inhi							
446	4	36.4	12	12	AAW10937	Residues 205-216 o							
447	4	36.4	12	13	AAW24217	Fragment of tenase							
448	4	36.4	12	13	AAW24220	Fragment of tenase							

## ALIGNMENTS

RESULT :

AAW88547

ID AAW88547 standard; peptide: 11 AA.

XX

AC AAW88547:

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Iq1 binding peptide #19.

XX

KW NCAM; neural cell adhesion molecule; Iq1; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

```

XX OS Synthetic.
XX AC WO200018801-A2.
XX PN 06-APR-2000.
XX PD 21-SEP-1999; 99WD-DK00500.
XX PF 29-SEP-1999; 98DK-0001212.
XX PR 29-APR-1999; 99DK-0000592.
XX XX (BENNY) KONN L C B.
XX PA (BENNY) BOCK E.
XX PA (HCLM) HOLM A.
XX PA (JLSE) OLSEN M.
XX PA (OSTE) OSTERGAARD S.
XX PA (JENS) JENSEN P H.
XX PA (POUL) POULSEN F M.
XX PA (SORU) SOROKA V.
XX PA (RALE) RAJETS I.
XX PA (HERE) BEREZIN V.
XX XX
XX PI Ronn LCB, Bock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH;
XX PI Poulsen FM, Soroka V, Rajets I, Berezin V.
XX XX
XX DR WPI: 2000-293111/25.
XX XX
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and diseases e.g. Alzheimer's
XX PT and Parkinson's diseases.
XX XX
XX PS Example 4: Page 25; 119pp; English.
XX XX
XX CC Neural cell adhesion molecule (NCAM) is a cell-surface adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting of five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminus. The present sequence represents a peptide which binds to the
XX CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
XX CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting
XX CC the proliferation of NCAM presenting cells. The compound may be used in
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.
XX CC The compound may in particular be used to treat diseases of the central
XX CC and peripheral nervous systems such as post-operative nerve damage,
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
XX CC dementia, sclerosis, nerve degeneration associated with diabetes,
XX CC mellitus, disorders affecting the circulation, block of neuro-muscular
XX CC transmission and schizophrenia. Conditions affecting the muscles may also
XX CC be treated with the compound, such as conditions associated with impaired
XX CC function of neuromuscular connections (e.g. genetic or traumatic stroke or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to
XX CC learn, and to stimulate the memory of a subject.
XX SQ Sequence 11 AA:
Query Match 100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEGGKKKKMRA 11
DB 1 AEGGKKKKMRA 11
RFSULT 2
ABG69347

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ID ARG69347 standard; Peptide: 11 AA.
XX AC ARG69347;
XX XX 21-OCT-2002 (first entry)
XX DE Human neural cell adhesion molecule (NCAM) peptide #19.
XX XX
XX KW Human: neural cell adhesion molecule: NCAM; heart muscle cell survival;
XX KW acute myocardial infarction; central nervous system disorder; stroke;
XX KW peripheral nervous system disorder; postoperative nerve damage;
XX KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
XX KW postischaemic damage; multiinfarct dementia; multiple sclerosis;
XX KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
XX KW atrophic muscle disorder; gonad degeneration; nephrosis.
XX OS Homo sapiens.
XX XX
XX PN WO200247719-A2.
XX PD 20-JUN-2002.
XX PF 12-DEC-2001; 2001WG-DK00822.
XX PR 12-DEC-2000; 2000DK-0001863.
XX XX
XX PA (ENKA-) ENKAM PHARM AS.
XX PI Hock E, Herezin V, Kohler LB;
XX DR WPI: 2002-583473/62.
XX XX
XX PT Use of a compound comprising a peptide of neural cell adhesion
XX PT molecule, in the preparation of medicament for preventing death of
XX PT cells presenting NCAM or NCAM ligand and treating central nervous
XX PT system diseases.
XX PS Disclosure; Page 16; 57pp; English.
XX XX
XX CC The invention relates to use of a compound (I) comprising a peptide
XX CC which comprises at least 5 contiguous amino acid residues of a sequence
XX CC of the neural cell adhesion molecule (NCAM), its fragment, variant or its
XX CC mimic, for the preparation of a medicament for preventing death of cells
XX CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
XX CC of a medicament for preventing death of cells presenting the NCAM or an
XX CC NCAM ligand. The medicament is for the stimulation of the survival of
XX CC heart muscle cells, such as survival after acute myocardial infarction.
XX CC The medicament is for the treatment of diseases or conditions of the
XX CC central and peripheral nervous system, such as postoperative nerve
XX CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
XX CC impaired myelination of nerve fibres, postischaemic damage, e.g.
XX CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
XX CC degeneration associated with diabetes mellitus, neuro-muscular
XX CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease
XX CC and Huntington's disease. The medicament is for the treatment of diseases
XX CC or conditions of the muscles including conditions with impaired function
XX CC of neuro-muscular connections, such as genetic or traumatic atrophic
XX CC muscle disorders, and for the treatment of diseases of conditions of
XX CC various organs, such as degenerative conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).
XX CC ABG69329-ABG69352 represent human NCAM peptides of the invention.
XX SQ Sequence 11 AA:
Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEGGKKKKMRA 11
DB 1 AEGGKKKKMRA 11

```

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RESULT 3
ABB74498
ID ABB74498 standard: Peptide: 13 AA
XX
AC ABB74498:
XX
DT 18-APR-2002 (first entry)
XX
DE 18-APR-2002 (first entry)
XX
KW Nuclear protein nuclear localisation signal peptide SEQ ID NO:617.
XX
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
XX liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
XX peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
XX breast carcinoma; prostate carcinoma.
XX
OS Bos taurus.
XX
PN WO200193836-A2.
XX
XX WO200193836-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US18657.
XX
PR 09-JUN-2000; 2000US-210925P.
XX
PA (BOUL/) BOULIKAS T.
XX
PI Boulikas T.
XX
DR WPI: 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 70; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC of delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptides produced can have cytostatic
CC and antitumour activities. The peptide-lipid polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention.
XX
SQ Sequence 13 AA.
XX
Query Match 63.6%; Score 7; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EGGKKKK 8
DB 3 EGGKKKK 9
RESULT 4
ABB74498
ID ABB74498 standard: Peptide: 13 AA
XX
AC ABB74498:
XX
DT 18-APR-2002 (first entry)
XX
DE 18-APR-2002 (first entry)
XX
KW Nuclear protein nuclear localisation signal peptide SEQ ID NO:617.
XX
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
XX liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
XX peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
XX breast carcinoma; prostate carcinoma.
XX
OS Bos taurus.
XX
PN WO200193836-A2.
XX
XX WO200193836-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US18657.
XX
PR 09-JUN-2000; 2000US-210925P.
XX
PA (BOUL/) BOULIKAS T.
XX
PI Boulikas T.
XX
DR WPI: 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 70; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC of delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic karyophilic peptides. The peptides produced can have cytostatic
CC and antitumour activities. The peptide-lipid polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention.
XX
SQ Sequence 13 AA.
XX
Query Match 63.6%; Score 7; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EGGKKKK 8
DB 3 EGGKKKK 9

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ID ABB74858 standard: Peptide: 13 AA.
XX
AC ABB74858:
XX
DT 18-APR-2002 (first entry)
XX
DE 18-APR-2002 (first entry)
XX
KW Nuclear protein nuclear localisation signal peptide SEQ ID NO:617.
XX
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
XX liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
XX peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
XX breast carcinoma; prostate carcinoma.
XX
OS Bos taurus.
XX
PN WO200193836-A2.
XX
XX WO200193836-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US18657.
XX
PR 09-JUN-2000; 2000US-210925P.
XX
PA (BOUL/) BOULIKAS T.
XX
PI Boulikas T.
XX
DR WPI: 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 85; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC of delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention.
XX
SQ Sequence 13 AA.
XX
Query Match 63.6%; Score 7; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EGGKKKK 8
DB 3 EGGKKKK 9
RESULT 5
AAR29147
ID AAR29147 standard: peptide: 8 AA.
XX
AC AAR29147:
XX

```

XX 24-MAR-1993 (first entry)  
 XX (2-thioacetyl)diacylglycylglycylpentyl-L-lysine  
 DE Protein conjugate; carrier peptide; diamine; therapeutic  
 XX blood clearance rate; diffusion; carrier; agent.  
 KW  
 XX Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= 2-Thioacetyl-L-lysine  
 FT Binding site 4.8  
 FT /note= "Antimycin Fab" attachment request"

XX J55162505-A.

XX 10-NOV-1992.

XX 19-SEP-1989; 89US-0409150.

XX 19-SEP-1989; 89US-0409150.

XX (GENZ ) GENP-COR.

XX Boston RH, Dean RT, Lister-James G.

XX WPI: 1992-358123/48.

XX New positively charged protein conjugate used as carrier for  
 FT diagnostic or therapeutic radiolabeled

XX Disclosure: Column 14, 11pp; English.

XX The sequence given is a portion of a protein conjugate which contains  
 CC a pharmaceutical protein (Fab') linked to at least one positively  
 CC charged agent. This peptide represents the carrier portion of the  
 CC conjugate. The whole conjugate may be used as a diagnostic or  
 CC therapeutic agent. By attaching positively charged agents to the  
 CC conjugates the blood clearance rate is decreased in vivo, thereby  
 CC increasing blood concentration without reducing diffusion of the conjugates.  
 CC Each positively charged agent can be used as a carrier of one or more  
 CC therapeutic or diagnostic agents. The conjugates may be used in  
 CC vivo tumor imaging or treatment.

XX Sequence 8 AA:

Query Match 54.5%; Score 6; DH 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8

DB 2 GKKKK 7

RESULT 6

AAR60836

XX AAR60836 standard; peptide; 8 AA.

XX AAR60838:

XX 25-MAR-2003 (updated)

DT 05-JUN-1995 (first entry)

XX Polyoxyime hexa-CXL baseplate.

XX Polyoxyime: homopolyoxyime; heteropolyoxyime; peptide presentation;  
 KW cell imaging; complementary orthogonal specifically active molecule.  
 KW COSM: baseplate; immunogen.

XX Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= OTHER  
 FT Modified site 4  
 FT /label= OTHER  
 FT Modified-site 5  
 FT /note= "glyoxyl-L-lysine"  
 FT Modified-site 6  
 FT /label= OTHER  
 FT Modified-site 7  
 FT /note= "glyoxyl-L-lysine"  
 FT Modified-site 8  
 FT /note= "glyoxyl-L-lysine"  
 FT Modified-site 9  
 FT /label= OTHER  
 FT Modified-site 10  
 FT /note= "glyoxyl-L-lysine"

W09425071-A1.

10-NOV-1994.

05-MAY-1994; 94WO-1B00093.

05-MAY-1994; 94US-0057594.

31-AUG-1993; 93US-0105504.

31-AUG-1993; 93US-0114877.

(OFFC//) OFFORD R E.

(ROSE//) ROSE K.

Offord RE, Rose K;

WPI: 1994-357918/44.

XX Homo- and hetero polyoxime compounds and their preparation - used  
 FT for peptide presentation to antibodies and in cell imaging etc.

XX Disclosure: Page 49-50; 85pp; English.

XX Peptides given in AAR60838-62 are used as baseplates and COSMs for the  
 CC preparation of polyoximes having varying spacing, charge,  
 CC lipophilicity, valency, conformational restraints, solubility and  
 CC other physical and biological properties. A hexa-CXL baseplate  
 CC structure is given in AAR60838.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA:

Query Match 54.5%; Score 6; DH 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8

DB 2 GKKKK 7

RESULT 7

AAR60837

1D AAR60837 standard; peptide; 9 AA.

XX AAR60837:

XX 25-MAR-2003 (updated)

DT 05-JUN-1995 (first entry)

XX Polyoxyime hexa-AcA baseplate.

XX Polyoxyime: homopolyoxyime; heteropolyoxyime; peptide presentation;



KW cell imaging; complementary orthogonal specifically active molecule;  
 KW COSM: baseplate; immunogen;  
 XX Synthetic;

OS Key Location/Qualifiers  
 FH Modified-site 1 /label OTHER  
 FT Modified-site 4 /note "aminooxyacetyl glycine"  
 FT Modified-site 4 /label OTHER  
 FT Modified-site 5 /note "aminooxyacetyl lysine"  
 FT Modified-site 5 /label OTHER  
 FT Modified-site 6 /note "aminooxyacetyl lysine"  
 FT Modified-site 6 /label OTHER  
 FT Modified-site 7 /note "aminooxyacetyl lysine"  
 FT Modified-site 7 /label OTHER  
 FT Modified-site 8 /note "aminooxyacetyl lysine"  
 FT Modified-site 8 /label OTHER  
 FT Modified-site 9 /note "aminooxyacetyl lysine"  
 FT Modified-site 9 /label OTHER

W09425071-A1  
 10 NOV-1994 94WO-1806093  
 05-MAY-1994 94WO-1806093  
 05-MAY-1994 93US-0057594  
 31-AUG-1994 94US-0105904  
 31-AUG-1994 93US-0114877

(OFF//) OFFORD R E.  
 (ROSE//) ROSE K.

Offord RE, Rose K;  
 WPI: 1994-3579;8/44.

Hemo- and heteropolyoxime compounds and their preparation - used  
 for peptide presentation to antibodies and in cell imaging etc.

Disclosures: Page 49; 85pp; English.

Peptides given in AAR60843-62 are used as baseplates and COSMs for the  
 preparation of polyoximes having varying spacing, charge,  
 lipophilicity, valency, conformational restraints, solubility and  
 other physical and biological properties. A penta-GXL baseplate  
 structure is given in AAR60847.

(Updated on 25-MAR-2003 to correct PN field.)

Sequence 9 AA:

Query Match 54.5%; Score 6; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKKK 8  
 DE 2 GKKKKK 7

RESULT 8  
 AAR60840  
 ID AAR60840 standard; peptide: 9 AA.  
 XX AAR60840;  
 XX

25-MAR-2003 (updated)  
 25-MAR-1995 (first entry)

XX Polyoxime penta-GXL baseplate.  
 DE  
 XX  
 KW Polyoxime; heteropolyoxime; heteropolyoxime; peptide presentation;  
 KW cell imaging; complementary orthogonal specifically active molecule;  
 KW COSM: baseplate; immunogen;  
 XX Synthetic;  
 OS Key Location/Qualifiers  
 FH Modified-site 1 /label OTHER  
 FT Modified-site 4 /note "aminooxyacetyl glycine"  
 FT Modified-site 4 /label OTHER  
 FT Modified-site 5 /note "aminooxyacetyl lysine"  
 FT Modified-site 5 /label OTHER  
 FT Modified-site 6 /note "aminooxyacetyl lysine"  
 FT Modified-site 6 /label OTHER  
 FT Modified-site 7 /note "aminooxyacetyl lysine"  
 FT Modified-site 7 /label OTHER  
 FT Modified-site 8 /note "aminooxyacetyl lysine"  
 FT Modified-site 8 /label OTHER  
 FT Modified-site 9 /note "aminooxyacetyl lysine"  
 FT Modified-site 9 /label OTHER

W09425071-A1

10 NOV-1994 94WO-1806093  
 05-MAY-1994 94WO-1806093  
 05-MAY-1994 93US-0057594  
 31-AUG-1994 94US-0105904  
 31-AUG-1994 93US-0114877

(OFF//) OFFORD R E.  
 (ROSE//) ROSE K.

Offord RE, Rose K;  
 WPI: 1994-3579;8/44.

Hemo- and heteropolyoxime compounds and their preparation - used  
 for peptide presentation to antibodies and in cell imaging etc.

Disclosures: Page 52; 85pp; English.

Peptides given in AAR60843-62 are used as baseplates and COSMs for the  
 preparation of polyoximes having varying spacing, charge,  
 lipophilicity, valency, conformational restraints, solubility and  
 other physical and biological properties. A penta-GXL baseplate  
 structure is given in AAR60840.

(Updated on 25-MAR-2003 to correct PN field.)

Sequence 9 AA:

Query Match 54.5%; Score 6; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKKK 8  
 DE 2 GKKKKK 7

RESULT 9  
 AAR60840  
 ID AAR60840 standard; peptide: 10 AA.  
 XX

AC AAR60841;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 05-JUN-1995 (first entry)  
 XX  
 XX Hexa-GXL-baseplate precursor.  
 DE  
 XX Polyoxyime; homopolyoxime; heteropolyoxime; peptide presentation;  
 KW cell imaging; complementary orthogonal specifically active molecule;  
 KW COSM; baseplate; immunogen.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 5  
 FT /label= OTHER  
 FT /note= "serine-lysine"  
 FT Modified-site 6  
 FT /label= OTHER  
 FT /note= "serine-lysine"  
 FT Modified-site 7  
 FT /label= OTHER  
 FT /note= "serine-lysine"  
 FT Modified-site 8  
 FT /label= OTHER  
 FT /note= "serine-lysine"  
 FT Modified-site 9  
 FT /label= OTHER  
 FT /note= "serine-lysine"  
 FT  
 XX W09425071-AL.  
 PN  
 XX 10-NOV-1994.  
 PD  
 XX 05-MAY-1994; 94WO-1B00093.  
 XX  
 XX 05-MAY-1993; 93US-0057594.  
 PR 31-AUG-1993; 93US-0105904.  
 PR 31-AUG-1993; 93US-0114877.  
 XX  
 XX (OFFD/) OFFORD R E.  
 PA (ROSE/) ROSE K.  
 XX  
 XX Offord RE. Rose K;  
 PI  
 XX WPI: 1994-457918/44.  
 DR  
 XX Homo- and hetero-polyoxime compounds and their preparation - used  
 FT for peptide presentation to antibodies and in cell imaging etc.  
 PT  
 XX Disclosure: Page 50-51; 85pp; English.  
 PS  
 XX Peptides given in AAR60833-62 are used as baseplates and COSMs for the  
 CC preparation of polyoximes having varying spacing, charge,  
 CC lipophilicity, valency, conformational restraints, solubility and  
 CC other physical and biological properties. Peptide AAR60839 was used  
 CC in the preparation of hexa-GXL-baseplate (AAR60841).  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 10 AA:  
 SQ

Query Match 54.5%; Score 6; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8  
 11111  
 QB 3 GKKKK 8

RESULT 10  
 AAR60841  
 ID: AAR60841 standard; peptide: 11 AA

XX  
 AC AAR60841;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 05-JUN-1995 (first entry)  
 XX  
 XX Polyoxyime octa-GXL baseplate.  
 DE  
 XX Polyoxyime; homopolyoxime; heteropolyoxime; peptide presentation;  
 KW cell imaging; complementary orthogonal specifically active molecule;  
 KW COSM; baseplate; immunogen.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /label= OTHER  
 FT /note= "glyoxyl-glycine"  
 FT Modified-site 4  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 5  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 6  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 7  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 8  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 9  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 10  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT  
 XX W09425071-AL.  
 PN  
 XX 10-NOV-1994.  
 PD  
 XX 05-MAY-1994; 94WO-1B00093.  
 XX  
 XX 05-MAY-1993; 93US-0057594.  
 PR 31-AUG-1993; 93US-0105904.  
 PR 31-AUG-1993; 93US-0114877.  
 XX  
 XX (OFFD/) OFFORD R E.  
 PA (ROSE/) ROSE K.  
 XX  
 XX Offord RE. Rose K;  
 PI  
 XX WPI: 1994-457918/44.  
 DR  
 XX Homo- and hetero-polyoxime compounds and their preparation - used  
 FT for peptide presentation to antibodies and in cell imaging etc.  
 PT  
 XX Disclosure: Page 53; 85pp; English.  
 PS  
 XX Peptides given in AAR60833-62 are used as baseplates and COSMs for the  
 CC preparation of polyoximes having varying spacing, charge,  
 CC lipophilicity, valency, conformational restraints, solubility and  
 CC other physical and biological properties. An octa-GXL baseplate  
 CC structure is given in AAR60841.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 11 AA:  
 SQ

Query Match 54.5%; Score 6; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 GKKKK 8  
 DB 11111  
 2 GKKKK 7

RESULT 11  
 ABB74856  
 ID ABB74856 standard; Peptide: 15 AA.  
 AC ABB74856;  
 XX  
 DT 18 APR-2002 (first entry)  
 DE Nuclear protein nuclear localisation signal peptide SpG ID No:620.  
 XX  
 KW Fusogenic nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; anti-tumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 CS Bos taurus.  
 UN WU2031948: A2.  
 XX  
 PD 14 DEC 2003.  
 XX  
 PF 08-JUN-2001: 2001WO-US18657.  
 PR 09-JUN-2000: 2000US-210925P.  
 XX  
 PA (BOL/) BOLLIKAS T.  
 PT bollikas T.  
 PS WPI: 2002-164245/21.  
 XX  
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PI nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes -  
 PS Claim 14: Page 85; 107pp: English.  
 XX  
 XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 10-99 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (1) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-1.0 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74856 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and anti-tumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid-polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74245 to ABB74255 are used in the exemplification of the present  
 CC invention.

QY Sequence 15 AA:  
 Query Match 54.5%; Score 6; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 11111  
 6 GKKKK 11

RESULT 12  
 AAR23932  
 ID AAR23932 standard; Protein: 8 AA.  
 XX  
 AC AAR23932;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 15-NOV-1992 (first entry)  
 XX  
 DE Lactoferrin induced peptide (2).  
 XX  
 KW Human lactoferrin; LF; transfection; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP04108390-A.  
 XX  
 PD 09-APR-1992.  
 XX  
 PF 29-AUG-1990: 90JP-0227619.  
 XX  
 PR 29-AUG-1990: 90JP-0227619.  
 XX  
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.  
 XX  
 DR WPI: 1992-171655/21.  
 XX  
 PT Introduction of foreign genes into animal cells - using a  
 PT complex comprising the gene with lactoferrin.  
 XX  
 PS Disclosure; Page 5; 10pp: Japanese.  
 XX  
 XX The sequences given in AAR23931 - AAR23938 are synthetic peptides which  
 CC were introduced into human lactoferrin (LF) by introducing the DNA  
 CC encoding the peptide into the human LF gene and then incubating the  
 CC mixture. The introduction of the peptide caused increased  
 CC transformation rates compared to unmodified LF and this method could  
 CC be used to introduce an exogenous gene into an animal cell with no  
 CC stress.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX Sequence 8 AA:  
 SQ  
 Query Match 45.5%; Score 5; DB 13; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 1 GKKKK 5

RESULT 13  
 AAR70582  
 ID AAR70582 standard; Peptide: 8 AA.  
 AC AAR70582;  
 XX  
 DT 14-FEB-1996 (first entry)  
 XX  
 DE HIV(H35)-1, human immunodeficiency virus epitope.  
 XX  
 KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW autoimmune disease syndrome; vaccine.  
 XX  
 CS Human immunodeficiency virus  
 XX  
 PN WG951125: A:

XX 27-APR-1995.  
 XX 19-OCT-1994; 94WO-0P01756.  
 XX 19-OCT-1995; 93JP-0261302.  
 XX (AJEN ) AJINOMOTO CO INC.  
 XX (AJEN ) AJINOMOTO KK.  
 XX Miwa K. Takiquehi M.  
 XX WPI: 1995-170188/22.  
 XX  
 XX HLA-binding peptide fragments from HIV proteins induce killer  
 XX cells which target HIV-infected cells and can be incorporated into  
 XX anti-HIV vaccines  
 XX  
 XX Example 1; Page 10; 61pp; Japanese.  
 XX  
 XX AAR70582 is a peptide fragment derived from an HIV (Human  
 XX Immunodeficiency Virus) protein and is capable of binding to a human  
 XX lymphocyte antigen. The peptide can induce killer cells which target  
 XX HIV-infected cells. It is also useful in the prevention and treatment of  
 XX HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may  
 XX incorporate a vector (such as vaccinia or bac) containing DNA encoding the  
 XX peptides.  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 45.5%; Score 5; DB 15; Length 4;  
 XX Best Local Similarity 100.0%; Pred. No. 9.4e+05;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB : GKKKK 7  
 RESULT 14  
 AAW#0767  
 ID AAW#0767 standard; peptide: 8 AA.  
 XX  
 XX AAW#0767;  
 XX  
 XX 04 DEC-1998 (first entry)  
 XX  
 XX Bioactive fragment acting as biospecificity enhancer.  
 XX  
 XX Factor XIIIa substrate domain; transglutaminase substrate domain;  
 XX bioactive factor; protein network; implant adhesion; wound healing;  
 XX cell growth promotion; tissue regeneration; tissue regeneration;  
 XX angiogenesis; tissue engineering; neovascular bed; surgical adhesive;  
 XX cell transplantation; sealant; fibrin.  
 XX  
 XX Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 XX Modified-site 1  
 XX /note- "damsylated leucine"  
 XX  
 XX WC984686-A1.  
 XX  
 XX 08-OCT-1998.  
 XX  
 XX 02-APR-1998; 98WO-US06617.  
 XX  
 XX 03-APR-1997; 97US-0042143.  
 XX  
 XX (CALY ) CALIFORNIA INST OF TECHNOLOGY  
 XX  
 XX Hubbell J. Schense JC;  
 XX

DR WPI: 1998-542404/46.  
 XX  
 XX A new modified fibrin containing a bioactive factor - useful to  
 XX promote cell growth, wound healing, and tissue regeneration  
 XX  
 XX Claim 32; Page 6; 42pp; English.  
 XX  
 XX This represents a bioactive fragment that can be used as a biosupportive  
 XX material in the composition of the invention. The composition comprises a  
 XX peptide with transglutaminase substrate domain (factor XIIIa substrate  
 XX domain) and a bioactive factor, covalently bound to a protein network,  
 XX particularly a fibrin network. The composition can be used in implantable  
 XX devices, for promotion of cell growth, wound healing and tissue  
 XX regeneration. They can be particularly used for nerve regeneration and  
 XX angiogenesis, in tissue engineering, for example to create neovascular  
 XX beds for cell transplantation, and as a surgical adhesive or sealant.  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 45.5%; Score 5; DB 19; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GKKKK 8  
 DB 3 GKKKK 7  
 RESULT 25  
 AAY10184  
 ID AAY10184 standard; peptide: 8 AA.  
 XX  
 XX AAY10184;  
 XX  
 XX 12-MAY-1999 (first entry)  
 XX  
 XX T cell epitope/MHC ligand SEQ ID NO:114.  
 XX  
 XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 XX immunisation; tumour; infectious disease; immunotherapy; cancer;  
 XX malignant melanoma; viral disease; hepatitis; AIDS.  
 XX  
 XX Synthetic.  
 XX Human immunodeficiency virus type 1.  
 XX  
 XX WC9902183-A2.  
 XX  
 XX 21-JAN 1999.  
 XX  
 XX 10-JUL-1998; 98WO-US14289.  
 XX  
 XX 10-DEC-1997; 97US-0988340.  
 XX  
 XX 10-JUL-1997; 97CA-2209815.  
 XX  
 XX (CTL1-) CTL IMMUNOTHERAPIES CORP.  
 XX  
 XX Kuendig TM, Simard JCL;  
 XX  
 XX WPI: 1999-120514/10.  
 XX  
 XX Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 XX of antigen in the lymphatic system of a mammal so as to provide a  
 XX sustained CTL response, used to treat, e.g. AIDS  
 XX  
 XX Disclosure: Page 27; 199pp; English.  
 XX  
 XX The present invention describes a method of inducing and/or sustaining  
 XX an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 XX method comprises: (a) delivering an antigen to the mammal at a level to  
 XX induce an immunological CTL response in the mammal; and (b) maintaining  
 XX the level of the antigen in the mammal's lymphatic system to maintain  
 XX the immunologic CTL response. The method can be used for the delivery of  
 XX e.g. a differentiation antigen, a tumour-specific multipeptide antigen,

an embryonic antigen, an oncogene antigen, a mutated tumor suppressor gene antigen, or a viral antigen. They can be used for the treatment of disease such as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent cell stimulation that takes place in the milieu of the lymphoid organ and it sustains stimulation that is necessary to keep CTL active, cytotoxic and reactive throughout the body. AAY10071 to AAY10089 represent examples of peptide antigens given in the present invention.

Sequence 8 AA;  
Query Match 45.58; Score 5; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; Acc. 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
L I I I I  
Eh 1 GKKKK 5

RESULTS 16  
AAY84922  
ID AAY84922 standard; peptides # AA;  
AA AAY84922;  
XX 05-OCT-2000 (first entry)  
XX HIV-1 gag p17 b8 restricted CTL epitope

XX Immunogen: particulate composition, immune response assessment, target, skin site; skin immune response; HIV-1, human immunodeficiency virus antibody; cell mediated immunity; antigen exposure; allergy.

US human immunodeficiency virus type 1

XX W0200014547 A1;  
XX 16 MAR-2000;  
XX 01-SEP-1999; 99WO-GR02915;

XX 04 SEP 1998; 98US-C099241;  
XX 15 JUN 1999; 99US-C149345;  
XX (F-900) F-900000000 RES L10;  
XX Sarpate EF, Roberts LK, Fuller M;  
XX WPI: 2000 257072/22;

XX Assessing an immune response against a selected agent in an individual comprises accelerating a particulate composition containing an immunogenic compound from a selected agent, and the target skin site of the individual.

XX Disclosure: Page 23; 41pp; English.

XX The invention relates to a method of using a particulate compound from a selected agent in the manufacture of a particulate composition for assessing an immune response against the selected agent in an individual. The method comprises: (a) accelerating the particulate composition into a target skin site on the body; and (b) assessing the target site to determine the presence of a response of a localized skin immune reaction, where the presence of the immune reaction is indicative of an immune response against the selected agent. Peptides AAY84916 Y83925 represent examples of peptides that could be used in the method as used to detect human immunodeficiency virus type 1. The method is useful for assessing immune response against a selected agent, mediated immunity, antigen exposure, or other immunomodulators in an individual.

XX

Sequence 8 AA;

Query Match 45.58; Score 5; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; Acc. 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
L I I I I  
Eh 1 GKKKK 5

RESULTS 17  
ABP16668  
ID ABP16668 standard; peptide; 8 AA;

XX ABP16668;  
XX 15-JUN-2002 (first entry)  
XX HIV B07 super motif gag peptide #1.

XX HIV, HIV 1; human immunodeficiency virus; env; pol; gag; nef; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1;

XX W0200124830 A1;

XX 12 APR 2001;

XX 05-OCT-2000; 2000WO-052766;

XX 05 OCT-1999; 99US-0412863;

XX (EPIM ) EPIKJUNE INC;

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI: 2001 354887/37;

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

XX Claim 2; Page 23; 44pp; English.

XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus 1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25497). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group based vaccine may be selected from conserved regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA;

XX Query Match 45.58; Score 5; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
DB 3 GKKKK 7

## RESULT 18

ABP18869 standard: Peptide: 8 AA.

XX  
AC ABP18869;

DT 15 JUL-2002 (first entry)

DE HIV 362 super motif gag peptide #272.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; virucide.

OS human immunodeficiency virus type 1.

PN WC200124810-A1.

PD 12-APR-2001.

PE 05-OCT-2000; 2000WO-US27766.

PR 05-OCT-1999; 99US-0412863.

PA (EPI-M) EPTIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R,  
PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI: 2001 354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1

PS Claim 32: Page 255; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25412). (I) has virucide activity and can be used in vaccines. (I)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL) and further to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC is not possible with traditional approaches. ABP1501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX Sequence 8 AA;

Query Match 45.5%; Score 5; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
DB 2 GKKKK 6

QY 3 GKKKK 7  
DB 3 GKKKK 7

## RESULT 19

ABP20439 standard: Peptide: 8 AA.

XX  
AC ABP20439;

DT 15 JUL-2002 (first entry)

DE HIV A03 motif gag peptide #102.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; virucide.

OS human immunodeficiency virus type 1.

PN WC200124810-A1.

PD 12-APR-2001.

PE 05-OCT-2000; 2000WO-US27766.

PR 05-OCT-1999; 99US-0412863.

PA (EPI-M) EPTIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R,  
PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI: 2001 354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1

PS Claim 32: Page 288; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25412). (I) has virucide activity and can be used in vaccines. (I)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL) and further to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC is not possible with traditional approaches. ABP1501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX Sequence 8 AA;

Query Match 45.5%; Score 5; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
DB 2 GKKKK 6

```

RESULT 22
ABP20619
ID ABP20619 standard: Peptide: # AA
XX
AC ABP20619
XX
DI 15-JUL-2002 (first entry)
XX
DE HIV A11 motif gag peptide #66.
XX
KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; net; vpr;
KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
CS Human immunodeficiency virus type 1.
XX
PN W0200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
DR WPI: 2001-354857/47.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 292; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABL1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence # AA:
XX
Query Match 45.5%; Score 5; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCKKK 7
DB 2 GCKKK 6
RESULT 21

```

```

ABP22587
ID ABP22587 standard: Peptide: # AA
XX
AC ABP22587
XX
DI 15-JUL-2002 (first entry)
XX
DE HIV A11 motif gag peptide #66.
XX
KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; net; vpr;
KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
CS Human immunodeficiency virus type 1.
XX
PN W0200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
DR WPI: 2001-354857/47.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 314; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABL1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence # AA:
XX
Query Match 45.5%; Score 5; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCKKK 7
DB 2 GCKKK 6
RESULT 22
ABP22808
ID ABP22808 standard: Peptide: # AA
XX

```

AC ABU22808;  
 DT 15-JUL-2002 (first entry)  
 DE HIV A11 motif gag peptide #187.  
 EE  
 KW HIV; HIV-1; human immunodeficiency virus; env; gag; pol; tat; rev; vif; vpr; vpx; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virulence.  
 XX  
 CS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124410-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston RB, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI: 2001-354887/37.  
 CC  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 42; Page 336; 448pp; English.  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HIV) and further to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABU1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 2 GKKKK 6  
 RESULT 23  
 AAU12533  
 ID AAU12533 standard; Peptide: 8 AA.  
 XX  
 AC AAU12533;  
 XX  
 DT 27-SEP-2001 (first entry)

XX Human HIV-1 Th-CTL overlapping epitope #40.  
 DE  
 XX  
 KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;  
 KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;  
 KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;  
 KW Vaccinia ankara.  
 XX  
 OS Homo sapiens.  
 CS Human immunodeficiency virus type 1.  
 XX  
 PN WO200156355-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US03540.  
 XX  
 PR 04-FEB-2000; 2000US-0497497.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Haynes BF, Liao R;  
 XX  
 DR WPI: 2001-488827/53.  
 XX  
 PT Vaccine for immunizing against human immunodeficiency virus has mixture  
 PT or linear array of peptides comprising immunodominant T-helper epitopes  
 PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes -  
 XX  
 PS Disclosure; Page 27; 33pp; English.  
 XX  
 CC The present invention relates to human immunodeficiency virus (HIV)  
 CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.  
 CC The vaccine comprises a mixture or linear array of peptides, or its  
 CC variants, where the peptides contain immunodominant T-helper (Th)  
 CC epitopes and major histocompatibility complex (MHC) cytotoxic T-  
 CC lymphocyte (CTL) epitopes and the linear array of peptides are  
 CC preferably expressed in modified Vaccinia ankara. The vaccine is useful  
 CC for immunising a patient against HIV and focuses immune response on many  
 CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with  
 CC linear arrays of CTL epitopes can be used as either primes or boosts of  
 CC peptides or of each other to optimally give CTL anti-HIV responses. The  
 CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558  
 CC represent the amino acid sequences of the Th-CTL epitopes and HIV  
 CC immunogenic peptides used in the invention.  
 XX  
 SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 1 GKKKK 5  
 RESULT 24  
 ABU57482  
 ID ABU57482 standard; Peptide: 8 AA.  
 XX  
 AC ABU57482;  
 XX  
 DT 08-APR-2003 (first entry)  
 XX  
 DE HIV cytotoxic lymphocyte epitope #46.  
 XX  
 KW MHC; major histocompatibility complex; human; cytostatic; anti-HIV;  
 KW antinflammatory; dermatological; antidiabetic; antirheumatic; virucide;  
 KW antiinfectious; antitumor; antitubercular; antileishmanial; AIDS;  
 KW antipsoriasis; immunosuppressive; inflammatory bowel disease; measles;  
 KW Crohn's disease; ulcerative colitis; scleroderma; type 1 diabetes; pox;  
 KW rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; chicken pox;



KW malignant melanoma; carcinoma; cancer; leukaemia; lymphoma; hepatitis;  
 KW rheila; herpes; human immunodeficiency virus.  
 XX Human immunodeficiency virus.  
 CS W:27022631-A2.  
 XX  
 XX  
 PN 15-MAR-2002; 2002WC-UK00169.  
 XX  
 XX 14-MAR-2001; 2001BK-0000435.  
 PR 14-MAR-2001; 2001BK-0000436.  
 PR 14-MAR-2001; 2001BK-0000437.  
 PR 14-MAR-2001; 2001US-275447P.  
 PR 14-MAR-2001; 2001US-275448P.  
 PR 14-MAR-2001; 2001US-275470P.  
 XX (DAKO) LAKOCYTOMATION DENMARK AS.  
 PA (DYNA-) DYNAL BIOTECH ASA.  
 XX  
 XX Winther L., Petersen LÖ, Buus S., Schreiner G., Roub E., Aamleim M.  
 DR WPI: 2002 759837/82.  
 XX  
 XX New Major Histocompatibility Complex (MHC) molecule construct, useful  
 PI for treating, preventing, stabilizing or alleviating a disease  
 PI involving MHC recognizing cells e.g. cancer  
 XX  
 XX Disclosure: Figure 37; 304pp: English.  
 XX  
 XX This invention relates to a new Major Histocompatibility Complex (MHC)  
 CC molecule construct comprising a carrier molecule to which one or more  
 CC MHC molecules are attached either directly or via one or more entities.  
 CC The construct of the invention may have cytostatic, antiinflammatory,  
 CC dermatological, antitumour, antidiabetic, anti-HIV, virucide,  
 CC antiproliferative, antitumor, antirheumatic, antiallergic,  
 CC antiparasitic and immunosuppressive activities and may be used in gene  
 CC therapy. The MHC molecule construct is useful as a therapeutic  
 CC composition in vivo or ex vivo therapy for treating, preventing,  
 CC stabilising or alleviating a disease involving MHC recognising cells,  
 CC for monitoring MHC recognising cells or establishing a prognosis of a  
 CC disease or diagnosing a disease, or determining the status of a disease  
 CC or the effectiveness of a medication against a disease, involving MHC  
 CC recognising cells, e.g., chronic inflammatory bowel disease, such as  
 CC Crohn's disease or ulcerative colitis, sarcoidosis, type 1 diabetes,  
 CC rheumatoid arthritis, psoriasis, allergic dermatitis, asthma, malignant  
 CC melanoma, renal carcinoma, liver cancer, lung cancer, cancer of the  
 CC uterus, cervical cancer, prostate cancer, brain cancer, head and neck  
 CC cancer, leukaemia, cutaneous lymphoma, squamous carcinoma, colorectal  
 CC cancer, bladder cancer, rejection related diseases, graft versus host-  
 CC related disease, or a viral disease associated with hepatitis. Acquired  
 CC immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rabies or  
 CC herpes. The MHC molecule construct is also useful for flow cytometry,  
 CC histology or cytology. The present sequence represents a peptide  
 CC used to create the MHC molecule construct of the invention.  
 XX  
 XX Sequence 8 AA:  
 SQ  
 Query Match 45.5%; Score 5; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 1 GKKKK 5  
 RESULT 25  
 ARG79866  
 ID ARG79866 standard; Peptide: 8 AA.  
 XX  
 AC ARG79866;

XX 15-NOV-2002 (first entry)  
 XX  
 XX MHC class I molecule, viral epitope #114.  
 XX  
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.  
 XX  
 XX Human immunodeficiency virus.  
 CS W:200262368 A2.  
 XX  
 XX 15-AUG-2002.  
 PD  
 XX 22-JAN-2002; 2002WC-US02033.  
 PF  
 XX 02-FEB-2001; 2001US-0776232.  
 PR  
 XX (CTL-) CTL IMMUNOTHERAPIES CORP.  
 PA  
 XX Kundig TM, Seward JLL  
 PF  
 XX WPI: 2002-657506/70.  
 DR  
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in  
 PI a mammal, useful for treating a mammal with malignant tumour or  
 PI infectious disease, by directly administering an antigen to the  
 PI lymphatic system of the mammal.  
 XX  
 XX Disclosure: Page 21; 73pp: English.  
 XX  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.  
 CC ARG79753-ABG6659 represent viral epitopes on major histocompatibility  
 CC complex (MHC) class I molecules, used in the method of the invention.  
 XX  
 XX Sequence 8 AA:  
 SQ  
 Query Match 45.5%; Score 5; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 1 GKKKK 5  
 RESULT 26  
 ABP96665  
 ID ABP96665 standard; peptide; 8 AA.  
 XX  
 AC ABP96665;  
 XX  
 XX 29-MAY-2003 (first entry)  
 DT  
 XX HIV p17 protein neutralising epitope related peptide SEQ ID NO:3.  
 DE  
 XX HIV; human immunodeficiency virus; p17; neutralising epitope;  
 KW vaccine; infection; antibody; immune response; immunostimulation.  
 XX  
 AC

US Human immunodeficiency virus type 1  
 XX WO2003016337 A1  
 XX 27-FEB-2003  
 XX 05 AUG 2002: 2002WO-180394  
 XX 07 AUG-2001: 2001FO-060796  
 XX 02 NOV 2001: 2001IT-0001042  
 XX (MEDE-) MEDISTEA INT SRL  
 XX Caruso A, Franzone JS;  
 P1 WPI: 2003-248147/25  
 DR  
 XX New isolated polypeptide based on the neutralising epitope of the p17  
 P1 protein of HIV, useful for the diagnosis, prevention and treatment of  
 P1 the human acquired immune deficiency syndrome  
 XX  
 P5 Claim 4: Page 28: 37pp: English  
 XX  
 CC The present invention describes an isolated polypeptide (1) capable of  
 CC reacting specifically with a neutralising antibody act. p17 of human  
 CC immunodeficiency virus (HIV), which comprises an amino acid sequence  
 CC which corresponds to the neutralising epitope of the protein p17 of HIV  
 CC that is the sequence lying between position 9 and position 22 of the  
 CC protein p17 of HIV. Also described: (1) a pharmaceutical vaccine or  
 CC inoculum composition comprising (1) and a carrier, (2) a monoclonal or  
 CC polyclonal antibody directed against (1), and (3) a pharmaceutical  
 CC composition comprising the antibody of (2) and a carrier. (1) has  
 CC anti-HIV activity, and can be used in vaccines. (1) is useful for the  
 CC preparation of a medicament capable of generating an immune response  
 CC neutralising the biological activity of the protein p17 of HIV in a  
 CC subject to which it is administered, or as a specific reagent for the  
 CC purification of neutralising antibodies act. p17 of HIV from a sample of  
 CC biological sample. The antibodies are useful for the preparation of a  
 CC therapeutic or prophylactic medicament capable of inhibiting the  
 CC immunostimulating activity of the protein p17 of HIV produced in the  
 CC course of an HIV infection. The polypeptide and antibody are also useful  
 CC as specific reagents in a test for detecting the presence of neutralising  
 CC antibodies anti-p17 of HIV in a sample of human biological material. The  
 CC present sequence represents a specifically defined HIV p17 protein  
 CC neutralising epitope related to the human immunodeficiency virus  
 XX  
 SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 GKKKK 7  
 DB 1 GKKKK 5  
 RESULT 27  
 AAN78854  
 ID AAK78854 standard; peptide: 9 AA.  
 XX  
 AC AAN78854;  
 XX  
 XX 25-SEP-1998 (first entry)  
 XX Peptide from HIV-1 gag p17 20-29.  
 XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
 KW vaccine; treatment.  
 XX Synthetic.  
 OS  
 XX W09613378 A1.  
 XX  
 XX 02-APR-1998  
 XX 25-SEP-1997: 97WO NL00536.  
 XX 26 SEP 1996: 96EP-0202701.  
 XX (OYLE-) RIJKSENIV LEIDEN.  
 PA  
 XX Deilhoet JW, Konink F.  
 P1  
 XX WPI: 1998-25041/20.  
 DR  
 XX Increasing uptake and presentation of antigen(s) - by adding mannose  
 KW glycoprotein; viruses; parasitic; tumour; and cancer treatment;  
 XX disease prevention.  
 XX  
 OS human immunodeficiency virus

XX WO9522317 A1.  
 XX 24 AUG 1995.  
 XX 16-FEB 1995: 95WO-US02121.  
 XX 16-FEB-1994: 94US 0197484.  
 XX (CYTE-) CYTEL CORP.  
 XX Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX WPI: 1995-302545/39.  
 DR  
 XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 P1 bacterial, parasitic or tumour antigens - useful in the treatment  
 P1 and prevention of diseases associated with the antigen e.g.  
 P1 hepatitis B  
 XX  
 PS Disclosure, Page 17: 109pp: English.  
 XX  
 CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC an antigen (Ag) in a mammal comprises, a CTL Ag response inducing  
 CC peptide (i.e. AAK78824-R78853) and a lipid conjugated helper T cell  
 CC inducing peptide. The compsn. induces a CTL response to bacterial,  
 CC viral or tumour Ags, and is therefore useful in the treatment and  
 CC prevention of diseases associated with the Ag.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 9 AA:  
 Query Match 45.5%; Score 5; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 GKKKK 7  
 DB 1 GKKKK 5  
 RESULT 28  
 AAN54640  
 ID AAN54640 standard; peptide: 9 AA.  
 XX  
 AC AAN54640;  
 XX  
 XX 25-SEP-1998 (first entry)  
 XX Peptide from HIV-1 gag p17 20-29.  
 XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
 KW vaccine; treatment.  
 XX Synthetic.  
 OS  
 XX W09613378 A1.  
 XX  
 XX 02-APR-1998  
 XX 25-SEP-1997: 97WO NL00536.  
 XX 26 SEP 1996: 96EP-0202701.  
 XX (OYLE-) RIJKSENIV LEIDEN.  
 PA  
 XX Deilhoet JW, Konink F.  
 P1  
 XX WPI: 1998-25041/20.  
 DR  
 XX Increasing uptake and presentation of antigen(s) - by adding mannose  
 KW glycoprotein; viruses; parasitic; tumour; and cancer treatment;  
 XX disease prevention.  
 XX  
 OS human immunodeficiency virus

XX Disclosures: Page 28: 47pp; English.

XX

CC The peptides AAY5459-W5480 are examples of peptides 1-10 which, at least

CC : (preferably 2) mannose can be attached to, to use them as uptake as

CC antigens by antigen presenting cells. Optimal amount may be varied

CC peptides will increase the T cell response, when as uptake of antigen most

CC peptides blocks the T cell response. Blockant binding of immunogenic

CC autoantigens can be used in treatment of type 1 diabetes, rheumatoid

CC arthritis, graft rejection etc. also to inhibit T cell non

CC responsiveness. Vaccines containing mannose attached and peptides used to

CC prevent or treat infections by viral, bacterial, viruses, fungi, B. malariae

CC and parasites.

XX

CC

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY < GKKKK 7

DB 5 GKKKK 9

RESULT 29

AAY5444

ID AAY5444 standard: Protein: 9 AA.

XX

AC AAY5444;

XX

DT 19 JAN 2000 (first entry)

XX

DE HIV-1 p17 protein (aa 20-28) binds HLA-A\*.

XX

KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;

KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;

KW human immunodeficiency virus; hepatitis B virus; papilloma virus;

KW melanoma; malaria; parasite.

XX

XX Synthetic.

OS

OS Human immunodeficiency virus type 1.

XX

PN FR276926-A1.

XX

PD 08-OCT-1999.

XX

PF 07-APR-1998; 98FR-0004323.

XX

PR 07-APR-1998; 98FR-0004323.

XX

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSP ) INST PASTEUR LILLE.

XX

PI Le Gal FA, Guillet JG, Gabery SH, Gras MH, Melnyk O, Tartar A;

XX

DR Wnt: 1999-58115/50.

XX

PI New lipopeptide containing lipid regions and two epitopes, all

PI separated by peptide spacers that impart hydrophilicity, useful in

PI vaccines .

XX

PS Disclosures: Page 21: 35pp; French.

XX

XX The invention relates to the generation of a lipopeptide comprising at

CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)

CC epitope and at least one lipid residue with (i) the epitopes and lipid

CC portion and (ii) the epitopes, being separated independently by peptide

CC spacers. These spacers comprise sequences of amino acids which carry an

CC overall electrical charge in neutral media to ensure that the

CC lipopeptide is hydrophilic. The peptides AAY5301-Y5359 represents

CC examples of peptide epitopes used to generate the lipopeptides. These are

CC used in therapeutic or prophylactic compositions and vaccines to induce

CC specific immune responses against human immunodeficiency, hepatitis B or

CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC used in therapeutic or prophylactic compositions and vaccines to induce

CC specific immune responses against human immunodeficiency, hepatitis B or

CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY < GKKKK 7

DB 5 GKKKK 9

RESULT 30

AAY5349

ID AAY5349 standard: Protein: 9 AA.

XX

AC AAY5349;

XX

DT 18 JAN 2000 (first entry)

XX

DE HIV-1 p17 protein (aa 24-32) binds HLA-B\*.

XX

KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;

KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;

KW human immunodeficiency virus; hepatitis B virus; papilloma virus;

KW melanoma; malaria; parasite.

XX

XX Synthetic.

OS

OS Human immunodeficiency virus type 1.

XX

PN FR276925-A1.

XX

PD 08-OCT-1999.

XX

PF 07-APR-1998; 98FR-0004323.

XX

PR 07-APR-1998; 98FR-0004323.

XX

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSP ) INST PASTEUR LILLE.

XX

PI Le Gal FA, Guillet JG, Gabery SH, Gras MH, Melnyk O, Tartar A;

XX

DR Wnt: 1999-58115/50.

XX

PI New lipopeptide containing lipid regions and two epitopes, all

PI separated by peptide spacers that impart hydrophilicity, useful in

PI vaccines .

XX

PS Disclosures: Page 21: 35pp; French.

XX

XX The invention relates to the generation of a lipopeptide comprising at

CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)

CC epitope and at least one lipid residue with (i) the epitopes and lipid

CC portion and (ii) the epitopes, being separated independently by peptide

CC spacers. These spacers comprise sequences of amino acids which carry an

CC overall electrical charge in neutral media to ensure that the

CC lipopeptide is hydrophilic. The peptides AAY5301-Y5359 represents

CC examples of peptide epitopes used to generate the lipopeptides. These are

CC used in therapeutic or prophylactic compositions and vaccines to induce

CC specific immune responses against human immunodeficiency, hepatitis B or

CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      3 GKKKK 7
DB      11111
        1 GKKKK 5

RESULT 31
AAV4544B
ID      AAY4544B Standard: Peptide: 9 AA
XX
AC      AAY4544B
XX
DT      01 DEC 1999 (first entry)
XX
DE      Immunogenic peptide having a human leukocyte antigen binding motif: #59.
XX
KW      Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW      immune response; T cell activation; major histocompatibility complex;
KW      cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW      prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW      vaccine; immunisation.
XX
CS      Synthetic.
OS      Homo sapiens.
XX
PM      W05945954 A1.
XX
PG      16 SEP 1999.
XX
PF      13 MAR 1998: 98WO-US05039.
XX
PR      23 MAR 1998: 98WO-US05039.
XX
PA      (EPIM-) EPIMMUNE INC.
XX
PI      Sette A, Kube RT, Sidney G, Cellis E, Grey HM. Southwest St.
XX
DR      WPI: 1999 551214/46.
XX
PT      New immunogenic peptides with HLA binding motif useful in treatment
PI      and diagnosis of cancers and viral diseases
XX
PS      claim 1; Page 29; 150pp; English.
XX
CC      AAY4544B to AAY48214 represent specifically claimed immunogenic peptides
CC      having a human major histocompatibility complex (MHC) class I false
CC      known as human leukocyte antigen (HLA); binding motif. The immunogenic
CC      peptides can bind to a specific HLA allele of the HLA A subtypes
CC      HLA-A2.1, A1, A3.2 or A24.1 or HLA-B*07:01 and induce a cytotoxic T cell
CC      response against the antigen from which the peptide is derived.
CC      Cytotoxic T lymphocytes (CTLs) which destroy antigen bearing cells are
CC      normally induced by an antigen in the form of a peptide fragment bound
CC      to a HLA molecule, rather than the intact foreign antigen itself, and
CC      are particularly important in tumour rejection and in fighting viral
CC      infections. The peptides are therefore useful therapeutically to treat
CC      or prevent viral infections and cancers in mammals (especially humans)
CC      e.g. prostate cancer, hepatitis B and C, AIDS and renal carcinoma.
CC      They can be administered as vaccines to elicit an immune response in
CC      individuals susceptible or otherwise at risk of viral infection or
CC      cancer, or used to treat chronic or acute conditions. They are also
CC      useful diagnostically, and can be used to induce a cytotoxic T cell
CC      response by contacting a cytotoxic T cell with the peptide e.g. to
CC      produce CTLs ex vivo for infusion back into a patient. The
CC      polynucleotides encoding the immunogenic peptides are also useful
CC      therapeutically and for immunisation as above.
XX
SQ      Sequence 9 AA:

Query Match      45.5% Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GKKKK 7
DB      11111
        5 GKKKK 9

RESULT 32
AAV40273
ID      AAY40273 Standard: Peptide: 9 AA
XX
AC      AAY40273
XX
DT      19-NOV-1999 (first entry)
XX
DE      Amino acid sequence of a HIV 1 epitope.
XX
KW      Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
KW      CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
KW      vaccine; tumor; infection; immune response; cytokine profile;
KW      acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
KW      autoimmune disease.
XX
OS      Human immunodeficiency virus type 1.
XX
FR      FR2774687-A1.
XX
PN      FN
XX
PD      13-AUG-1999.
XX
PF      06-FEB-1998: 96FR-0001439.
XX
PR      06-FEB-1998: 96FR-0001439.
XX
PA      (INRM ) INSRM INST NAT SANTE & RECH MEDICALE.
PA      (INSP ) INST PASTEUR LILLE.
XX
PI      Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
XX
DR      WPI: 1999-510734/43.
XX
PT      New lipopeptide comprising C-terminal interferon-gamma fragment with
PI      attached lipophilic groups, used as interferon mimic, e.g. for treating
XX      cancer or virus infection
XX
PS      Disclosure: Page 38; 53pp; French.
XX
CC      AAY40123-Y40179 represent epitopes that are able to activate cytotoxic
CC      T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
CC      B epitopes recognized by corresponding antibodies. The epitopes may be
CC      used in the composition of the invention. The specification describes a
CC      lipopeptide that has a peptide part derived from mammalian interferon
CC      gamma (IFNg) and one or more lipophilic parts comprising a linear or
CC      branched, (unsaturated 4-20C hydrocarbyl chain or a steroid. The
CC      lipopeptide mimics the activity of IFNg. Compositions comprising the
CC      lipopeptide are used to treat or prevent any condition that responds
CC      to IFNg, and as adjuvant for vaccines (particularly those directed
CC      against tumors, viral or parasitic infections), to stimulate or
CC      (re)orient the immune response between types 1 and 2 cytokine profiles.
CC      Particular applications are treatment of infections (particularly
CC      viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
CC      hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
CC      (particularly of kidney, cutaneous T cells or ovary, chronic
CC      myelogenous leukemia or mesothelioma), allergy; and autoimmune
XX      diseases.
XX
SQ      Sequence 9 AA:

Query Match      45.5% Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GKKKK 7
DB      11111
        5 GKKKK 9

RESULT 33

```

AAV40304  
 ID AAY40304 standard; Peptide: 9 AA.  
 XX  
 AC AAY40308;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Amino acid sequence of a HIV-1 epitope.  
 XX  
 KW Cytotoxic T cells; T lymphocyte; CD8+ epitope; T helper cells;  
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
 KW vaccine; tumor; infection; immune response; cytokine profile;  
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
 KW autoimmune disease.  
 XX  
 OS human immunodeficiency virus type 1.  
 XX  
 PN FR2774687-A1.  
 XX  
 PD 13-AGO-1999.  
 XX  
 PF 06-FEB-1998; 98FR-0001439.  
 XX  
 PR 06-FEB-1998; 98FR-0001439.  
 XX  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 PI Titum K, Guillet JG, Ver Waerde C, Amadiot C, Gras MH, Loring E;  
 DR WPI: 1999 510734/43.  
 XX  
 PT New lipopeptide comprising C-terminal interferon gamma3 treatment with  
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating  
 PT cancer or virus infection  
 XX  
 PS Disclosure: Page 39; 53pp; French.  
 XX  
 CC AAY40123-Y40179 represent epitopes that are able to activate cytotoxic  
 CC T lymphocytes (CD8+ epitopes). T helper cells (CD4+ epitopes), or  
 CC B epitopes recognized by corresponding antibodies. The epitopes may be  
 CC used in the composition of the invention. The specification describes a  
 CC lipopeptide that has a peptide part derived from mammalian interferon  
 CC gamma (IFN $\gamma$ ) and one or more lipophilic parts comprising a linear or  
 CC branched, (un)saturated 4-200 hydrocarbon chain of a steroid. The  
 CC lipopeptide mimics the activity of IFN $\gamma$  and epitopes comprising the  
 CC lipopeptide are used to treat or prevent any condition that responds  
 CC to IFN $\gamma$ , and as adjuvant for vaccines (particularly those directed  
 CC against tumors, viral or parasitic infections), to stimulate or  
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.  
 CC Particular applications are treatment of infections (particularly  
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and  
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers  
 CC (particularly of kidney, cutaneous T cells or hairy, chronic  
 CC myelogenous leukemia or mesothelioma); allergy and autoimmune  
 CC diseases.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9 3e-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CY 3 GGRKK 7  
 DB 11111  
 1 GGRKK 5  
 RESULT 34  
 AAY26765  
 ID AAY26765 standard; peptide: 9 AA.  
 XX  
 AC AAY26765;  
 XX  
 DT 14-SEP-1999 (first entry)  
 XX  
 DE HIV-derived lipopeptide epitope #70 for mixed micelles.  
 XX  
 KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
 KW melanoma; Plasmodium falciparum; malaria.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 PN FR2771640-A1.  
 XX  
 PD 04-JUN-1999.  
 XX  
 PF 03-DEC-1997; 97FR-0015246.  
 XX  
 PR 03-DEC-1997; 97FR-0015246.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 PI Bossus M, Bourgaud VJ, Gras-Masse H, Guillet JG, Lippens G;  
 PI Tartar A, Wieruszski JM;  
 DR WPI: 1999-349509/30.  
 XX  
 PT Immunogenic lipopeptide micelles - comprising lipopeptides  
 PT containing cytotoxic and helper T-lymphocyte epitopes  
 XX  
 PS Disclosure: Page 33; 60pp; French.  
 XX  
 CC The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprise: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit  
 CC different from that of the first lipopeptide. This peptide represents  
 CC an example of a lipopeptide epitope used in the invention and is derived  
 CC from a human immunodeficiency virus type 1 (HIV-1) protein. The  
 CC immunogenic lipopeptide micelles are used in vaccines, especially  
 CC against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma  
 CC or Plasmodium falciparum malaria.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9 3e-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CY 3 GGRKK 7  
 DB 11111  
 1 GGRKK 5  
 RESULT 35  
 AAY26800  
 ID AAY26800 standard; peptide: 9 AA.  
 XX  
 AC AAY26800;  
 XX  
 DT 14-SEP-1999 (first entry)  
 XX  
 DE HIV-derived lipopeptide epitope #70 for mixed micelles.  
 XX  
 KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
 KW melanoma; Plasmodium falciparum; malaria.  
 XX

OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 PN FR2771840-A1.  
 XX  
 XX  
 PD 04-JUN-1999.  
 XX  
 PF 01-DEC-1997; 97FR-0015246.  
 XX  
 PR 03-DEC-1997; 97FR-0015246.  
 XX  
 XX (CNRS ) CNRS CENT NAT RECH SNT.  
 PA (INM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 PI Bossus M, Bourgault VI, Gras-Masse H, Guillet DS, Lippens G;  
 PI Tartat A, Wieruszkeski JM;  
 XX  
 XX WPI: 1999-349509/30.  
 XX  
 PT Immunogenic lipopeptide micelles comprising lipopeptides  
 PT containing cytotoxic and helper T-lymphocyte epitopes  
 XX  
 PS Disclosure: Page 34; 60pp; French.  
 XX  
 CC The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprising: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit,  
 CC different from that of the first lipopeptide. This peptide represents  
 CC an example of a lipopeptide epitope used in the invention and is derived  
 CC from a human immunodeficiency virus type 1 (HIV 1) protein. The  
 CC immunogenic lipopeptide micelles are used in vaccines, especially  
 CC against HIV, hepatitis B virus (HBV), papilloma viruses, P53, melanoma  
 CC or Plasmodium falciparum malaria.  
 XX  
 XX Sequence 9 AA;  
 SO

Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.36+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGKKK 7  
 DE 1 GGKKK 5

RESULT 36  
 AAY10176  
 ID AAY10176 standard; Peptide: 9 AA.  
 XX  
 AC AAY10176;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE 1 cell epitope/MHC ligand SEQ ID NO:106  
 XX  
 KW Cytotoxic T lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; hepatitis; AIDS.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9902183-A2.  
 XX  
 PD 21 JAN-1999.  
 XX  
 PF 10 JUL 1998; 98WO-US:4289.  
 XX  
 PR 10-DEC 1997; 97US-0988320.  
 XX  
 PR 10-JUL-1997; 97CA-2209815.

XX  
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.  
 XX  
 PI Kuendig TM, Simard JLL;  
 XX  
 XX WPI: 1999-120514/10.  
 XX  
 PT Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS  
 XX  
 PS Disclosure: Page 27; 19pp; English.  
 XX  
 CC The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC throughout the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.  
 XX  
 XX Sequence 9 AA;  
 SO

Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.36+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 DE 5 GGKKK 9

RESULT 37  
 AAY10575  
 ID AAY10575 standard; Peptide: 9 AA.  
 XX  
 AC AAY10575;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE RLA Class 1 motif peptide SEQ ID NO:505.  
 XX  
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; hepatitis; AIDS.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9902183-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 10-JUL-1998; 98WO-US14289.  
 XX  
 PR 10-DEC-1997; 97US-0988320.  
 XX  
 PR 10-JUL-1997; 97CA-2209815.  
 XX  
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.  
 XX  
 PI Kuendig TM, Simard JLL;  
 XX  
 XX WPI: 1999-120514/10.

PT Inducing a cytotoxic T lymphocyte response, by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 E3 sustained CTL response, used to treat, e.g. AIDS  
 XX  
 PS Disclosure: Page 47; 1999p; English.  
 XX  
 CC The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour specific multipeptide antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10073 to AAY1569 represent examples of peptide  
 CC antigens given in the present invention.

Sequence 9 AA;

Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 P 1 1 1  
 D 5 GGKKK 9

RESULT 48

ABP1448;  
 ID ABP1448; standard; Peptide: 9 AA

AC  
 AC ABP1448;  
 XX 15-JUL-2002 (first entry)

XX HIV A27 super motif gag peptide #26.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WC200124810-A1.  
 XX 12-APR-2001.

XX 05-OCT-2000; 2000W0-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 P1 Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1  
 XX  
 PS Claim 42; Page 165; 448pp; English.

CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497).

CC ABP25497). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

Sequence 9 AA;

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 P 1 1 1  
 D 5 GGKKK 9

RESULT 39

ABP17150;  
 ID ABP17150; standard; Peptide: 9 AA.

AC  
 AC ABP17150;  
 XX 15-JUL-2002 (first entry)

XX HIV B27 super motif gag peptide #26.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WC200124810-A1.  
 XX 12-APR-2001.

XX 05-OCT-2000; 2000W0-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 P1 Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1  
 XX  
 PS Claim 32; Page 220; 446pp; English.

CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CII and HTL), and further to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ARP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 9 AA;  
 Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIIL  
 DB 4 GKKKK 8

RESULT: 40  
 ABP20400  
 ID ABP20400 standard; Peptide: 9 AA

AC ARI-20400;

DT 15 JUL-2002 (first entry)

XX HIV A03 motif gag peptide #63.

LE HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide;  
 KW  
 XX Human immunodeficiency virus type 1

OS  
 XX  
 XX W0200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2500WD-US27766.

XX 05-OCT-1999; 990S-0412#53.

XX (EPIM) EPIMMUNE INC.

XX Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI: 2001-354887/37.

PI Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PI peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 288; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.

CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CII and HTL), and further to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ARP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIIL  
 DB 1 GKKKK 5

RESULT: 41  
 ABP20552

ID ABP20552 standard; Peptide: 9 AA.

AC ABP20552;

DT 15 JUL-2002 (first entry)

XX HIV A03 motif gag peptide #215.

KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide;  
 XX

OS Human immunodeficiency virus type 1.

XX W0200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2500WD-US27766.

XX 05-OCT-1999; 990S-0412#53.

XX (EPIM) EPIMMUNE INC.

XX Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI: 2001-354887/37.

PI Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PI peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 291; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of



CC escape mutants. Furthermore, immunosuppression groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 7

DB 1 GKKKK 5

RESULT 42

ABP20742  
 ID ABP20742 standard; Peptide: 9 AA

XX

AC ABP20742;

XX

DT 15-JUL-2002 (first entry)

XX

DE HIV A13 motif gag peptide #405.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr;

KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

CS Human immunodeficiency virus type 1

XX

PN W0200124810-A1

XX

DT 12-APR-2001

XX

PF 05-OCT-1999; 99JS-0412063

XX

PR 05-OCT-1999; 99JS-0412063

XX

PA (EPRM) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX

DT WPI: 2001-054887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1

XX

PS Claim 42; Page 294; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 7

DB 5 GKKKK 9

RESULT 43

ABP22667  
 ID ABP22667 standard; Peptide: 9 AA

XX

AC ABP22667;

XX

DT 15-JUL-2002 (first entry)

XX

DE HIV A13 motif gag peptide #46.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

CS Human immunodeficiency virus type 1

XX

PN W0200124810-A1

XX

DT 12-APR-2001

XX

PF 05-OCT-1999; 99JS-0412063

XX

PR 05-OCT-1999; 99JS-0412063

XX

PA (EPRM) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX

DT WPI: 2001-054887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1

XX

PS Claim 42; Page 433; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

SQ Sequence 9 AA:  
 Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIII  
 DB 1 GKKKK 5

RESULT 44  
 ABP22764  
 ID ABP22764 standard; Peptide: 9 AA.

AC ABP22764;

XX ABP22764;

DT 15-JUL-2002 (first entry)

XX HIV All motif gag peptide #143.

DE HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PS WO200124810 A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27765.

XX 05-OCT-1999; 99US-0412863.

PA (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI: 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 335; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations, which therefore reduces the likelihood of  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present

CC invention.  
 XX Sequence 9 AA:  
 SQ

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIII  
 DB 1 GKKKK 5

RESULT 45

ABP22885  
 ID ABP22885 standard; Peptide: 9 AA.

XX ABP22885;

XX ABP22885;

DT 15-JUL-2002 (first entry)

XX HIV All motif gag peptide #264.

DE HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PS WO200124810 A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

PA (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI: 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 338; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations, which therefore reduces the likelihood of  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:  
 SQ

Query Match 45.5% Score 5; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKXXX 7  
IIII  
DB 5 GKXXX 9

RESULT 4b  
AAB59211  
ID AAB59211 standard; peptide; 9 AA.

AC AAB59211;  
DT 23-MAR-2001 (first entry)

CE Peptide #2 used in invention.

KW Nucleic acid imaging.

XX Synthetic.

OS WO200075125-A1.

PN 14-OCT-2000.

XX 25-MAY-2003; 2003WO-US14439.

PR 03-JUN-1999; 94US-0324665.

PA (GENO) GEN HOSPITAL CORP.

PI Bogdanov A, Tung C, Weissleder R;

XX WPI; 2001-080571/09.

XX New nucleic acid-imaging compounds comprising a base-binding group, a phosphate-binding group, and a metal-binding group for quantitative assessment of the biodistribution of introduced nucleic acid.

PS Example 2; Page 14; 24pp; English.

XX The present invention relates to a nucleic acid binding compound comprising a base-binding group, a phosphate-binding group, and a metal-binding group. The nucleic acid binding compound is useful for noninvasive imaging for the quantitative assessment of the biodistribution of introduced nucleic acid.

XX Sequence 9 AA;

Query Match 45.5% Score 5; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8  
IIII  
DB 4 GKXXX 8

RESULT 47  
AB057445  
ID AB057445 standard; Peptide; 9 AA.

AC AB057445;

XX 09-APR-2003 (first entry)

XX HIV cytotoxic lymphocyte epitope #9.

XX MHC, major histocompatibility complex; human; cytostatic; anti HIV; antiinflammatory; dermatological; antidiabetic; virucide;

KW antiarteriosclerotic; antiulcer; antirheumatic; antiarthritic; AIDS;  
KW antipruritic; immunosuppressive; inflammatory bowel disease; measles;  
KW Crohn's disease; ulcerative colitis; sclerosis; type I diabetes; pox;  
KW rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; chicken pox;  
KW malignant melanoma; carcinoma; cancer; leukaemia; lymphoma; hepatitis;  
KW rubella; herpes; human immunodeficiency virus.

OS Human immunodeficiency virus.

XX WO200272631-A2.

PN 19-SEP-2002.

XX 13-MAR-2002; 2002WO DK03169.

XX 14-MAR-2001; 2001DK-0000435.

PR 14-MAR-2001; 2001DK-0000436.

PR 14-MAR-2001; 2001DK-0000441.

PR 14-MAR-2001; 2001US-2754479.

PR 14-MAR-2001; 2001US-2754489.

PR 14-MAR-2001; 2001US-2754709.

XX (DAKO) DAKOCYTOMATION DENMARK AS.

PA (DYNA) DYNAL BIOTECH ASA.

XX Winther L, Petersen LO, Ruus S, Schoeller J, Ruub E, Aamellem O;

XX WPI; 2002-759837/82.

XX New Major Histocompatibility Complex (MHC) molecule construct, useful for treating, preventing, stabilizing or alleviating a disease involving MHC recognizing cells e.g., cancer.

PS Disclosure; Figure 37; 304pp; English.

XX This invention relates to a new Major Histocompatibility Complex (MHC) molecule construct comprising a carrier molecule to which one or more MHC molecules are attached either directly or via one or more entities. The construct of the invention may have cytostatic, antiinflammatory, dermatological, antiallergic, antidiabetic, antirheumatic, antiarthritic, antipruritic and immunosuppressive activities and may be used in gene therapy. The MHC molecule construct is useful as a therapeutic composition in vivo or ex vivo therapy, for treating, preventing, stabilizing or alleviating a disease involving MHC recognizing cells, for monitoring MHC recognizing cells or establishing a prognosis of a disease or diagnosing a disease, or determining the status of a disease or the effectiveness of a medicament against a disease, involving MHC recognizing cells, e.g., chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, cervical cancer, prostate cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, graft-versus-host-related disease, or a viral disease associated with hepatitis. Acquired immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rubella or herpes. The MHC molecule construct is also useful for flow cytometry, histology or cytology. The present sequence represents a peptide used to create the MHC molecule construct of the invention.

XX Sequence 9 AA;

Query Match 45.5% Score 5; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKXXX 7  
IIII  
DB 5 GKXXX 9

RESULT 48

ABR82016  
ID: ABR82016 standard; protein; 9 AA.  
XX AC ABR82016;  
XX AC ABR82016;  
XX DT 05 DEC-2002 (first entry)  
XX DE CP02 enzyme immunogenic region peptide (residues 33-48).  
XX KW CP02: carboxypeptidase G2; gene-directed enzyme producing therapy; enzyme;  
KW immunogenicity; antibody-directed enzyme producing therapy; cytostatic;  
KW ACEP1; GDEPT.  
XX OS Pseudomonas sp.  
XX PN US2002050709-A1.  
XX PD 11 JUL 2002.  
XX PF 05-JUL-2001: 2001US-0898461.  
XX PR 07 JUL 2002: 2000US-216689P.  
XX PA (REGG/) BEGENT R H J.  
XX PA (CHES/) CHESTER K.  
XX PA (MINT/) MINTON N P.  
XX PA (REES/) REES A R.  
XX PA (SHAR/) SHARMA S K.  
XX PA (SPEN/) SPENCER D I R.  
XX P1 Bequent KHJ, Chester K, Minton NP, Rees AP, Sharma SK, Spencer LR.  
XX WP1: 2002 681730/73.  
XX Novel carboxypeptidase G2 enzyme used in antibody directed enzyme  
producing therapy and gene-directed enzyme producing therapy, comprises  
immunogenic regions modified to reduce or alter immunogenicity to  
immune system.  
XX Claim 1; Page 12; 23pp; English.  
XX The invention provides a Pseudomonas derived carboxypeptidase G2 (CPG2)  
enzyme in which an immunogenic residue is modified to reduce or alter  
immunogenicity to a mammalian immune system, with a reducing CPG2  
activity, or a CPG2 enzyme where the CPG2 has an extension comprising  
an extension such as histidine, myc tag, or a CPG2 enzyme is  
useful in therapy, particularly antibody directed enzyme producing therapy  
(ADEPT) and gene-directed enzyme producing therapy (GDEPT). A fusion  
protein comprising an antibody fused to the CPG2, as useful in ADEPT  
therapy, or used in the provision of vectors such as viral vectors for  
GDEPT therapies. ADEPT therapy has use in the treatment of tumours  
associated with tumour specific markers, which may be targeted for an  
antibody. Sequences ABR82032-36 represented immunogenic region peptides of  
the CPG2 enzyme, that can be modified to reduce or alter immunogenicity.  
XX Sequence 9 AA;  
Query Match 45.5%; Score 5; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EGGKK 6  
DB 1 EGGKK 5  
RESULT 45  
ABR79858  
ID: ABR79858 standard; Peptide; 9 AA.  
XX AC ABR79858;  
XX AC ABR79858;  
XX DT 15-NOV-2002 (first entry)

XX MHC class I molecule, viral epitope #106.  
DE Major histocompatibility complex; MHC; MHC class I molecule; virus;  
XX epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
KW acquired immune deficiency syndrome; AIDS.  
XX Human immunodeficiency virus.  
OS WO200262368-A2.  
XX PN 15-AUG-2002.  
XX PD 22-JAN-2002: 2002WO-US02033.  
XX PF 02-FEB 2001: 2001US-0776232.  
XX PR (CTL1-) CTL IMMUNOTHERAPIES CORP.  
XX PA Kundiag TM, Simard JDL;  
XX P1 WP1: 2002-657506/70.  
XX Inducing or sustaining immunological cytotoxic T lymphocyte response in  
a mammal, useful for treating a mammal with malignant tumour or  
infectious disease, by directly administering an antigen to the  
lymphatic system of the mammal.  
XX Disclosure; Page 21; 73pp; English.  
XX The invention relates to a method of inducing and/or sustaining an  
immunological cytotoxic T lymphocyte (CTL) response in a mammal  
comprising administering directly to the lymphatic system of the mammal:  
(a) an antigen in the form of a polypeptide; (b) a vector comprising a  
nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
method is useful for inducing and/or sustaining CTL response in a mammal.  
This is particularly useful for treating a mammal having a malignant  
tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
malaria, measles or tuberculosis), or in an animal having a  
predisposition to these diseases. The mammal may be dogs, cats, mice,  
cattle, sheep, pigs, goats, rabbits, or preferably humans.  
XX ABR79753; ABR80319 represent viral epitopes on major histocompatibility  
complex (MHC) class I molecules, used in the method of the invention.  
XX Sequence 9 AA;  
Query Match 45.5%; Score 5; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGGKK 7  
DB 5 GGGKK 9  
RESULT 50  
ABR80258  
ID: ABR80258 standard; Peptide; 9 AA.  
XX AC ABR80258;  
XX AC ABR80258;  
XX DT 15-NOV-2002 (first entry)  
XX DE MHC class I molecule, viral epitope #506.  
XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
KW acquired immune deficiency syndrome; AIDS.

```

XX Viridae.
XX
XX W:20022266-A2.
XX
XX 15-AUG 2002.
XX
XX 22 JAN+2002; 2002R0-USC2000.
XX
XX 02-FEB+2001; 2001US-0776232.
XX
XX (C111 ) C11. IMMUNOTHERAPIES (APP.
XX
XX Kundiq TM, Simard JUL.
XX
XX W61; 2002-657566/70.
XX
XX inducing or sustaining immunological cytotoxic T lymphocyte response in
XX a mammal, useful for treating a mammal with malignant tumour or
XX infectious disease, by directly administering an antigen to the
XX lymphatic system of the mammal.
XX
XX Disclosures: Page 41: 73pp: English.
XX
XX The invention relates to a method of inducing antigen specific an
XX immunological cytotoxic T lymphocyte (CTL) response in a mammal
XX comprising administering directly to the lymphatic system of the mammal:
XX (a) an antigen in the form of a polypeptide; (b) a vector comprising a
XX nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
XX method is useful for inducing and/or sustaining CTL response in a mammal.
XX This is particularly useful for treating a mammal having a malignant
XX tumour (e.g. carcinoma, melanoma), vaccine in an lymphatic or infectious
XX disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
XX malaria, measles or tuberculosis), or in an animal having a
XX predisposition to these diseases; the mammal may be dogs, cats, mice,
XX cattle, sheep, pigs, goats, rabbits, or preferably humans.
XX AM07475-A5380319 represent viral epitopes on major histocompatibility
XX complex (MHC) class I molecules, used in the method of the invention.
XX
XX Sequence 9 AA:
XX
XX Query Match: 45.5%, Score 51, ID: 1, Length 97
XX Best Local Similarity 100.0%, Pos: 9, Score 51
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 5 GAKKK 7
XX
XX 5 GAKKK 9
XX

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Search completed: September 30, 2003 11:07:00  
 Job time: 47.1667 secs

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OM proteins - protein search, using SW mode.

Run on: September 30, 2003, 10:07:44, Search time 11.443 Seconds  
(without alignment)  
90,440 Million cell updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: 1 AGGKKKKMRA 1:

Scoring table: G200

Gapop 60.0, Gapext 60.0

Searched: 293308 seqs, 96166682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2064

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database:

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	4	46.4	15	2	129501			fibronectin A
2	4	46.4	15	2	429601			fibronectin A
3	4	27.3	9	2	157635			sperrin alpha cha
4	4	27.3	10	2	164760			hypothetical prote
5	4	27.3	10	2	877960			cytochrome oxid
6	4	27.3	11	2	140020			338 proteins 4218
7	4	27.3	11	2	167237			tracylqyositol li
8	4	27.3	11	2	857575			T cell receptor V-
9	4	27.3	11	2	856294			tubulin 2 beta-s c
10	4	27.3	12	2	869022			33 proteins - whea
11	4	27.3	12	2	864573			hypothetical prote
12	4	27.3	12	2	848204			zinc-metallophosph
13	4	27.3	12	2	860757			enterotoxin C1
14	4	27.3	12	2	A60751			hydriin 1 - Arctia
15	4	27.3	12	2	A39900			lipovitellin - Afr
16	4	27.3	12	2	S10626			T cell receptor V-
17	4	27.3	12	2	S57570			T cell receptor al
18	4	27.3	12	2	PH1189			T cell receptor al
19	4	27.3	12	2	PH1175			T cell receptor al
20	4	27.3	12	2	PH1481			T cell receptor be
21	4	27.3	13	1	JIJ03			trimeric alpha -
22	4	27.3	13	2	G24565			K phycoerythrin ca
23	4	27.3	13	2	JO1350			Aspartyl prote
24	4	27.3	13	2	PH1585			14 H chain V-D J r
25	4	27.3	14	2	S2140			Aspartyl prote
26	4	27.3	14	2	S14864			serine protease M
27	4	27.3	14	2	PA0109			protein 15 - Acl
28	4	27.3	14	2	PA0045			protein 15 - Acl
29	4	27.3	14	2	PH1623			14 H chain V-D J r

30	3	27.3	15	2	S26524			T-cell receptor al
31	3	27.3	15	2	S26534			T-cell receptor al
32	3	27.3	15	2	J60101			fibronogen alpha c
33	3	27.3	15	2	A36786			pineloyl-CoA synth
34	3	27.3	15	2	S47387			T-cell antigen rec
35	3	27.3	15	2	A27504			histone H2A - mous
36	3	27.3	15	2	H26501			lipoprotein lipase
37	2	18.2	8	1	LFSAME			probable msra lead
38	2	18.2	8	2	PI0184			capsid protein Vp-
39	2	18.2	8	2	I10077			hypothetical prote
40	2	18.2	8	2	S19288			acylase - Kluyvera
41	2	18.2	8	2	S63493			disulfatase - Kluyvera
42	2	18.2	8	2	S21273			cellulase (EC 3.2
43	2	18.2	8	2	B39745			endoglycosylcerami
44	2	18.2	8	2	D51512			variant surface gl
45	2	18.2	8	2	A21440			calliPMRFamide 8 -
46	2	18.2	8	2	H41978			acetylcholinestera
47	2	18.2	8	2	A41117			Ig heavy chain CRD
48	2	18.2	8	2	PT0279			phosphatidylethano
49	2	18.2	8	2	PN0043			T-cell receptor be
50	2	18.2	8	2	PT0595			T-cell receptor be
51	2	18.2	8	2	PT0530			T-cell receptor be
52	2	18.2	8	2	PT0527			T-cell receptor be
53	2	18.2	8	2	PT0509			T-cell receptor be
54	2	18.2	8	2	PT0639			T-cell receptor be
55	2	18.2	8	2	PT0613			T-cell receptor be
56	2	18.2	8	2	PT0557			T-cell receptor be
57	2	18.2	8	2	PT0554			T-cell receptor be
58	2	18.2	8	2	PT0716			T-cell receptor be
59	2	18.2	8	2	PT0725			T-cell receptor be
60	2	18.2	8	2	PT0588			T-cell receptor be
61	2	18.2	8	2	A35180			neutral proteinase
62	2	18.2	8	2	PC4372			telomeric and tetr
63	2	18.2	8	2	T48890			hypothetical prote
64	2	18.2	8	4	I55411			hypothetical histo
65	2	18.2	9	1	YFPG			thymic factor - pi
66	2	18.2	9	2	S59902			glutathione transf
67	2	18.2	9	2	A60957			thymocyte growth p
68	2	18.2	9	2	A61230			calsequestrin, car
69	2	18.2	9	2	D28854			fibronopeptide B -
70	2	18.2	9	2	E28854			fibronopeptide B -
71	2	18.2	9	2	F28854			fibronopeptide B -
72	2	18.2	9	2	D24180			fibronogen beta ch
73	2	18.2	9	2	S30494			cat gene leader pe
74	2	18.2	9	2	H43622			chloramphenicol O-
75	2	18.2	9	2	A60522			sperm-activating p
76	2	18.2	9	2	S79329			sperm-activating p
77	2	18.2	9	2	Q0RB			delta sleep-induci
78	2	18.2	9	2	H45020			probable minipolyp
79	2	18.2	9	2	S02484			probable membrane
80	2	18.2	9	2	S66608			quinoline 2-oxidor
81	2	18.2	9	2	PI0139			orf AB protein - S
82	2	18.2	9	2	S19523			carbon-monoxide de
83	2	18.2	9	2	S70334			endosperm protein,
84	2	18.2	9	2	A57444			neuropeptide Grb-A
85	2	18.2	9	2	B57444			neuropeptide Grb-A
86	2	18.2	9	2	C57444			neuropeptide Grb-A
87	2	18.2	9	2	A41978			calliPMRFamide 1 -
88	2	18.2	9	2	A44787			calliPMRFamide 10
89	2	18.2	9	2	D44787			calliPMRFamide 13
90	2	18.2	9	2	B41978			calliPMRFamide 2 -
91	2	18.2	9	2	C41978			calliPMRFamide 3 -
92	2	18.2	9	2	D41978			calliPMRFamide 4 -
93	2	18.2	9	2	E41978			calliPMRFamide 5 -
94	2	18.2	9	2	F41978			calliPMRFamide 6 -
95	2	18.2	9	2	G41978			calliPMRFamide 7 -
96	2	18.2	9	2	B20569			serum amyloid P-co
97	2	18.2	9	2	A53797			3',5'-cyclic-GMP p
98	2	18.2	9	2	I50633			c-rel protein - ch
99	2	18.2	9	2	PT0225			Ig heavy chain CDR
100	2	18.2	9	2	PC2197			zymogen granule me
101	2	18.2	9	2	C60070			gastrin - domestic
102	2	18.2	9	2	S56636			alpha-2-macroglobu

104	2	18.2	9	2	PHO136	late gl 19 protein	176	2	18.2	10	2	PT0245	Ig heavy chain CRD
104	2	18.2	9	2	PT0670	T-cell receptor be	177	2	18.2	10	2	PT0289	Ig heavy chain CRD
105	2	18.2	9	2	PT0634	T-cell receptor be	178	2	18.2	10	2	PT0309	Ig heavy chain CRD
106	2	18.2	9	2	PT0562	T-cell receptor be	179	2	18.2	10	2	PT0310	Ig heavy chain CRD
107	2	18.2	9	2	PT0706	unidentified 48.7K	180	2	18.2	10	2	H45482	platelet activatin
108	2	18.2	9	2	PT0935	T-cell receptor be	181	2	18.2	10	2	S23370	T-cell receptor al
109	2	18.2	9	2	PT0937	T-cell receptor be	182	2	18.2	10	2	S23371	T-cell receptor al
110	2	18.2	9	2	PT0938	T-cell receptor be	183	2	18.2	10	2	F49033	T-cell receptor ga
111	2	18.2	9	2	S78424	52.1K protein sf	184	2	18.2	10	2	S68638	acetylcholinestera
112	2	18.2	9	2	PT0027	per tachykinin-1 f	185	2	18.2	10	2	S26506	collagen alpha 1(V
113	2	18.2	9	4	S15595	cat 2 rat V-prot	186	2	18.2	10	2	S71948	matrix metalloprot
114	2	18.2	10	1	GM0412	leucosulfakinin II	187	2	18.2	10	2	PT0212	T-cell receptor al
115	2	18.2	10	2	S15139	hydrofolate redu	188	2	18.2	10	2	PT0632	T-cell receptor be
116	2	18.2	10	2	S65384	cytochrome-c oxida	189	2	18.2	10	2	PT0664	T-cell receptor be
117	2	18.2	10	2	S24190	trypsin (EC 3.4.2	190	2	18.2	10	2	PT0215	T-cell receptor be
118	2	18.2	10	2	PT00346	prosin (EC 3.4.24	191	2	18.2	10	2	F41946	T-cell receptor ga
119	2	18.2	10	2	S33844	alpha 2 macroglobu	192	2	18.2	10	2	S65387	cytochrome-c oxida
120	2	18.2	10	2	S10926	inhibin beta-A era	193	2	18.2	10	2	PH0944	T-cell receptor be
121	2	18.2	10	2	A61131	lydlin 2 - bullfro	194	2	18.2	10	2	PH0925	T-cell receptor be
122	2	18.2	10	2	A60430	beta-neomorphin	195	2	18.2	10	2	PH0926	T-cell receptor be
123	2	18.2	10	2	PT02172	triacylglycerol II	196	2	18.2	10	2	S152645	gene B-50 protein
124	2	18.2	10	2	F60747	sperm-activation p	197	2	18.2	10	2	PA0116	ferredoxin-NADP re
125	2	18.2	10	2	H60787	sperm-activation p	198	2	18.2	10	2	PS0220	ferredoxin-NADP re
126	2	18.2	10	2	S60744	sperm-activation p	199	2	18.2	10	2	S74147	glyceraldehyde-3-p
127	2	18.2	10	2	C60748	sperm-activation p	200	2	18.2	11	1	GM0051	leucosulfakinin -
128	2	18.2	10	2	PT0748	sperm-activation p	201	2	18.2	11	2	S66196	alcohol dehydrogen
129	2	18.2	10	2	PT0748	sperm-activation p	202	2	18.2	11	2	A33917	dihydroorotase (EC
130	2	18.2	10	2	C60748	sperm-activation p	203	2	18.2	11	2	PT0682	photosystem 1 17.5
131	2	18.2	10	2	A60747	sperm-activation p	204	2	18.2	11	2	C53652	rhIR protein - Pse
132	2	18.2	10	2	H60787	sperm-activation p	205	2	18.2	11	2	YH01	morphogenetic neur
133	2	18.2	10	2	A60748	sperm-activation p	206	2	18.2	11	2	YH01	morphogenetic neur
134	2	18.2	10	2	A60527	sperm-activation p	207	2	18.2	11	2	YH01	morphogenetic neur
135	2	18.2	10	2	PT0527	sperm-activation p	208	2	18.2	11	2	YH01	morphogenetic neur
136	2	18.2	10	2	PT0527	sperm-activation p	209	2	18.2	11	2	YH01	morphogenetic neur
137	2	18.2	10	2	PT0527	sperm-activation p	210	2	18.2	11	2	S42449	anti protein - pha
138	2	18.2	10	2	PT0527	sperm-activation p	211	2	18.2	11	2	C58501	42K bile stone pro
139	2	18.2	10	2	C60527	sperm-activation p	212	2	18.2	11	2	PT0395	hypothetical prote
140	2	18.2	10	2	C60527	sperm-activation p	213	2	18.2	11	2	PT0395	beta-glucosidase (
141	2	18.2	10	2	PT0527	sperm-activation p	214	2	18.2	11	2	S66606	pyrroloquinoline q
142	2	18.2	10	2	PT0527	sperm-activation p	215	2	18.2	11	2	S58244	nifs protein - Bra
143	2	18.2	10	2	PT0527	sperm-activation p	216	2	18.2	11	2	S04875	nifs protein - Bra
144	2	18.2	10	2	C60589	sperm-activation p	217	2	18.2	11	2	E60691	phycoerythrin 8K1
145	2	18.2	10	2	PT0527	sperm-activation p	218	2	18.2	11	2	S33519	probable secreted
146	2	18.2	10	2	PT0527	sperm-activation p	219	2	18.2	11	2	PT0383	hypothetical prote
147	2	18.2	10	2	PT0527	sperm-activation p	220	2	18.2	11	2	S19775	wound-induced prot
148	2	18.2	10	2	PT0527	sperm-activation p	221	2	18.2	11	2	S41747	chaperonin 10 homo
149	2	18.2	10	2	PT0527	sperm-activation p	222	2	18.2	11	2	A38590	transforming prote
150	2	18.2	10	2	PT0527	sperm-activation p	223	2	18.2	11	2	A61512	variant surface gl
151	2	18.2	10	2	PT0527	sperm-activation p	224	2	18.2	11	2	A35594	buccalin - Califor
152	2	18.2	10	2	A60589	sperm-activation p	225	2	18.2	11	2	A60589	perisulfakinin - A
153	2	18.2	10	2	PT0527	sperm-activation p	226	2	18.2	11	2	S65395	chemical-sense-rel
154	2	18.2	10	2	X3H0E	cytotoxic membra	227	2	18.2	11	2	S41978	calliphramide 9 -
155	2	18.2	10	2	GM01	gastric juice pep	228	2	18.2	11	2	D37196	bradykinin-potenti
156	2	18.2	10	2	S58591	48K bile/whole blood	229	2	18.2	11	2	S165231	CKK-B gastrin rece
157	2	18.2	10	2	S06944	hypothetical prote	230	2	18.2	11	2	PT0349	Ig heavy chain CRD
158	2	18.2	10	2	A60742	cytochrome-c oxida	231	2	18.2	11	2	PT0302	Ig heavy chain CRD
159	2	18.2	10	2	PT0442	S-layer protein	232	2	18.2	11	2	PH1343	Ig heavy chain DJ
160	2	18.2	10	2	A60742	processing enzyme	233	2	18.2	11	2	S51732	T-cell receptor al
161	2	18.2	10	2	S66248	protein P11 - S-14	234	2	18.2	11	2	S60354	retinal oxidase -
162	2	18.2	10	2	S28927	triase-phosphate 1	235	2	18.2	11	2	PT0004	protein kinase C 1
163	2	18.2	10	2	A27617	triase-phosphate 1	236	2	18.2	11	2	PT0209	T-cell receptor al
164	2	18.2	10	2	PT0209	24K protein 4407 -	237	2	18.2	11	2	PT0218	T-cell receptor be
165	2	18.2	10	2	C61460	polygalacturonase	238	2	18.2	11	2	S141946	T-cell receptor ga
166	2	18.2	10	2	S62880	polygalacturonase	239	2	18.2	11	2	C49037	tCR gamma V-J regi
167	2	18.2	10	2	PT0165	triose-phosphate 1	240	2	18.2	11	2	PD0441	translation elonga
168	2	18.2	10	2	S19617	glutathione - polychaet	241	2	18.2	11	2	S177447	urinary protein -
169	2	18.2	10	2	B61656	leucosulfakinin II	242	2	18.2	11	2	S65377	cytochrome-c oxida
170	2	18.2	10	2	A42089	transcription fact	243	2	18.2	11	2	S78422	ribosomal protein
171	2	18.2	10	2	C44787	calliphramide 12	244	2	18.2	11	2	PH0947	T-cell receptor be
172	2	18.2	10	2	B56899	serum heterodimer	245	2	18.2	11	2	S52304	gene rSSTR4 protei
173	2	18.2	10	2	A41196	acetylcholinestera	246	2	18.2	11	2	A34243	H-hyoscyamin - Ja
174	2	18.2	10	2	S43630	cytochrome-c oxida	247	2	18.2	11	2	A61575	Trimeresurus scrin
175	2	18.2	10	2	S77969	cytochrome-c oxida	248	2	18.2	11	4	S19015	hypothetical prote

249	2	18.2	11	4	154081	retinoic acid rece	322	2	18.2	13	2	S22995	hypothetical prote
250	2	18.2	12	2	PN0577	tyrosine 3-monooxy	323	2	18.2	13	2	H36042	oxfx protein - Esc
251	2	18.2	12	2	PN0578	tyrosine 3-monooxy	324	2	18.2	13	2	H64124	hypothetical prote
252	2	18.2	12	2	PN0579	tyrosine 3-monooxy	325	2	18.2	13	2	S36668	hypothetical prote
253	2	18.2	12	2	PN0580	tyrosine 3-monooxy	326	2	18.2	13	2	PC2371	probable endopepti
254	2	18.2	12	2	PN0581	tyrosine 3-monooxy	327	2	18.2	13	2	A01825	botulinum toxins -
255	2	18.2	12	2	PN0576	tyrosine 3-monooxy	328	2	18.2	13	2	S36887	ribosomal protein
256	2	18.2	12	2	A29169	phospholipase A2 (	329	2	18.2	13	2	S41209	F420-non-reducing-
257	2	18.2	12	2	C49215	urease (EC 3.5.1.5	330	2	18.2	13	2	PN0176	acidic ribosomal p
258	2	18.2	12	2	S65409	5-stere H2H - huma	331	2	18.2	13	2	PA0023	protein QA300052 -
259	2	18.2	12	2	S15815	translation, e-onga	332	2	18.2	13	2	S00316	photosystem I prot
260	2	18.2	12	2	S65649	protoporphyrinogen	333	2	18.2	13	2	S09733	protein P18 - comm
261	2	18.2	12	2	S71034	p-tB protein - Sal	334	2	18.2	13	2	H44957	protein P18 - comm
262	2	18.2	12	2	S43013	hypothetical prote	335	2	18.2	13	2	PS0325	tetrahydroberberin
263	2	18.2	12	2	D28551	hypothetical prote	336	2	18.2	13	2	PO0700	unidentified 6.3/4
264	2	18.2	12	2	S49547	hypothetical prote	337	2	18.2	13	2	PA0089	protein QF200053 -
265	2	18.2	12	2	S36899	ribosomal protein	338	2	18.2	13	2	S04013	lignin peroxidase
266	2	18.2	12	2	T46794	hypothetical prote	339	2	18.2	13	2	PC1149	equinatoxin 1A - s
267	2	18.2	12	2	PA0030	protein QA300025 -	340	2	18.2	13	2	A26999	carboxylesterase (
268	2	18.2	12	2	S70337	nopin small chain	341	2	18.2	13	2	H58533	CD61 homolog - cha
269	2	18.2	12	2	S28215	gluca: endo-1,3-be	342	2	18.2	13	2	S09019	hemolytic protein
270	2	18.2	12	2	PS0213	28K protein: 44.2 -	343	2	18.2	13	2	A33660	osteoclast functio
271	2	18.2	12	2	PO0730	unidentified 5.4/3	344	2	18.2	13	2	A54326	gladular kallikre
272	2	18.2	12	2	PN0170	alcohol dehydrogen	345	2	18.2	13	2	S52356	hypothetical prote
273	2	18.2	12	2	PN0162	malate dehydrogena	346	2	18.2	13	2	PT0263	Ig heavy chain CRD
274	2	18.2	12	2	T46656	hypothetical prote	347	2	18.2	13	2	S57567	T cell receptor V-
275	2	18.2	12	2	C33099	148K exoantigen	348	2	18.2	13	2	S47382	T-cell antigen rec
276	2	18.2	12	2	A33099	163K exoantigen -	349	2	18.2	13	2	S47383	T-cell antigen rec
277	2	18.2	12	2	S16204	4 phosphofructokin	350	2	18.2	13	2	S47388	T-cell antigen rec
278	2	18.2	12	2	A09985	gamma-crystallin	351	2	18.2	13	2	S47389	T-cell antigen rec
279	2	18.2	12	2	A43261	coagulation factor	352	2	18.2	13	2	S47374	T-cell antigen rec
280	2	18.2	12	2	S24830	dimethylamino mo	353	2	18.2	13	2	H56046	urinary tract ston
281	2	18.2	12	2	PT0253	Ig heavy chain CRD	354	2	18.2	13	2	G56046	sperm motility inh
282	2	18.2	12	2	PT0359	Ig heavy chain CRD	355	2	18.2	13	2	S66235	tubulin alpha-chai
283	2	18.2	12	2	S21205	Ig heavy chain V :	356	2	18.2	13	2	S65612	Ig kappa-1 chain J
284	2	18.2	12	2	S43170	kinesin: light chai	357	2	18.2	13	2	R20907	Ig H chain V-D-J r
285	2	18.2	12	2	S47363	T cell antigen rec	358	2	18.2	13	2	PH1636	Ig kappa chain J r
286	2	18.2	12	2	PH1181	T-cell receptor al	359	2	18.2	13	2	A33933	Ig kappa chain J r
287	2	18.2	12	2	PH1186	T-cell receptor al	360	2	18.2	13	2	H26406	Ig kappa chain J r
288	2	18.2	12	2	PH1172	T-cell receptor al	361	2	18.2	13	2	S22761	Ig lambda-2 chain
289	2	18.2	12	2	A45033	T-cell receptor de	362	2	18.2	13	2	PH0796	T-cell receptor al
290	2	18.2	12	2	C49033	T-cell receptor de	363	2	18.2	13	2	PH0787	T-cell receptor al
291	2	18.2	12	2	A60526	insulin-like growt	364	2	18.2	13	2	PH0799	T-cell receptor al
292	2	18.2	12	2	F26907	Ig kappa-2 chain J	365	2	18.2	13	2	PH0783	T-cell receptor al
293	2	18.2	12	2	PH1606	Ig H chain V-D-J :	366	2	18.2	13	2	PH0786	T-cell receptor al
294	2	18.2	12	2	PH1611	Ig H chain V-D-J :	367	2	18.2	13	2	PH0805	T-cell receptor al
295	2	18.2	12	2	S25039	Ig heavy chain V :	368	2	18.2	13	2	PH0928	T-cell receptor be
296	2	18.2	12	2	A42324	cytochrome P450c27	369	2	18.2	13	2	A47630	Ig kappa chain J r
297	2	18.2	12	2	B42523	hexokinase (EC 2.7	370	2	18.2	13	2	S74130	NADH oxidase - Gia
298	2	18.2	12	2	PH0940	T-cell receptor be	371	2	18.2	13	2	A86126	hypothetical prote
299	2	18.2	12	2	PH0946	T-cell receptor be	372	2	18.2	13	2	S01904	H+-transporting tw
300	2	18.2	12	2	PC4377	telomeric and tetr	373	2	18.2	13	2	PS0277	glyceraldehyde-3-p
301	2	18.2	12	2	S71680	lebetin 1 isoform	374	2	18.2	14	1	NTPG14	hypochalamic tetra
302	2	18.2	12	2	A50375	microcin B17 - Esc	375	2	18.2	14	1	QMVAVV	mastoparan - yello
303	2	18.2	12	2	A53252	pollen mator aller	376	2	18.2	14	1	QMVHMM	mastoparan M - hor
304	2	18.2	12	2	141235	glutamine-tRNA lig	377	2	18.2	14	1	QMVHXX	mastoparan X - hor
305	2	18.2	12	2	S21163	NAD ADP-ribosyltra	378	2	18.2	14	1	QMVHP2	mastoparan C - Eur
306	2	18.2	12	4	PC2122	aminotransferase c	379	2	18.2	14	1	QMVAPP	pollistes mastopara
307	2	18.2	13	1	XAV19B	angiotensin-conver	380	2	18.2	14	1	QMVAPP	alpha-conotoxin MI
308	2	18.2	13	1	MTCMAD	melanotropin alpha	381	2	18.2	14	2	PC2373	probable IMP dehyd
309	2	18.2	13	1	MTMOAD	melanotropin alpha	382	2	18.2	14	2	A33798	D-amino-acid oxida
310	2	18.2	13	1	N7KN20	alpha-conotoxin GI	383	2	18.2	14	2	C40944	hypothetical prote
311	2	18.2	13	1	N7KNAS	alpha-conotoxin SI	384	2	18.2	14	2	JN0389	histamine-releasein
312	2	18.2	13	2	A32734	enkephalin precurs	385	2	18.2	14	2	JN0390	histamine-releasein
313	2	18.2	13	2	S48213	collagen alpha 1(V	386	2	18.2	14	2	A58963	alpha-conotoxin Cn
314	2	18.2	13	2	A23695	myosin heavy chain	387	2	18.2	14	2	S15130	hemoglobin beta ch
315	2	18.2	13	2	S15755	actin 7 - soybean	388	2	18.2	14	2	S19803	ubiquitin - potato
316	2	18.2	13	2	A59778	lactose phosphotra	389	2	18.2	14	2	S15132	histone H4-1 precu
317	2	18.2	13	2	S50173	alpha-2 collagen -	390	2	18.2	14	2	A35377	GTP-binding protei
318	2	18.2	13	2	A61351	bradykinin-like pe	391	2	18.2	14	2	R29743	translation initia
319	2	18.2	13	2	A60409	bombesin-like pept	392	2	18.2	14	2	A42473	ermK leader peptid
320	2	18.2	13	2	T08533	hypothetical prote	393	2	18.2	14	2	A32654	fibrinopeptide A -
321	2	18.2	13	2	154984	aeq 46.5 protein -	394	2	18.2	14	2	JH0328	probrusin tetradece



995	2	18.2	14	2	S29632	xyran 1,4-beta-xyl	468	2	18.2	15	2	S26527	T-cell receptor al
996	2	18.2	14	2	S59495	tormate dehydrogen	469	2	18.2	15	2	S26528	T-cell receptor al
997	2	18.2	14	2	S54945	gene C protein - E	470	2	18.2	15	2	A28497	neurotensin-relate
998	2	18.2	14	2	H54606	hypofunctional prote	471	2	18.2	15	2	149407	placental calcium-
999	2	18.2	14	2	S58806	butalinum zeutox	472	2	18.2	15	2	P00681	photosystem I 19.0
400	2	18.2	14	2	S36892	ribosomal protein	473	2	18.2	15	2	P00692	photosystem I 18.5
401	2	18.2	14	2	S74126	superoxide dismuta	474	2	18.2	15	2	140665	ilvBN leader pepti
402	2	18.2	14	2	P00615	photosystem II oxy	475	2	18.2	15	2	P00545	capsid protein VP1
403	2	18.2	14	2	P00615	photosystem II oxy	476	2	18.2	15	2	S02381	probable membrane
404	2	18.2	14	2	P01497	seed protein 45-21	477	2	18.2	15	2	A60929	dichloromethane de
405	2	18.2	14	2	A61062	photosystem II oxy	478	2	18.2	15	2	C48401	ribosomal protein
406	2	18.2	14	2	G44957	photosystem II oxy	479	2	18.2	15	2	PC4213	bphB protein - Com
407	2	18.2	14	2	P00147	acada-gliadine 1 a	480	2	18.2	15	2	B60929	dichloromethane de
408	2	18.2	14	2	P00151	acada-gliadine 2	481	2	18.2	15	2	B35389	urease (EC 3.5.1.5
409	2	18.2	14	2	S13803	chapone, TCp1-re	482	2	18.2	15	2	A35389	urease (EC 3.5.1.5
410	2	18.2	14	2	P00258	18K protein 3228	483	2	18.2	15	2	E41383	32K variable histo
411	2	18.2	14	2	S35267	acetyl-CoA carboxy	484	2	18.2	15	2	C41383	32K variable histo
412	2	18.2	14	2	B34135	2NA-binding protei	485	2	18.2	15	2	S29386	nglerythrin - Desu
413	2	18.2	14	2	E33998	214K exoantigen (v	486	2	18.2	15	2	C43334	orf3 3' to aadr -
414	2	18.2	14	2	S23476	collagen alpha cha	487	2	18.2	15	2	S03353	plastocyanin - Mic
415	2	18.2	14	2	A56642	zeosultakinin-1	488	2	18.2	15	2	PC2374	unidentified 22K p
416	2	18.2	14	2	S14356	mastoparan B - hor	489	2	18.2	15	2	A60156	cellulase (EC 3.2.
417	2	18.2	14	2	S12904	protein kinase (EC	490	2	18.2	15	2	S36893	ribosomal protein
418	2	18.2	14	2	S43629	cytochrome-c oxida	491	2	18.2	15	2	S36897	ribosomal protein
419	2	18.2	14	2	S11074	alcohol dehydrogen	492	2	18.2	15	2	S36896	ribosomal protein
420	2	18.2	14	2	P10492	Ig heavy chain CR2	493	2	18.2	15	2	A61145	dihydrofolate redu
421	2	18.2	14	2	S57564	T cell receptor V	494	2	18.2	15	2	A40634	orf19 3' of eryk -
422	2	18.2	14	2	S27674	T cell receptor V	495	2	18.2	15	2	PA0036	glycine cleavage s
423	2	18.2	14	2	S47465	T cell antigen rec	496	2	18.2	15	2	PA0040	malate dehydrogena
424	2	18.2	14	2	S22369	T-cell receptor al	497	2	18.2	15	2	PA0002	photosystem II oxy
425	2	18.2	14	2	E49339	T-cell receptor be	498	2	18.2	15	2	PA0038	protein QA100030 -
426	2	18.2	14	2	S58426	spectrin-delta: ANK b	499	2	18.2	15	2	PA0046	protein QA100044 -
427	2	18.2	14	2	A47471	leukotriene B-4 12	500	2	18.2	15	2	PA0034	protein QA300024 -
428	2	18.2	14	2	S64244	sperm motility inh							
429	2	18.2	14	2	F46194	glycoprotein compo							
430	2	18.2	14	2	I45474	thiobiosphindin 2 -							
431	2	18.2	14	2	S36678	dodecenyl-CoA Del							
432	2	18.2	14	2	PH1574	Ig H chain V-D-J r							
433	2	18.2	14	2	PH1508	Ig H chain V-D-J r							
434	2	18.2	14	2	PH1448	T cell receptor al							
435	2	18.2	14	2	PH0600	T cell receptor al							
436	2	18.2	14	2	PH0795	T-cell receptor al							
437	2	18.2	14	2	PH0834	T-cell receptor al							
438	2	18.2	14	2	PH0776	T-cell receptor al							
439	2	18.2	14	2	PH1450	T-cell receptor al							
440	2	18.2	14	2	PT0210	T cell receptor al							
441	2	18.2	14	2	PH0742	T cell receptor al							
442	2	18.2	14	2	PH0747	T cell receptor be							
443	2	18.2	14	2	PH0774	T-cell receptor be							
444	2	18.2	14	2	D35141	T-cell receptor de							
445	2	18.2	14	2	S35141	T-cell receptor de							
446	2	18.2	14	2	S35141	T-cell receptor de							
447	2	18.2	14	2	F49037	Tck delta chain V							
448	2	18.2	14	2	PC7379	unidentified 27.2K							
449	2	18.2	14	2	A37789	heat shock cognate							
450	2	18.2	14	2	PH0345	T-cell receptor be							
451	2	18.2	14	2	S29878	Na+/K+-exchanging							
452	2	18.2	14	2	A12150	glucose 1 dehydro							
453	2	18.2	14	2	F52618	hemoglobin beta ch							
454	2	18.2	15	1	SFR1	scotophobin - rat							
455	2	18.2	15	1	NTKNAG	alpha-conotoxin G1							
456	2	18.2	15	1	LTWL	leu leader peptide							
457	2	18.2	15	2	S21241	oligo-1,6-glucosid							
458	2	18.2	15	2	S21243	alpha-glucosidase							
459	2	18.2	15	2	S21262	glucan 1,4 alpha-g							
460	2	18.2	15	2	S24159	leukocyte elastase							
461	2	18.2	15	2	PC2215	fibrinogenolytic p							
462	2	18.2	15	2	S57201	basic proteinase I							
463	2	18.2	15	2	A54397	ubiquitin-carrier							
464	2	18.2	15	2	P00232	cystatin G1-4a - m							
465	2	18.2	15	2	F52734	gene c-KI ras prot							
466	2	18.2	15	2	A22789	platelet derived g							
467	2	18.2	15	2	S26516	T cell receptor al							

## ALIGNMENTS

## RESULT 1

129501  
 fibrinopeptide A kanaroc  
 C:Species: Macropus sp. (kanaroc)  
 C:Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 18-Aug-2000  
 C:Accession: 129501  
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.  
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and  
 A:Reference number: A29501  
 A:Accession: 129501  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <81/0>  
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 36.4%; Score 4; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEGG 4

IIII

Db 9 AEGG 12

## RESULT 2

fibrinopeptide A - wombat  
 C:Species: Vombatidae gen. sp. (wombat)  
 C:Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 18-Aug-2000  
 C:Accession: F29501  
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.  
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and  
 A:Reference number: A29501  
 A:Accession: F29501  
 A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-15 <BLD>  
C:Similarity: fibrinogen alpha chain; fibrinogen subunit alpha ring homology

Query Match 46.4% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5; AEG 2;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 4  
DB 9 AEG 12

RESULT 5  
PC7076

Spectrin alpha chain, non-erythrocyte mouse (fragment)  
N:Alternate names: lodrin alpha chain  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-2000 #sequence\_revision 18 Aug 2000 #text\_change 18-Aug-2000  
C:Accession: PC7076

K:Tsukita, A.; Kawakami, T.; Gehda, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.  
Electrophoresis 21, 1853-1871, 2000  
A:Title: Proteome analysis of mouse brain. Two-dimensional electrophoresis profiles of b  
A:Reference number: PC7072  
A:Accession: PC7076  
A:Molecule type: protein  
A:Residues: 1-9 <TSU>  
A:Experimental source: strain: C57BL/6J; Site: brain; brain; striatum  
C:Keywords: brain

Query Match 27.3% Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2; AEG 2;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
DB 5 KKK 8

RESULT 4  
PC7097

Hypothetical protein (tpi 57 region) - bacteriophage phi85 T (fragment)  
C:Species: Bacteriophage phi85 T  
C:Date: 28 Apr 1993 #sequence\_revision 28 Apr 1993 #text\_change 17 Mar 1999  
C:Accession: PC7397

K:Laksimidevi, G.; Davidson, R.R.; Hillier, A.  
Appl. Environ. Microbiol. 56, 944-947, 1990  
A:Title: Molecular characterization of bacteriophage phi85 T (tphi57) and its replicative  
activity.  
A:Reference number: A47397; MUID:96254170; PDB:1A118  
A:Accession: PC7397  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <LAK>  
A:Cross-References: GB:M34497

Query Match 27.3% Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3; AEG 2;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KMR 10  
DB 7 KMR 9

RESULT 5  
S77990

Cytochrome c oxidase (EC 1.9.3.1) chain VIII - bovine heart (fragment)  
C:Species: Bos taurus (biquey line)  
C:Date: 17-Sep-1997 #sequence\_revision 17 Sep 1997 #text\_change 18 Jan 1998  
C:Accession: S77990

R:Arnold, S.; Lee, J.; Kim, M.; Socha, P.; Cohen, T.; Gaspard, D.; Kadenbach, B.  
Submitted to the Protein Sequence Database, 1998

A:Reference number: S77980  
A:Accession: S77990  
A:Molecule type: protein  
A:Residues: 1-16 <ARN>  
A:Experimental source: heart; liver  
C:Genetics:  
A:Genome: nuclear  
C:Function:  
A:Pathway: oxidative phosphorylation; respiratory chain  
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner mem

Query Match 27.3% Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3; AEG 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 4  
DB 4 AEG 5

RESULT 5  
P00029

33K protein 3218 - rice (strain Nohonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C:Accession: P00029

K:Tsukita, A.; Miyatake, N.  
Submitted to JPIB, April 1993  
A:Reference number: P00029  
A:Accession: P00029  
A:Molecule type: protein  
A:Residues: 1-11 <TSU>  
A:Experimental source: brain  
C:Comment: molecular weight 33K, pI 6.0.

Query Match 27.3% Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4; AEG 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 3 EGG 5

RESULT 7  
PC2173

Triacylglycerol lipase (EC 3.1.1.3) 11 - Rhizopus niveus (strain IFO 4759) (fragment)  
C:Species: Rhizopus niveus  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C:Accession: PC2173

R:Kohno, M.; Kujiyama, M.; Hashimoto, Y.; Morita, Y.  
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994  
A:Title: Purification, characterization, and crystallization of two types of lipase  
A:Reference number: PC2171; MUID:94319059; PMID:7765029  
A:Accession: PC2174  
A:Molecule type: protein  
A:Residues: 1-10; 11 <KCH>  
C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds of triacylglycer  
C:Comment: This enzyme is produced from lipase I by limited proteolysis due to the  
C:Keywords: carboxylic ester hydrolase

Query Match 27.3% Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4; AEG 3;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5  
DB 3 GKK 5

RESULT 8  
S57676

11 cell receptor VLA-1 protein and alpha chain (human) (fragment)



Q1 9 GKK 11

RESULT 14

A:Accession: A33500; S30176  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide  
A:Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Iys, in Xenopus  
A:Reference number: S30176; NCID:94200145; PMID:8452872  
A:Accession: S30176  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 9 GKK 11  
DB 9 GKK 11

RESULT 15

A:Accession: S10625  
A:Title: Placement of small lipovitellin subunit's within the vitellogenin precursor in X  
A:Reference number: S10624; NCID:9027455; PMID:202215  
A:Accession: S10625  
A:Molecule type: protein  
A:Residues: 1-12 <WA>  
A:Keywords: neuropeptide  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 9 GKK 11  
DB 9 GKK 11

RESULT 16

A:Accession: S57570  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: S57494  
A:Accession: S57570  
A:Molecule type: mRNA  
A:Keywords: neuropeptide  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Residues: 1-12 <RQ>  
A:Cross-references: EMBL:Z49954; NID:9887488; PTDN:CAA90225.1; PID:9887489  
C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 9 MKA 11  
DB 3 MKA 5

RESULT 17

A:Accession: PH1189  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: S26512; NCID:92364546; PMID:1380061  
A:Accession: PH1189  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Keywords: neuropeptide  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 2 EGG 4  
DB 5 EGG 7

RESULT 18

A:Accession: PH1180  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: S26512; NCID:92364546; PMID:1380061  
A:Accession: PH1180  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Keywords: neuropeptide  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 2 EGG 4  
DB 5 EGG 7

RESULT 19

A:Accession: PH1175  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: S26512; NCID:92364546; PMID:1380061  
A:Accession: PH1175  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Keywords: neuropeptide  
A:Title: Hydrins, hydrosomatic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; NCID:8915779; PMID:274509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <RQ>  
A:Keywords: neuropeptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 2 EGG 4  
DB 5 EGG 7

A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 27.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 5 EGG 7

#### RESULT 20

PH1481  
T-cell receptor beta chain (clone A24/PE12) mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 1; #text\_change 1; Apr-1995  
C:Accession: PH1481  
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, B.; Pennetier, C.; Regnault, A.; Kieffer, J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex peptides  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1481  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
A:Note: the authors translated the cDNA obtained for residue 2 as Ala and Gln for residue 3  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 27.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
DB 4 AEG 6

#### RESULT 21

PH1585  
Trematode a-13 - jelly fungus (Trematid mesenterica)  
C:Species: Trematid mesenterica  
C:Date: 09-Aug-1984 #sequence\_revision 0; #text\_change 0; Nov-1997  
C:Accession: A01641  
R:Sakaguchi, Y.; Yoshida, M.; Isigai, A.; Saito, A.  
Science 224, 1525-1527, 1981  
A:Title: Trematid sex hormones inducing development in compatible mating partners  
A:Reference number: A94256  
A:Accession: A01641  
A:Molecule type: protein  
A:Residues: 1-13 <SAK>  
C:Comment: Trematogen a-13 is produced by the a-13 type cells and induces formation of a-13 type cells  
C:Keywords: extracellular protein; hormone; lipoprotein; photomicro; prolylated cysteine  
F:13/Binding site: farnesyl (Cys) (covalent) #status experimental  
F:13/Modified site: methyl ester carboxyl end (Cys) #status absent

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 1 EGG 3

#### RESULT 22

G22565  
R-phycoerythrin gamma-B chain - red alga (Gastrocoulonm coulteri) (fragment)  
C:Species: Gastrocoulonm coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 0; #text\_change 23-Mar-1993  
C:Accession: G22565

R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 268, 4856-4863, 1993

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:3886644  
A:Accession: G22565  
A:Molecule type: protein  
A:Residues: 1-13 <KLO>

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
DB 2 AEG 4

#### RESULT 23

QJ1350  
hypothetical protein, 1.3k (rps16 5' region) - Emericella nidulans  
C:Species: Emericella nidulans, Aspergillus nidulans  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Sep-1997  
C:Accession: QJ1350  
R:Bradshaw, R.E.; Pillar, T.M.  
Gene 108, 157-162, 1991  
A:Title: Isolation and nucleotide sequence of the ribosomal protein S16-encoding gene from the fungus Emericella nidulans  
A:Reference number: QJ1349; MUID:92104500; PMID:1761226  
A:Accession: QJ1350  
A:Molecule type: DNA  
A:Residues: 1-13 <BRA>  
A:Cross-references: GB:M65259; NID:g168087; PID:g168089  
A:Experimental source: strain K153

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6  
DB 9 GKK 11

#### RESULT 24

PH1585  
Iq H chain V-D-J region (wild-type clone 9) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1585  
R:Levinson, D.A.; Campos-Torres, J.; Ieder, P.  
J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1585  
A:Molecule type: DNA  
A:Residues: 1-13 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 5 EGG 7

#### RESULT 25

S27140  
hypothetical protein 1 estrogen receptor 5'-region - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Mar-1994 #sequence\_revision 12-May-1995 #text\_change 18-Aug-2000  
C:Accession: S27140

R:Keaveney, M.; Klug, J.; Gannon, F.  
DNA Seq. 2, 347-358, 1992

A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene  
A:Reference number: S27140; MUID:93075998; PMID:1476547

A:Accession: S27140

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-14 <K&A>

A:Cross-references: EMBL:X62462; NID:G1271; PIR:G0AA4419.1; PIR:G1272

C:Superfamily: unassigned leader peptides

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MRA 11

DB 1 MRA 3

RESULT 26

SI7864

methy: coenzyme M reductase (EC 1.8.1.2) 1; alpha chain - Methanobacterium thermoautotro-

C:Species: Methanobacterium thermoautotrophicum

A:Variety: Strain Marburg

C:Date: 19-Mar-1997 #sequence\_revision 13-Sep-1998 #text\_change 30-Oct-1998

C:Accession: SI7864

R:Kosper, S.; Linder, D.; Ellermann, J.; Ihauer, R.K.

Eur. J. Biochem. 194, 871-877, 1990

A:Title: Two genetically distinct methyl coenzyme M reductases in Methanobacterium therm

A:Reference number: SI7864; MUID:91099473; PMID:2265066

A:Accession: SI7864

A:Molecule type: protein

A:Residues: 1-14 <K&S>

A:Experimental source: strain Marburg

C:Keywords: methanogenesis; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7

DB 12 KKK 14

RESULT 27

PA0109

porin por 18 - Arabidopsis thaliana (flower)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 30-Jun-1995

C:Accession: PA0109

R:Kamo, M.; Kawakami, T.; Tsugita, A.

submitted to JIPID, March 1995

A:Reference number: PA0109

A:Accession: PA0109

A:Molecule type: protein

A:Residues: 1-14 <K&A>

A:Experimental source: root

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6

DB 11 GKK 13

RESULT 28

PA0045

porin por1 - Arabidopsis thaliana (flower)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995

C:Accession: PA0045

R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimen

A:Reference number: PA0001

A:Accession: PA0045

A:Molecule type: protein

A:Residues: 1-14 <K&A>

A:Experimental source: root

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6

DB 11 GKK 14

RESULT 29

PH1626

Ig H chain V-D-J region (clone B-less 118) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1626

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1626

A:Molecule type: DNA

A:Residues: 1-14 <L&E>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MRA 11

DB 2 MRA 4

RESULT 30

S26524

T-cell receptor alpha chain V region (clone Cw3/5B8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Variety: Clone Cw3/5B8

C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C:Accession: S26524

R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.

J. Exp. Med. 176, 439-447, 1992

A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell rec

A:Reference number: S26512; MUID:92364546; PMID:1380061

A:Accession: S26524

A:Molecule type: mRNA

A:Residues: 1-15 <C&S>

A:Cross-references: EMBL:X67975

A:Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4

DB 5 EGG 7

**RESULT 31**  
**S26534**  
 T-cell receptor alpha chain V region (Cane CW/263) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 A:Variant: Clone CW3/2C3  
 C:Date: 11-Mar-1988 #sequence\_revision 17 Apr-1992 #extl\_change 17 Mar-1999  
 C:Accession: S26534  
 K:Casanova, J.L.; Corbelli, J.C.; Mathis, M.; Melnick, A.; Gough, H.; Baria, C.; Wad  
 3: Exp. Med. 176, 439-447, 1992  
 A:Title: H-2 restricted cytolytic T lymphocytes specific for H-2A display T cell receptor  
 A:Reference number: S26512; MUID:9246546; PK:1134661  
 A:Accession: S26534  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <CAS>  
 A:Cross-references: EMBL:X67995  
 A:Experimental source: cytolytic T-lymphocytes from CW3/2C3  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: T-cell receptor  
  
 Query Match 27.3% Score 31 18 21 Length 15:  
 Best local Similarity 100.0% Pred. No. Score 0:  
 Matches 3: Conservative 0: Mismatches 0: Gaps 0:  
  
 QY 2 EGG 4  
 DE 1 1  
 4 EGG 7  
  
**RESULT 32**  
**JP0101**  
 fibrinogen alpha chain - duck (fragment)  
 N:Contains: fibrinopeptide A  
 C:Species: Anas platyrhynchos (domestic duck)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Dec-1987 #extl\_change 26-Jan-1996  
 C:Accession: JP0101  
 K:Min, Y.; Ping, Z.; Yaoshi, Z.  
 Sci. Sin. B Chem. Biol. Agric. Med. Earth Space Sci. 16, 65, 1995  
 A:Title: Purification and primary structures of duck fibrinopeptides A and B.  
 A:Reference number: A94238  
 A:Accession: JP0101  
 A:Molecule type: protein  
 A:Residues: 1-16 <MIN>  
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide chain homology  
 C:Keywords: blood coagulation; plasma; fibrinogen; duck  
 E1/Modified sites: pyrolysine carboxyl group; aspartic acid  
  
 Query Match 27.3% Score 31 18 21 Length 15:  
 Best local Similarity 100.0% Pred. No. Score 0:  
 Matches 3: Conservative 0: Mismatches 0: Gaps 0:  
  
 QY 2 EGG 4  
 DE 1 1  
 4 EGG 12  
  
**RESULT 33**  
**A56786**  
 Pim-2/1 CoA synthase - Bacillus sphaericus  
 C:Species: Bacillus sphaericus  
 C:Date: 18-Aug-1995 #sequence\_revision 16-Aug-1997 #extl\_change 18-Aug-1995  
 C:Accession: A56786  
 K:Ploux, O.; Soullier, P.; Marquet, A.; Ghackler, B.; Lacroix, Y.  
 Biochem. J. 297, 685-690, 1992  
 A:Title: Investigation of the first step of bacterial synthesis in Bacillus sphaericus.  
 A:Reference number: A56786; MUID:93075613; PK:1141212  
 A:Accession: A56786  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <PLO>  
 A:Experimental source: Bacillus sphaericus protein overexpressed in Escherichia coli  
 A:Note: sequence extracted from NCBI Fackbook (NCBI:P:11639)  
 C:Genetics:  
 A:Gene: btoW

C:Keywords: carboxylester hydrolase

Query Match 27.4% Score 2: DB 2: Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3: Conservative 0; Mismatches 0; Indels 0;

QY 4 OK 5

DB 1 1

QY 4 OK 5

RESULT 47

LFSAME

C:Species: Staphylococcus epidermidis

C:Date: 30-Sep-1991 #sequence\_revision 10 Sep 1991 #text\_change 16-Jul-1999

C:Accession: S1157

R:Ross, J. L.; Eady, E. A.; Cove, J. H.; Gaultier, W. S.; Baumberg, S.; Wootten, J. C.

Mol. Microbiol. 4: 1207-1214, 1990

A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member of the

A:Reference number: S1157; M010:91047707; PMID:2233255

A:Accession: S1157

A:Molecule type: DNA

A:Residues: 1-8 <ROS>

A:Cross-references: EMBL:X52065; N10047600; F11N:25A6333.1; F11N:4541653

C:Suprafamily: probable msrA leader: peptide

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0;

QY 9 OK 10

DB 5 OK 6

RESULT 48

PL0184

C:Species: murine poliovirus (fragment)

C:Date: 20-Feb-1995 #sequence\_revision 20 Feb 1995 #text\_change 20 Feb 1995

C:Accession: PL0184

R:Zurbriggen, A.; Hogle, J. M.; Fujiwara, R. S.

J. Exp. Med. 170: 2037-2049, 1989

A:Title: Alteration of amino acid 101 within capsid protein VP1 enhances the pathogenicity

A:Reference number: PL0184; M010:90664480; PMID:2473766

A:Accession: PL0184

A:Molecule type: genomic RNA

A:Residues: 1-8 <OR>

C:Keywords: capsid protein

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0;

QY 4 OK 4

DB 2 OK 3

RESULT 49

PL0377

C:Species: Methylophilus methylotrophus

C:Date: 16-Jul-1999 #sequence\_revision 16 Jul 1999 #text\_change 27-Jul-2000

C:Accession: PL0377

R:Christoserdov, A. Y.; McIntire, W. S.; Mathews, F. S.; Johnston, M. B.

J. Bacteriol. 176: 4073-4080, 1994

A:Title: Organization of the methylamine utilization (mnu) genes in Methylophilus methyl-

A:Reference number: PL0377; M010:94292427; PMID:21188

A:Accession: PL0377

A:Status: preliminary

A:Molecule type: DNA

C:Date: 04-Nov-1992 #sequence\_revision 04-Dec-1992 #text\_change 22-Nov-1996

A:Residues: 1-8 <SHL>

A:Cross-references: EMBL:L25407; N1004561931; PIDN:AAB46955.1; PID:9561933

A:Experimental source: strain W3A1

C:Genetics:

A:Gene: mauH

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 OK 10

DB 1 OK 2

RESULT 40

SL9238

C:Species: Kluyvera cryocrescens

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C:Accession: SL9238

R:Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280: 659-662, 1991

A:Title: Chemical modification of serine at the active site of penicillin acylase f

A:Reference number: SL9238; M010:92106664; PMID:1764029

A:Accession: SL9238

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 5

DB 7 OK 8

RESULT 41

S63493

C:Species: Desulfovibrio desulfuricans

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S63493; S63494

R:Steuber, J.; Arendsen, A. F.; Hagen, W. R.; Kroneck, P. M. H.

Eur. J. Biochem. 233: 873-879, 1995

A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A:Reference number: S63493; M010:96085152; PMID:8521853

A:Accession: S63493

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STE>

A:Accession: S63494

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <ST2>

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2

DB 1 AE 2

RESULT 42

S21273

C:Species: Clostridium thermocellum (fragment)

C:Date: 04-Nov-1992 #sequence\_revision 04-Dec-1992 #text\_change 22-Nov-1996



C:Accession: S21273  
 R:Komunie, M.P.M.; Fauth, U.; Kobayashi, T.; Huskisson, N.S.; Barker, P.J.; Demain, A.L.  
 Biochem. J. 283, 69-73, 1992  
 A:Title: Purification and characterization of a low molecular weight (fragment)  
 A:Reference number: S21273; MUID:92231850; PMID:156737  
 A:Accession: S21273  
 A:Molecule type: protein  
 A:Residues: 1-8 <PAR>  
 A:Function: hydrolysis of 1,4-beta-D-glucosidase  
 A:Pathway: cellulose degradation  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 4  
 DB 5 AE 6

RESULT 44  
 B39745  
 endoglycosyltransferase (EC 3.2.1.129) from *Glucospora* sp. (fragment)  
 C:Species: *Glucospora* sp.  
 C:Date: 30 Dec 1994; sequence\_revision 30-Dec-1994; #text\_change 41-Dec-1993  
 C:Accession: B39745  
 R:Itto, M.; Ikegami, Y.; Yamada, T.  
 J. Biol. Chem. 265, 7919-7926, 1991  
 A:Title: Activator proteins for glycosyltransferase hydrolysis by endoglycosyltransferases. E  
 ble using these activator proteins  
 A:Reference number: B39745; MUID:91210421; PMID:1856127  
 A:Accession: B39745  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <PAR>  
 C:Keywords: glycosidase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EA 11  
 DB 7 EA 8

RESULT 45  
 B61512  
 variant surface glycoprotein M181 from *Trypanosoma brucei* (fragment)  
 C:Species: *Trypanosoma brucei*  
 C:Date: 28 Oct 1994; sequence\_revision 28-Oct-1994; #text\_change 07 May 1999  
 C:Accession: B61512  
 R:Reed, A.A.; Cross, G.A.M.  
 Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A:Title: Glycopeptides from variant surface glycoproteins of *Trypanosoma brucei*. C-term  
 A:Reference number: B61512; MUID:91172843; PMID:7181214  
 A:Accession: B61512  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <PAR>  
 C:Keywords: glycoprotein

Query Match 18.2% Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Prod. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EA 3  
 DB 2 EA 3

RESULT 45  
 A21440  
 variant surface glycoprotein pSLel - *Trypanosoma brucei* (fragment)  
 C:Species: *Trypanosoma brucei*  
 C:Date: 19-Nov-1988; sequence\_revision 19-Nov-1988; #text\_change 20-Mar-1998  
 C:Accession: A21440  
 R:Parsons, M.; Neisner, K.G.; Watkins, K.P.; Agabian, N.  
 Cell 38, 309-316, 1984  
 A:Title: *Trypanosoma* mRNAs share a common 5' spliced leader sequence.  
 A:Reference number: A21440; MUID:84282716; PMID:6088073  
 A:Accession: A21440  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <PAR>  
 A:Cross-references: GB:K02195; MUID:dl62150; PID:gl62151  
 C:Keywords: glycoprotein

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4  
 DB 7 GG 8

RESULT 46  
 H41978  
 calliphoramide B, blood-bottle fly (*Calliphora vomitoria*)  
 C:Species: *Calliphora vomitoria*  
 C:Date: 30-Sep-1993; sequence\_revision 30-Sep-1993; #text\_change 17-Mar-1999  
 C:Accession: H41978  
 R:Dave, H.; Johsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Tl  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides  
 A:Reference number: H41978; MUID:92196111; PMID:1549595  
 A:Accession: H41978  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <PAR>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MR 10  
 DB 6 MR 7

RESULT 47  
 A41117  
 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)  
 C:Species: *Naja naja oxiana* (Asian cobra, Oxus cobra)  
 C:Date: 27-Mar-1992; sequence\_revision 27-Mar-1992; #text\_change 23-Jun-1993  
 C:Accession: A41117  
 R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Ravikumar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from *Torp*  
 A:Reference number: A41117; MUID:91296772; PMID:2068091  
 A:Accession: A41117  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <PAR>  
 C:Keywords: carboxylic ester hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 4  
 DB 1

Db 2 AE 3

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 EG 4  
II  
DB 4 EG 5

Search completed: September 30, 2003, 10:09:53  
Job time : 12.4167 secs

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Query Match 18.2% Score 23 DB 23 Length 83  
Best Local Similarity 100.0% Pred. No. 2.8e+5  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 GG 4  
II  
DB 7 GG 8

RESULT 49

PN0043

phosphatidylethanol amine-binding protein mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Oct-1997 #sequence\_revision 29 Oct-1997 #text\_change 23-Jan-1998  
C:Accession: PN0043  
S:Kato, H.  
Kawasaki, I.; Kaishii, 22, 245-259, 1996  
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro  
A:Reference number: PN0041  
A:Accession: PN0043  
A:Molecule type: protein  
A:Residues: 1-8 <YAM>  
A:Experimental source: neuroblastoma cells  
C:Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked  
C:Keywords: brain

Query Match 18.2% Score 23 DB 23 Length 83  
Best Local Similarity 100.0% Pred. No. 2.8e+5  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GK 5  
II  
DB 7 GK 8

RESULT 50

PT0595

T cell receptor beta chain V-D-J region (100-2AA) mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17 Jul 1992 #text\_change 30-May 1997  
C:Accession: PT0595  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; M010:91277601; PM01:171169  
A:Accession: PT0595  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-8 <FEE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 18.2% Score 23 DB 23 Length 83  
Best Local Similarity 100.0% Pred. No. 2.8e+5

GenCore version 5.1.6  
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1M Protein - protein search, using sw mod-1

Run on: September 30, 2003, 10:07:04 : Search time: 0.25 seconds

(without alignments)  
82.763 M/s, 60.00 updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: AEGGKKKKMRA 11

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 707

Minimum hit seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	15	PIR4_SYNCA	P14463 synectes ca
2	3	27.3	9	DL_NEPRI	P24816 nepriops no
3	3	27.3	9	NEP_HV7c	P12481 hepan immun
4	3	27.3	10	COX2_HUMAN	P92982 trammus oke
5	3	27.3	11	PKCL_CARM	P82684 carausius m
6	3	27.3	12	RS19_CARP	Q52251 tomato bnf
7	3	27.3	12	V14K_WRSV	P62606 white spot
8	3	27.3	13	TA13_TREME	P21470 tremella me
9	3	27.3	14	FIBA_HHPSE	P14452 equus cabal
10	3	27.3	14	MAST_FABID	P42716 parapolybia
11	3	27.3	14	MCRX_METIM	P58815 methanobact
12	3	27.3	15	FIBA_AKAPL	P12801 anas platyr
13	3	27.3	15	ONCL_NMY	P83287 oncorhynch
14	3	27.3	15	UC26_MAIZE	P50626 zea mays (m
15	3	18.2	8	ALL6_CARMA	P81819 carcinus ma
16	2	18.2	8	ALL9_CARMA	P81812 carcinus ma
17	2	18.2	8	CLP_HBHV	P63488 throbactilu
18	2	18.2	8	FAR5_CALVO	P41863 calliphora
19	2	18.2	8	LM12_LUEMI	P22496 locusta mig
20	2	18.2	8	LPMS_STAEP	P23211 staphylococ
21	2	18.2	8	NS3_MYCTU	P81152 mycobacteri
22	2	18.2	8	UC26_MAIZE	P50632 zea mays (m
23	2	18.2	8	UF06_MOUSE	P18644 mus musculu
24	2	18.2	8	WPL_PEARF	P83195 perkinsus a
25	2	18.2	9	DSIP_RABIT	P01158 oryctolagus
26	2	18.2	9	FAR1_CALVO	P41856 calliphora
27	2	18.2	9	FAR2_CALVO	P41857 calliphora
28	2	18.2	9	FAR3_CALVO	P41858 calliphora
29	2	18.2	9	FAR3_PENMO	P84118 penaeus men
30	2	18.2	9	FAR4_CALVO	P41859 calliphora
31	2	18.2	9	FAR4_PENMO	P84319 penaeus men
32	2	18.2	9	FAR5_AKAPL	P43170 ascaris suu
33	2	18.2	9	FAR5_CALVO	P41860 calliphora

P82661	panagrellus
P41861	calliphora
P83279	macrobrachi
P41862	calliphora
P41865	calliphora
P41868	calliphora
P19346	erythrocebu
P19344	papio anubi
P19343	papio hamad
P19342	theropithec
P83350	sarcophaga
P82992	rhodopseu
P36884	staphylococ
P41492	sarcophaga
P19095	mustelus ca
P24047	stomopneute
P101255	sus scrofa
P81736	leucophaea
P31929	homo sapien
P31934	homo sapien
P81355	clostridium
P81731	heiiicoverpa
P80331	oncorhynch
P80431	rattus norv
P80432	rattus norv
P80336	oryctolagus
P11735	locusta mig
P81012	schizaphis
P41867	calliphora
P01358	homo sapien
P02728	homo sapien
P09039	leucophaea
P80466	comamonas t
P49325	bacillus th
Q10997	halocynthia
P19118	nicotiana p
P81738	leucophaea
P81739	leucophaea
P81741	leucophaea
P32118	homo sapien
P38007	chlamydia t
P80717	dictyoglomu
P83147	bacteroides
P30424	bothrops in
P81095	bacillus su
P56571	rattus norv
P41864	calliphora
P81018	oncorhynch
P04428	leucophaea
P36885	periplaneta
P00580	klebsiella
P01163	homo sapien
P49820	canis fami
P55173	pseudomonas
P41837	periplaneta
P80464	comamonas t
P13179	chandipura
P83328	oncorhynch
Q05055	tetrahymena
P56246	litorea xan
P83327	oncorhynch
P47733	locusta mig
O22426	lotus japon
Q46490	clover yell
Q47881	elm yellows
P80863	bacillus su
P80852	methanosarc
P31144	homo sapien
P04561	cyprinus ca
P15987	glycine max
P82386	litorea ran
P82387	litorea ran

107	13	18.2	3	18.2	242771	use at 443	180	2	18.2	15	1	PLCB_VIG	P20034	sus scrofa
108	13	18.2	2	18.2	P01754	leucophaea	181	2	18.2	15	1	PLAS_MICAE	P10625	microcystis
109	13	18.2	2	18.2	P01759	leucophaea	182	2	18.2	15	1	RL11_STRAU	Q9X520	streptomyces
110	13	18.2	2	18.2	P45618	capitis fami	183	2	18.2	15	1	RS20_BACST	P59681	bacillus st
111	13	18.2	2	18.2	P10398	aplysia ca	184	2	18.2	15	1	RS6_BACST	P59682	bacillus st
112	13	18.2	2	18.2	P17235	vespa acut	185	2	18.2	15	1	SCUT_RAT	P01155	rattus norv
113	13	18.2	2	18.2	P17235	vespa acut	186	2	18.2	15	1	TAL_TREBR	P34070	tremella br
114	13	18.2	2	18.2	P17235	vespa acut	187	2	18.2	15	1	TRPA_LEUMA	P81753	leucophaea
115	13	18.2	2	18.2	P17235	vespa acut	188	2	18.2	15	1	UC11_MAIZE	P80607	zea mays (m
116	13	18.2	2	18.2	P17235	vespa acut	189	2	18.2	15	1	UC14_MAIZE	P80620	zea mays (m
117	13	18.2	2	18.2	P17235	vespa acut	190	2	18.2	15	1	UC17_MAIZE	P80623	zea mays (m
118	13	18.2	2	18.2	P17235	vespa acut	191	2	18.2	15	1	UC25_MAIZE	P80631	zea mays (m
119	13	18.2	2	18.2	P17235	vespa acut	192	2	18.2	15	1	UC27_MAIZE	P80633	zea mays (m
120	13	18.2	2	18.2	P17235	vespa acut	193	2	18.2	15	1	UC28_MAIZE	P80634	zea mays (m
121	13	18.2	2	18.2	P20011	truncatus ve	194	2	18.2	15	1	UN04_PINPS	P81673	pinus pinas
122	13	18.2	2	18.2	P41559	duclius rati	195	2	18.2	15	1	URE1_MORMO	P17337	morganelia
123	13	18.2	2	18.2	P41559	duclius rati	196	2	18.2	15	1	URE2_MORMO	P17338	morganelia
124	13	18.2	2	18.2	P49624	capitis fami	197	2	18.2	15	1	VORA_MEITM	P80907	methanobact
125	13	18.2	2	18.2	P20118	pisum sativ	198	2	18.2	15	1	YAA3_RHOPA	Q02006	rhodospseud
126	13	18.2	2	18.2	P57229	pisum sativ	199	2	18.2	15	1	ACT_THUAL	P18691	thunmus alb
127	13	18.2	2	18.2	P47716	mycoplasma	200	1	9.1	8	1	ACT_CARMA	P80709	carcinus ma
128	13	18.2	2	18.2	P44552	ash yellow	201	1	9.1	8	1	AKHG_GRYBI	P14086	gryllus bim
129	13	18.2	2	18.2	P56921	rattus tempor	202	1	9.1	8	1	AKH_TABAT	P14595	tabanus atr
130	13	18.2	2	18.2	P49948	homo sapien	203	1	9.1	8	1	AL12_CARMA	P81815	carcinus ma
131	13	18.2	2	18.2	P35586	liamulus po	204	1	9.1	8	1	AL15_CARMA	P81818	carcinus ma
132	13	18.2	2	18.2	P17236	vespa acut	205	1	9.1	8	1	AL17_CARMA	P81820	carcinus ma
133	13	18.2	2	18.2	P56923	canus canis	206	1	9.1	8	1	AL18_CARMA	P81821	carcinus ma
134	13	18.2	2	18.2	P14474	mandrillus	207	1	9.1	8	1	AL11_CYDPO	P82152	cydia pomon
135	13	18.2	2	18.2	P21155	sus scrofa	208	1	9.1	8	1	AL13_CYDPO	P82154	cydia pomon
136	13	18.2	2	18.2	P41303	pacallius li	209	1	9.1	8	1	AL14_CALVO	P41840	calliphora
137	13	18.2	2	18.2	P29399	ditrogonus	210	1	9.1	8	1	AL14_CYDPO	P82155	cydia pomon
138	13	18.2	2	18.2	P51577	pellistes ja	211	1	9.1	8	1	AL15_CALVO	P41841	calliphora
139	13	18.2	2	18.2	P21654	vespa basal	212	1	9.1	8	1	AL15_CYDPO	P82156	cydia pomon
140	13	18.2	2	18.2	P01516	vespa acut	213	1	9.1	8	1	AL16_CYDPO	P82157	cydia pomon
141	13	18.2	2	18.2	P01516	vespa acut	214	1	9.1	8	1	AL17_CARMA	P81809	carcinus ma
142	13	18.2	2	18.2	P04235	vespa acut	215	1	9.1	8	1	AL18_CARMA	P81811	carcinus ma
143	13	18.2	2	18.2	P17248	vespa acut	216	1	9.1	8	1	ANG2_BOTJA	Q10582	bothrops ja
144	13	18.2	2	18.2	P01515	vespa acut	217	1	9.1	8	1	B4K_PORGI	P81886	porphyromon
145	13	18.2	2	18.2	P01515	vespa acut	218	1	9.1	8	1	CAD1_ENTIA	P13268	enterococcu
146	13	18.2	2	18.2	P51493	serotus beqa	219	1	9.1	8	1	CKKN_MACED	P30369	macropus eu
147	13	18.2	2	18.2	P45428	glucosid brax	220	1	9.1	8	1	CKW2_CONPU	P58785	canus purpu
148	13	18.2	2	18.2	P45428	glucosid brax	221	1	9.1	8	1	CKW2_RAT	P80430	rattus norv
149	13	18.2	2	18.2	P22093	pruned pea	222	1	9.1	8	1	CPH1_ENTIA	P13269	enterococcu
150	13	18.2	2	18.2	P41160	prunus arce	223	1	9.1	8	1	FAR1_PANRE	P41872	panagrellus
151	13	18.2	2	18.2	P11760	atriaria ful	224	1	9.1	8	1	FAR1_PENMO	P83316	penaeus mon
152	13	18.2	2	18.2	P42479	Schistocerca	225	1	9.1	8	1	FAR2_MACRS	P83275	macrobrachi
153	13	18.2	2	18.2	P42479	Schistocerca	226	1	9.1	8	1	FAR3_HOMAM	P41486	homarus ame
154	13	18.2	2	18.2	P42479	Schistocerca	227	1	9.1	8	1	FAR4_HOMAM	P41487	homarus ame
155	13	18.2	2	18.2	P42479	Schistocerca	228	1	9.1	8	1	FAR7_MACRS	P83277	macrobrachi
156	13	18.2	2	18.2	P42479	Schistocerca	229	1	9.1	8	1	FAR7_ASCSU	P43171	ascaris suu
157	13	18.2	2	18.2	P42479	Schistocerca	230	1	9.1	8	1	FUSS_FUSSO	P81010	fusarium so
158	13	18.2	2	18.2	P42479	Schistocerca	231	1	9.1	8	1	GLUR_HUMAN	P02729	homo sapien
159	13	18.2	2	18.2	P42479	Schistocerca	232	1	9.1	8	1	LCK1_LEUMA	P21140	leucophaea
160	13	18.2	2	18.2	P42479	Schistocerca	233	1	9.1	8	1	LCK2_LEUMA	P21141	leucophaea
161	13	18.2	2	18.2	P42479	Schistocerca	234	1	9.1	8	1	LCK3_LEUMA	P21142	leucophaea
162	13	18.2	2	18.2	P42479	Schistocerca	235	1	9.1	8	1	LCK4_LEUMA	P21143	leucophaea
163	13	18.2	2	18.2	P42479	Schistocerca	236	1	9.1	8	1	LCK5_LEUMA	P19987	leucophaea
164	13	18.2	2	18.2	P42479	Schistocerca	237	1	9.1	8	1	LCK6_LEUMA	P19988	leucophaea
165	13	18.2	2	18.2	P42479	Schistocerca	238	1	9.1	8	1	LCK7_LEUMA	P19989	leucophaea
166	13	18.2	2	18.2	P42479	Schistocerca	239	1	9.1	8	1	LCK8_LEUMA	P19990	leucophaea
167	13	18.2	2	18.2	P42479	Schistocerca	240	1	9.1	8	1	LCK9_LEUMA	P13049	leucophaea
168	13	18.2	2	18.2	P42479	Schistocerca	241	1	9.1	8	1	LCK10_LEUMA	P15507	bos laurus
169	13	18.2	2	18.2	P42479	Schistocerca	242	1	9.1	8	1	NPB_BOVIN	P82455	orionectes
170	13	18.2	2	18.2	P42479	Schistocerca	243	1	9.1	8	1	NPB_BRANA	P81707	brassica na
171	13	18.2	2	18.2	P42479	Schistocerca	244	1	9.1	8	1	PKK2_PERAM	P82692	periplaneta
172	13	18.2	2	18.2	P42479	Schistocerca	245	1	9.1	8	1	PKK3_PERAM	P82618	periplaneta
173	13	18.2	2	18.2	P42479	Schistocerca	246	1	9.1	8	1	RPHL_PANBO	P08939	pandalus bo
174	13	18.2	2	18.2	P42479	Schistocerca	247	1	9.1	8	1	RS1_ERWCH	P37985	erwinia chr
175	13	18.2	2	18.2	P42479	Schistocerca	248	1	9.1	8	1	RS7_MYCIT	P33564	mycobacteri
176	13	18.2	2	18.2	P42479	Schistocerca	249	1	9.1	8	1	RT34_BOVIN	P82929	bos laurus
177	13	18.2	2	18.2	P42479	Schistocerca	250	1	9.1	8	1	SC09_RAT	P56575	rattus norv
178	13	18.2	2	18.2	P42479	Schistocerca	251	1	9.1	8	1	UPAL_HUMAN	P30687	homo sapien
179	13	18.2	2	18.2	P42479	Schistocerca	252	1	9.1	8	1	UPAL_HUMAN	P40096	homo sapien

253	8	9.1	8	1	VLGQ_RSV20	P81780 herpes simp	326	1	9.1	10	1	CAER_LITXA	P56264 litoria xax
254	9	9.1	9	1	ALLO_CARMA	P81813 carcinus ma	327	1	9.1	10	1	CATB_SHEEP	P83205 ovis aries
255	9	9.1	9	1	ALLO_CARMA	P81814 carcinus ma	328	1	9.1	10	1	COXA_ONCMY	P80328 oncorhynch
256	9	9.1	9	1	ALLO_CHERE	P82678 chlamydomo	329	1	9.1	10	1	COXK_ONCMY	P80332 oncorhynch
257	9	9.1	9	1	BS43_SERFL	P84375 serralia pl	330	1	9.1	10	1	COXQ_SHEEP	P80337 ovis aries
258	9	9.1	9	1	BYK_GLAPA	P81837 elostridius	331	1	9.1	10	1	ESL_LACCA	P81758 lartobacill
259	9	9.1	9	1	BYK_GLAPA	P82550 eucetius ma	332	1	9.1	10	1	FAK2_PENMO	P84317 penaeus mon
260	9	9.1	9	1	CONL_CORGE	P85486 comus gearr	333	1	9.1	10	1	FAK5_MACRS	P83278 macrobrachi
261	9	9.1	9	1	CONL_CORGE	P85487 comus stria	334	1	9.1	10	1	FAK6_PANRE	P82660 panayrelus
262	9	9.1	9	1	COWO_CINVE	P84047 comus ventr	335	1	9.1	10	1	FAK7_MACRS	P82680 macrobrachi
263	9	9.1	9	1	COXE_CHAPS	P82975 trioncus abe	336	1	9.1	10	1	FARP_LOCOMI	P83553 locusta mig
264	9	9.1	9	1	DNF1_LOCOMI	P81639 locusta mig	337	1	9.1	10	1	FARP_MANSE	P83523 manduca sex
265	9	9.1	9	1	FAK2_PANRE	P81874 panagrellus	338	1	9.1	10	1	FARP_MYTED	P42560 mytilus edu
266	9	9.1	9	1	FAK3_MACRS	P43276 macrobrachi	339	1	9.1	10	1	FIBB_CERST	P43537 caratotheri
267	9	9.1	9	1	FAK5_PENMO	P83620 penaeus mon	340	1	9.1	10	1	CONI_ALLMI	P37041 alligator m
268	9	9.1	9	1	FAK6_MACRS	P81261 macrobrachi	341	1	9.1	10	1	CONI_CHEPR	P80677 cheilosoma
269	9	9.1	9	1	FAK9_ASRSO	P43174 ascaris su	342	1	9.1	10	1	GONI_CLUPA	P81749 clupea pall
270	9	9.1	9	1	FARP_CALST	P83495 callinectes	343	1	9.1	10	1	GONI_PETMA	P804378 petromyzon
271	9	9.1	9	1	FIBB_MACFO	P49345 macaca lusc	344	1	9.1	10	1	GON2_CHEPR	P80678 cheilosoma
272	9	9.1	9	1	FLA2_TKHEH	P80159 treponema h	345	1	9.1	10	1	GON2_CHICK	P37043 gallus gall
273	9	9.1	9	1	ROTO_KLEAE	P42481 klebsiella	346	1	9.1	10	1	GON3_ONCKE	P37043 gallus gall
274	9	9.1	9	1	ISAE_CYPICA	P42593 cyprinus ca	347	1	9.1	10	1	GON3_PETMA	P37043 gallus gall
275	9	9.1	9	1	KNLS_B-WVA	P83058 bombina var	348	1	9.1	10	1	GONI_SQUAC	P30948 petromyzon
276	9	9.1	9	1	LITR_LITLAI	P80945 litoria aur	349	1	9.1	10	1	GRP_RANRI	P23260 rana ridibu
277	9	9.1	9	1	LITR_PHYPS	P80946 phyllomedus	350	1	9.1	10	1	GRS9_BACSU	P80243 bacillus su
278	9	9.1	9	1	LMIF_LORNY	P41759 locusta mig	351	1	9.1	10	1	HTF1_ROMMI	P81810 romalea mic
279	9	9.1	9	1	LMF3_LORNY	P41489 locusta mig	352	1	9.1	10	1	HTF2_CARMO	P11385 carausius m
280	9	9.1	9	1	MUSF_CLYCA	P41985 clypeaster	353	1	9.1	10	1	HTF_HELZE	P16353 heliothis z
281	9	9.1	9	1	MUSH_CLYCA	P41985 clypeaster	354	1	9.1	10	1	HTF_NAUCI	P10939 nauphoeta c
282	9	9.1	9	1	NEPU_CAYRE	P44952 cavia porc	355	1	9.1	10	1	HTF_TABAT	P14596 tabanus atr
283	9	9.1	9	1	NEPU_HUMAN	P44956 cavia porc	356	1	9.1	10	1	LABA_JATMU	P13270 jatropa mu
284	9	9.1	9	1	OXYA_S-YIVA	P42977 homo sapien	357	1	9.1	10	1	LCMS_LEUMA	P21144 leucophaea
285	9	9.1	9	1	OXYA_S-YIVA	P42999 scyllorhinu	358	1	9.1	10	1	LPK2_LOCOMI	P41488 locusta mig
286	9	9.1	9	1	OXYF_S-YIVA	P42997 scyllorhinu	359	1	9.1	10	1	MALE_KLEPN	O05564 klebsiella



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QY 1 AEGG 4
DB 9 AEGG 12

RESULT 2
DL_NEPNG STANDARD: PRT: 9 AA.
AC P24815;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Gastrin/cholecystokinin-like peptide 9L
OS Nephrops norvegicus (Norway lobster)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Nephrops
GX NCBI_TaxID=6829;
FN [1]
RP SEQUENCE
KC TISSUE=Stomach;
RX MEDLINE=92082847; PubMed=1747338;
RA Favrel P., Kegel G., Sedlmeyer D., Kellier R., van Kemmoudt A.;
RT "Structure and biological activity of crustacean gastrointestinal
RT peptides identified with antibodies to gastrin/cholecystokinin.";
RL Biochimie 73:1233-1239(1991);
CC -!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
LR PIR: S47432; S47432.
KW Hormone.
SQ SEQUENCE 9 AA: 1038 MW: 606279CAG68787B CRC64;

Query Match 27.3%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 2 EGG 4

RESULT 4
NEF_HV128 STANDARD: PRT: 9 AA.
AC P12481;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (c-act) (fragment).
GN NEF.
OS Human immunodeficiency virus type-1 (ZM4 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
GX NCBI_TaxID=11691;
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3355517;
RA Yairino J., Josephs S.F., Reitz M.S. Jr., Zairany D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1.";
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
CC activities. It seems to down-regulate the CD4(T4) antigen.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.

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CC EMBL: J03453; AAA44687.1; -
DR HIV; J03653; NEFSJY1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT NON_TER 5 9
SQ SEQUENCE 9 AA: 967 MW: 319CB325A3733878 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 2 GSK 4

RESULT 4
COXO_THUOB STANDARD: PRT: 10 AA.
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
GX NCBI_TaxID=8241;
FN [1]
RP SEQUENCE.
KC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
DR PIR: S77990; S77990.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1059 MW: 126DE76768781DCB CRC64;

Query Match 27.3%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3
DB 4 AEG 6

RESULT 5
PKCL_CARMO STANDARD: PRT: 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPR-1-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoides;
OC Heteronemidae; Carausius.

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GN NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC Tissue-corpora cardiaca;
RA Predel R., Kellner R., Gaele S.;
RT "Myotropic neuropeptides from the retroectoderm complex of the stick
insect, Carausius morosus (Phasmatodea: Isopodomorpha)";
RL Eur. J. Entomol. 96:275-278(1999);
CC 1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTIONS; ACTIVITY
CC 1- (MYOTROPIC ACTIVITY);
CC 1- MASS SPECTROMETRY: MW: 2255; METHOD=RAPI;
CC 1- SIMILARITY: BELONGS TO THE PEPTIDIN FAMILY;
DR INTERPLOT: IPR001484; PYROKININ;
DR PROSITE: PS00539; PYROKININ; FALSE NEG.;
KW Neuropeptide; Amidation; Pyrokinin;
FT MOLECULES 11
SQ SEQUENCE 11 AA: 1236 MW: 265225EBB4501AB CR664;

Query Match 27.3% Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 1
2 EGG 4

RESULT 5
RS19_TUBP
ID RS19_TUBP STANDARD: PRI: 12 AA.
DT 10-MAY-2000 (Rel. 39, Created)
BT 10-MAY-2000 (Rel. 39, Last sequence update)
DF 28-FEB-2003 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S19 (Fragment);
GN RPS19 OR RPS19;
OS Tomato big bud phytoplasma;
NC Bacteria; Firmicutes; Mollicutes; Actinobacteriales;
OC Actinobacteriales; Mollicutes; Actinobacteriales;
GX NCBI_TaxID=35770;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94350802; PubMed-8071178;
RA Gundersen D.E., Lee T.M., Kehler S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmids): a basis for
their classification";
RL J. Bacteriol. 176:5244-5254(1994);
CC 1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S 3 LEAF LINDS STRONGLY
CC 1- TO THE 16S RIBOSOMAL RNA (BY SIMILARITY);
CC 1- SIMILARITY: BELONGS TO THE SHIP FAMILY OF RIBOSOMAL PROTEINS.
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CC or send an email to license@isb-sib.ch);
DR HAMAP: L27034; AAA83952.1;
DR HAMAP: MF_00531; 1;
DR InterPro: IPR002222; Ribosomal S19;
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL;
KW Ribosomal protein; rRNA-binding;
FT NON_TER 1
SQ SEQUENCE 12 AA: 1470 MW: 4CC88BE98333A3 CR664;

Query Match 27.3% Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKM 9
DB 1

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DB 7 KKM 9

RESULT 7
V14K_WSSV
ID V14K_WSSV STANDARD: PRI: 12 AA.
AC P82006;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE 14.5 kDa structural polyprotein (Fragment);
OS White spot syndrome virus (WSSV);
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae;
GX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE: 20214217; PubMed:10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
virus";
RL Arch. Virol. 145:263-274(2000);
CC 1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12
SQ SEQUENCE 12 AA: 1242 MW: 24B8DE4FFD21A338 CR664;

Query Match 27.3% Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKG 5
DB 4 GKG 6

RESULT 8
TAL3_TREME
ID TAL3_TREME STANDARD: PRI: 13 AA.
AC P01370;
DT 21-JUL-1986 (Rel. 01, Created);
DT 21-JUL-1986 (Rel. 01, Last sequence update);
DT 01-NOV-1991 (Rel. 20, Last annotation update);
DE Tremmerogen A-13;
OS Tremella mesenterica (Jelly fungus);
NC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella;
GX NCBI_TaxID=5217;
RN [1]
RP SEQUENCE.
RA Sakaqami Y., Yoshida M., Isogai A., Suzuki A.;
RT "Peptide sex hormones inducing conjugation tube formation in
RT compatible mating-type cells of Tremella mesenterica.";
RL Science 212:1525-1527(1981);
CC 1- FUNCTION: TREMEROGEN A-13 IS PRODUCED BY THE A MATING-TYPE CELLS
CC AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
DR PIR: A01641; JTJG3;
KW Lipoprotein; Prenylation; Pheromone;
FT LIPID 13
SQ SEQUENCE 13 AA: 1204 MW: 680304A9697BA864 CR664;

Query Match 27.3% Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 1 EGG 3

RESULT 9
FIBA_HORSE
ID FIBA_HORSE STANDARD: PRI: 14 AA.
AC P14452;

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BT 01 JAN-1990 (Rel. 13, Created)
DI 01-JAN-1990 (Rel. 13, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN EGA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID:9796;
KN [1]
KP SEQUENCE.
RA Blomback B., Blomback M., Gresslind N.
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SET COTE.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 14 FIBRINOPEPTIDE A.
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1517 MW: 4594966.024627 Da;
Query Match 27.3% Score 3: DB 13; Length 14;
Best Local Similarity 100.0% Pred No. 1.7e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FGG 4
DB 9 EGS 11
RESULT 10
MAST_PART:
ID MAST_PART: STANDARD: PRT: 14 AA.
AC P42716;
DI 01-NOV-1995 (Rel. 32, Created)
DI 01-NOV-1995 (Rel. 32, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparsin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hymenoptera;
OC Neoptera; Endopterygota; Hymenoptera; Chalcidoidea; Vespinoidea;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID: 31921;
KN [1]
KP SEQUENCE.
RA Tissi Vencel;
RT "Isolation and sequential analysis of peptides in the venom of
RT Parapolybia indica."
RL Fisiol. Indus. 39:105-111(1988).
CC -1- FUNCTION: Mast cell degranulating peptide. Activates 2 proteins
CC that couple to phospholipase C.
KW Mast cell degranulation; Activation.
FT RES 14 14 AMILIPIN.
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1619 MW: 163766.061604 Da;
Query Match 27.3% Score 3: DB 13; Length 14;
Best Local Similarity 100.0% Pred No. 1.7e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KKM 9
DB 4 KKM 5
RESULT 11

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MCRX_METTM STANDARD: PRT: 14 AA.
ID MCRX_METTM
AC P58815;
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.1.1) (MCR II
DE alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriia; Methanothermobacter.
OX NCBI_TaxID:75929;
KN [1]
KP SEQUENCE.
RA MEDLINE:91099370; PubMed 2269306;
RA Rospert S., Linder D., Eilermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in
RT Methanobacterium thermoautotrophicum strain Marburg and delta H.":
RL Eur. J. Biochem. 194:871-877(1990).
CC -1- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreosine phosphate
CC to methane and an heterodisulfide.
CC -1- CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP -> CH(4) + COM-S-S-HTP.
CC -1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
CC TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
CC Porphyrinoid.
CC -1- PATHWAY: Methanogenesis; last step.
CC -1- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -1- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CC CONTAINS MOSTLY MCR I.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT NON_TER 14 14
FT SEQUENCE 14 AA: 1718 MW: D317CCC562F00E29 CRC64;
Query Match 27.3% Score 3: DB 13; Length 14;
Best Local Similarity 100.0% Pred No. 1.7e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKM 7
DB 12 KKM 14
RESULT 12
FIBA_AKAP1
ID FIBA_AKAP1 STANDARD: PRT: 15 AA.
AC P22801;
DI 01-NOV-1987 (Rel. 12, Created)
DI 01-OCT-1989 (Rel. 12, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Anseriformes; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID:8839;
KN [1]
KP SEQUENCE.
RA MEDLINE:85168194; PubMed-3984613;
RA Min Y., Ping Z., Yao S.
RT "Purification and primary structures of duck fibrinopeptides A and
RT B."
RL Sin. Ser. B. Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THE BRIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

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QC      RESPONSIBLE FOR THE FORMATION OF THE SPOT COL.
KW      PIR: J10111 J10101;
KW      Blood coagulation; Plasmas; Fibrinogen; Carboxypeptidase;
FT      PEPTIDE      1 15
FT      MOD_RES      1 1
FT      NON_TER      15 15
SQ      SEQUENCE      15 AA: 1580 MW: 127465.484 Da; 164.3604,
Query Match: 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 EGG 4
DB      1 EGG 12
RESULT 14
ALL9_CARMA
ID      ALL9_CARMA      STANDARD:      PRT:      15 AA.
AC      P81287;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Oncorhynchus mykiss (Rainbow trout) (Salmo salar L.)
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OT      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX      NCBI_TaxID:8022;
RN      [1]
RP      TISSUE: SKIN;
SA      Fernandes J.M.O., Smith V.J., Kemp G.J.
SC      Purification and N-terminal sequencing of a 15 kDa antifibrinolytic
      peptide from skin secretions of rainbow trout.
      Submitted (MAY 2002) to the SWISS Prot data bank.
      ** FUNCTION: Has antibacterial activity against gram positive
      bacteria: P. citreus.
      ** SUBCELLULAR LOCATION: Secreted.
      ** TISSUE SPECIFICITY: SKIN.
      ** GO:0005576; C:extracellular; NAS.
      ** GO:0005795; F:antimicrobial; peptide activity; NAS.
      ** GO:0006095; P:phenotypic metabolic process; NAS.
      ** Antibiotic.
KW      UNSURE      4 4
FT      UNSURE      7 9
FT      NON_TER      15 15
SQ      SEQUENCE      15 AA: 1601 MW: 4522.296 Da; 164.3604,
Query Match: 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 GKK 6
DB      4 GKK 5
RESULT 14
9C20_MAIZE
ID      9C20_MAIZE      STANDARD:      PRT:      15 AA.
AC      P81626;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Unknown protein from 20-page of electrophoretogram (Spot 436)
      (Fragment).
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OT      Spermatophyta; Magnoliophyta; Equisetidae; Liliaceae;
OC      Poaceae; Pooideae; Panicoideae; Andropogoneae.
OX      NCBI_TaxID:4577;

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RN      SEQUENCE.
KW      TISSUE: Neuroptera;
KW      Touzel P., Richard F., Marin C., Damerval C., Huet J.-C.,
      Pernollet J.-C., Zivy M., de Vienne D.;
      "The maize two dimensional gel protein database: towards an integrated
      genome analysis program";
      1999; Appl. Genet. 9:197-205(1996).
KW      ** MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKN/AN
      PROTEIN IS 6.1; ITS MW IS 45.3 KDa.
      ** SIMILARITY: TO ALA-ME; SYNTHETASES.
OR      MAIZE_2DPAGE_P81626; C:NEUROPTILE.
OR      MAIZE_DB; 123952;
FT      NON_TER      15 15
FT      NON_TER      15 15
SQ      SEQUENCE      15 AA: 1597 MW: 426610.156 Da; 164.3604,
Query Match: 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 EGG 4
DB      1 EGG 12
RESULT 15
ALL16_CARMA
ID      ALL16_CARMA      STANDARD:      PRT:      8 AA.
AC      P81819;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Carcinus maenas (Common shore crab) (Green crab).
OS      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Brachyura;
OT      Eubrachyura; Portunidea; Portunidae; Carcinus.
OX      NCBI_TaxID:6759;
RN      [1]
RP      SEQUENCE.
KW      TISSUE: Cerebral ganglion, and thoracic ganglion;
KW      MESLINE-9812191; EMBL-9461295;
RA      Dave H., Johnson A.H., Maestro J.L., Scott A.G., Jaros P.P.,
      Thorpe A.;
      "Isolation and identification of multiple neuropeptides of the
      allatostatins superfamily in the shore crab Carcinus maenas";
      Eur. J. Biochem. 250:727-734(1997).
CC      ** FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
      ** SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW      Neuropeptide; Amidation; Multigene family.
FT      MOD_RES      5 8
FT      AMIDATION.
SQ      SEQUENCE      8 AA: 613 MW: 70286.845 Da; 164.3604,
Query Match: 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 GG 4
DB      1 GG 2
RESULT 16
ALL19_CARMA
ID      ALL19_CARMA      STANDARD:      PRT:      8 AA.
AC      P81812;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Carcinus maenas (Common shore crab) (Green crab).
OS      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
[1]
KP SEQUENCE FROM N.A.
KC STRAIN=968;
RX MEDLINE=9104.730; PubMed=2233255;
RA Ross J.L., Eady E.A., Cove J.H., Gunthrie W.J., Baumberg S.,
RA Weatton J.C.;
RT "Inducible erythromycin resistance in staphylococci is encoded by a
RL member of the ATP-binding transport supergene family."
RL Mol. Microbiol. 4:1207-1214(1992);
CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC PROTEIN.
CC -----
CC This SWISS-PROT entry is copyrighted. It is provided through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announc/
CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL: X52085; CAA36303.1; -.
DR PIR: S11157; LFSAME.
KW Leader peptide; Plasmid.
SQ SEQUENCE 8 AA; 937 MW; FA37440E5F6C1A67B094.

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 5 MR 6

RESULT 23
NS3_MOUSE
ID NS3_MOUSE STANDARD; PRT; 8 AA.
AC P81152;
DT 15-JUN-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 15-OCT-2003 (Rel. 40, Last annotation update)
DE 40 kDa non-secretory protein 3 (fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
[1]
RP SEQUENCE.
RX MEDLINE=95069907; PubMed 7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:745-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 919 MW; 8D5DC4E793C24C75764

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RA 11
DB 6 RA 7

RESULT 24
UC26_MOUSE
ID UC26_MOUSE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
[1]
RP SEQUENCE.
RX TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Motin C., Damerval C., Huet J.-C.;
RA Pernoillet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 1 AE 2

RESULT 23
CF06_MOUSE
ID CF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE.
RX TISSUE:Fibroblast;
RX MEDLINE=95069907; PubMed 7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:745-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4
DB 5 GG 6

RESULT 24
WPI_PERAT
ID WPI_PERAT STANDARD; PRT; 8 AA.
AC P83195;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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28-FEB-2003 (Rel. 41, Last annotation update)  
DE Wall protein-1 (PWP-1) (Fragment).  
OS Perkinsus atlanticus.  
OC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.  
OX NCBI\_TaxID-106964;  
RN [1]  
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RX MEDLINE-22044350; PubMed-12049410;  
RA Montes J.F., Durfort M., Llado A., Garcia Varela J.,  
RT "Characterization and immunolocalization of a 24kD proteinaceous  
RT component of the cell wall of the protozoan parasite Perkinsus  
RT atlanticus.";  
RZ Parasitology 124:477-484(2002).  
CC -!- FUNCTION: Is a major protein component of the cell wall. May play  
CC a key role in the organization of the cell wall and in promoting  
CC the survival of this parasite.  
CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell  
CC wall components.  
CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental  
CC stages.  
KW Cell wall.  
FT NON\_TER  
SQ SEQUENCE 8 AA: 765 MW: 81787D087B1AAB16 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EG 3  
DB 4 EG 5  
RESULT 26  
DSIP-RAB17  
ID DSIP-RAB17 STANDARD; PRT; 9 AA.  
AC P01158;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DI 15-OCT-2001 (Rel. 40, Last annotation update)  
DE Delta sleep-inducing peptide (DSIP).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID-9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE-77185424; PubMed-862709.  
RA Monnier M., Didier L., Gachet R., Maier P.F., Tobler H.J., Monnier M.,  
RA Schoenenberger G.A.;  
RT "The delta sleep inducing peptide (DSIP): Comparative properties of  
RT the original and synthetic nonapeptide.";  
RL Experientia 33:548-552(1977).  
RN [2]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE-79054421; PubMed-568769;  
RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilsch K., Monnier M.;  
RT "The delta EEG (sleep)-inducing peptide (DSIP): X-ray amino-acid  
RT analysis, sequence, synthesis and activity of the nonapeptide.";  
RL Pflügers Arch. 376:119-129(1978).  
RN [3]  
RP REVIEW.  
RX MEDLINE-87175129; PubMed-3556726;  
RA Graf M.V., Kastin A.J.;  
RT "Delta-sleep-inducing peptide (DSIP): an update.";  
RL Peptides 7:1165-1187(1986).  
CC -!- FUNCTION: WHEN INFUSED INTO THE MESOENCEPHALIC VENTRICLE OF  
CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND  
CC REDUCED MOTOR ACTIVITIES.  
CC -!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF  
CC CIRCULATING VENOUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC  
CC STIMULATION OF THE THALAMUS.  
CC -!- DATABASE: NAME-Protein Spotlight;

NOTE-Issue 8 of March 2001;  
WWW-<http://www.expasy.org/spotlight/articles/sptlt008.html>.  
DR PIR; A01422; GDRB.  
SQ SEQUENCE 9 AA: 849 MW: DDD365BDDAA8787D CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GG 4  
DB 4 GG 4  
RESULT 26  
FAR1-CALVO  
ID FAR1-CALVO STANDARD; PRT; 9 AA.  
AC P41856;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DI 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallipMRamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID-27454;  
RN [1]  
RP SEQUENCE.  
RX TISSUE-Rhotactic ganglion;  
RX MEDLINE-92196111; PubMed-1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callipMRamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
CC SALIVARY GLAND OF CALLIPHORA.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A41978; A41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9  
SQ SEQUENCE 9 AA: 1169 MW: 29D00699CAB6C6C7 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MR 10  
DB 7 MR 8  
RESULT 27  
FAR2-CALVO  
ID FAR2-CALVO STANDARD; PRT; 9 AA.  
AC P41857;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DI 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallipMRamide 2.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID-27454;  
RN [1]  
RP SEQUENCE.  
RX TISSUE-Thoracic ganglion;  
RX MEDLINE-92196111; PubMed-1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

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RA Rehfeld J.F., Thorpe A.;
KT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
KT neuropeptides (designated callifemr-famides) from the blowfly
KT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2325-2330(1992)
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR: H41978; H41978.
CC Neuropeptide; Amidation.
CC MOD.RES 9 9 AA: 25060699AB06-6A7 100.0%
SQ SEQUENCE 9 AA: 1128 MW: 25060699AB06-6A7 100.0%

Query Match 18.2% Score 2: DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 7 MR 8

RESULT 2/4
FAR4_PENMO STANDARD; PRT: 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created);
DT 01-NOV-1995 (Rel. 32, Last sequence update);
DT 01-NOV-1995 (Rel. 32, Last annotation update);
DE Callifemrfamide 3;
OS Calliphora vomitoria (Blue blowfly);
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Aestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN 11;
RP SEQUENCE.
KC TISSUE: Thoracic ganglion;
RX MEDLINE: 92196111; PubMed: 1549595;
RA Duve H., Jørgensen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
KT "Isolation, structure, and activity of the Met-Arg-Phe-NH2
KT neuropeptides (designated callifemr-famides) from the blowfly
KT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2325-2330(1992)
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR: H41978; H41978.
CC Neuropeptide; Amidation.
CC MOD.RES 9 9 AA: 25060699AB06-6A7 100.0%
SQ SEQUENCE 9 AA: 1114 MW: 25060699AB06-6A7 100.0%

Query Match 18.2% Score 2: DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 7 MR 8

RESULT 2/4
FAR3_PENMO STANDARD; PRT: 9 AA.
AC P41859;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE FMRFamide-like neuropeptide-FLP3 (AOPSRLRF amide);
OS Penaeus monodon (Penaeid shrimp);

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
GX NCBI_TaxID=6687;
RN 11;
RP SEQUENCE, AND MASS SPECTROMETRY.
KC TISSUE: Eye stalk;
RX MEDLINE: 21956277; PubMed: 11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
KT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
KT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002);
CC -1- SURCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW 1121.2; METHOD: MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
CC MOD.RES 9 9 AA: 1105 MW: CDD107340685A776 CRC64;
SQ SEQUENCE 9 AA: 1105 MW: CDD107340685A776 CRC64;

Query Match 18.2% Score 2: DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 5 MR 6

RESULT 30
FAR4_CALVO STANDARD; PRT: 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created);
DT 01-NOV-1995 (Rel. 32, Last sequence update);
DT 01-NOV-1995 (Rel. 32, Last annotation update);
DE Callifemrfamide 4;
OS Calliphora vomitoria (Blue blowfly);
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Aestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN 11;
RP SEQUENCE.
KC TISSUE: Thoracic ganglion;
RX MEDLINE: 92196111; PubMed: 1549595;
RA Duve H., Jørgensen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
KT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
KT neuropeptides (designated callifemr-famides) from the blowfly
KT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2325-2330(1992)
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR: H41978; H41978.
CC Neuropeptide; Amidation.
CC MOD.RES 9 9 AA: 1182 MW: 31730699CAB6D457 CRC64;
SQ SEQUENCE 9 AA: 1182 MW: 31730699CAB6D457 CRC64;

Query Match 18.2% Score 2: DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 7 MR 8

RESULT 31
FAR4_PENMO STANDARD; PRT: 9 AA.
AC P41859;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLH4 (SQSMACRF-amide)
OS Penaeus monodon (Penaeid shrimp)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca
OC Eucaridacea; Eucarida; Decapoda; Penaeodromachida; Penaeoidea;
OC Penaeidae; Penaeus
OX NCBI_TaxID=6687
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE: Eye-stalk;
RX MEDLINE=21956277; PubMed=17559675;
RA Sittlermagul P., Pupem J., Krumakson C., Langyant S.,
RA Chavisuthangkura P., Sittlermagul W., Jongs A.
RT "Seven novel FMRamide-like neuropeptide sequences from the eye-stalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 133B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW 1119.8; METHOD: MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 AA; 1052 MW; 340B065D06F74507264;
SQ SEQUENCE 9 AA; 1121 MW; DA0B0740658A776A7C64;

Query Match 18.2% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 5 MR 6

RESULT 32
FAR5_ASCSD STANDARD; PRT; 9 AA.
AC 343170;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRamide-like neuropeptide AF5.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae.
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE 95480462; PubMed=7451904
RA Cowden C., Stretton A.O.W.
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 AA; 1052 MW; 340B065D06F74507264;
SQ SEQUENCE 9 AA; 1052 MW; 340B065D06F74507264;

Query Match 18.2% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 5
DB 2 GK 3

RESULT 33
FAR5_CALVO STANDARD; PRT; 9 AA.
AC 341860;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 5.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Ephemeroptera; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE: Thoracic ganglion;
RX MEDLINE=9216611; PubMed=1549545;
RA Dure H., Johnson A.B., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.
RT "Isolation, structure, and activity of -Phe-Met-Arg-phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 AA; 1068 MW; 35D10699CAB6D867 CRC64;
SQ SEQUENCE 9 AA; 1068 MW; 35D10699CAB6D867 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MR 10
DB 7 MR 6

RESULT 34
FAR5_PANKE STANDARD; PRT; 9 AA.
AC 382661;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE FMRamide-like neuropeptide PF5 (AMRNALVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=5233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Mollet G.L., Marks N.J., Hallon D.W., Thomson D.P., Geary T.G.,
RA Maple A.G.
RT "Isolation, characterization and pharmacology of FMRamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 AA; 1077 MW; A0D112C72DB45406 CRC64;
SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DB45406 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 2 MR 4

RESULT 35
FAR6_CALVO STANDARD; PRT; 9 AA.
AC 341860;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MK 10
DB 7 MK 8

RESULT: 39
FARD_CALVO
ID FARD_CALVO STANDARD; PRT: 9 AA
AC P41968;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DE CalliPMPFamide 13.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID-27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE-92196111; PubMed-1549595;
KA Dave W., Johnson A.H., Sewell J.C., Scott A.G., Orchard L.,
KA Reitel D.J.F., Thorpe A.;
KT "Isolation, structure, and activity of Fibrinogen-Aquaphorin-2
KT neuropeptides (designated calliPMPFamides) from the blowfly
KT Calliphora vomitoria.";
KL Proc. Natl. Acad. Sci. U.S.A. 93:2325-2330(1996).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: D44787; D44787.
KW Neuropeptide: Amidation.
FT MOD_RES 9 AMIBALL-N.
SQ SEQUENCE 9 AA: 1028 MW: 22010699C87A86B8 C8764;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MK 10
DB 7 MK 8

RESULT 40
FIBB_ERYPA
ID FIBB_ERYPA STANDARD; PRT: 9 AA
AC P19346;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DE 28-FEB-2003 (rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Erythrocybus patas (Red quebon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
CC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID-9538;
RN [1]
RP SEQUENCE.
RX MEDLINE-85289140; PubMed-3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT quibons, and baboons.";
KL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MK 10
DB 7 MK 8

RESULT 41
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT: 9 AA
AC P19344;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DE 28-FEB-2003 (rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
CC Cercopitheciinae; Papio.
OX NCBI_TaxID-9555;
RN [1]
RP SEQUENCE.
RX MEDLINE-84161822; PubMed-6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
KL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GC 4
DB 7 GC 8

RESULT 42
FIBB_PAPHA

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CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR: D24180; D24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 1 9
SQ SEQUENCE 9 AA: 1020 MW: 69FE7879C732CB1B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GC 4
DB 7 GC 8

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RESULT 41
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT: 9 AA
AC P19344;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DE 28-FEB-2003 (rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
CC Cercopitheciinae; Papio.
OX NCBI_TaxID-9555;
RN [1]
RP SEQUENCE.
RX MEDLINE-84161822; PubMed-6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
KL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 3 EG 4

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RESULT 42
FIBB_PAPHA
ID FIBB_PAPHA STANDARD; PRT: 9 AA
AC P19346;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DE 28-FEB-2003 (rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Erythrocybus patas (Red quebon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
CC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID-9538;
RN [1]
RP SEQUENCE.
RX MEDLINE-85289140; PubMed-3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT quibons, and baboons.";
KL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 3 EG 4

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ID FIBR_PAPHA STANDARD: PRT: 9 AA.
AC P19342:
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment);
GN FGB;
OS Papio hamadryas (Hamadryas baboon);
OC Eukaryota; Metazoa; Chordata; Gracilaria; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio;
OX NCBI_TaxID=9557;
RN [1];
RP SEQUENCE:
RX MEDLINE=84161822; PubMed=6424621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT *Fibrinopeptides A and B of baboons (Papio anubas, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.*;
RL J. Biochem. 94:1973-1978(1983);
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NON-IDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR: E28854; E28854;
DR InterPro: IPR002181; Fibrinogen_C;
DR PROSITE: PS00514; FIBRIN_AC_C_DOMAIN; PARTIAL;
KW Blood coagulation; Plasma;
FT PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT NON TER 1 9
SQ SEQUENCE 9 AA: 1057 MW; 1057787227306 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 1
3 EG 4

RESULT 43
FIBR_THERG STANDARD: PRT: 9 AA.
AC P19342:
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment);
GN FGB;
OS Theropithecus gelada (Gelada baboon);
OC Eukaryota; Metazoa; Chordata; Gracilaria; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Theropithecus;
OX NCBI_TaxID=9565;
RN [1];
RP SEQUENCE:
RX MEDLINE=84161822; PubMed=6424621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT *Fibrinopeptides A and B of baboons (Papio anubas, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.*;
RL J. Biochem. 94:1973-1978(1983);
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NON-IDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR: E28854; E28854;
DR InterPro: IPR002181; Fibrinogen_C;
DR PROSITE: PS00514; FIBRIN_AC_C_DOMAIN; PARTIAL;
KW Blood coagulation; Plasma;
FT PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT NON TER 1 9
SQ SEQUENCE 9 AA: 977 MW; 1057787227306 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 1
3 EG 4

RESULT 44
FIBL_SARBU STANDARD: PRT: 9 AA.
AC P83350:
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Neb-FMRamide 1;
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga;
OX NCBI_TaxID=7385;
RN [1];
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen J., Mertens J., Clynen E., Baggerman G., Nichols R.,
RA Nulman K.J., Huybrechts R., De Loof A., Schoofs L.;
RT *Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor.*;
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002);
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1155 MW; 25810699CAB6C5A7 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 1
7 MR 6

RESULT 45
IPYR_RHOVI STANDARD: PRT: 9 AA.
AC P82992:
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (Phase) (Fragment);
GN PPA;
OS Riodopseudomonas viridis.

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CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC Hyphomicrobiales; Blastochloris.
CX NCBI_TaxID=1079;
RN [1]
RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RA Gomez R., Losada M., Serrano A.,
RA Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2O) -> 2 phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS PROTEIN IS:
CC 23 kDa.
CC -!- SIMILARITY: Belongs to the Pseu family.
DR HAWAP; M03049; -.
DR InterPro: IP001596; Pyrophosphatase.
DR PROSITE: PS00387; PPRASE; PARTIAL.
KW Hydrolyase.
FT NON_TER 9
FT PIR: B24362; B24362.
SQ SEQUENCE 9 AA: 1014 MW: 5864AA50DAAC34 CR664;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MR 10
DB 1 MR 2
RESULT 46
LPCA_STAAU STANDARD; PRT; 9 AA
AC P36804;
DT 01-JUN-1994 (rel. 29, Created)
DT 01-JUN-1994 (rel. 29, Last sequence update)
DT 01-OCT-1994 (rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus aureus.
CG Plasmid pSC86. Plasmid pSC87, Plasmid pSC88, and Plasmid pIP501.
CC Bacteria; Firmicutes; Bacillales; Staphylococcus
CX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus; STRAIN=406; PLASMID=pSC87.
RX MEDLINE=92027652; PubMed=1929426;
RA Schwartz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSC87 from Staphylococcus
RT aureus."
RL Antimicrob. Agents Chemother. 35:1061-1064(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus; PLASMID=pSC86;
RX MEDLINE=94288047; PubMed=1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSC86 from
RT Staphylococcus aureus."
RL J. Appl. Bacteriol. 72:289-293(1992)
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus; PLASMID=pIP501;
RX MEDLINE=86081739; PubMed=1805770;
RA Becknick K., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid pIP12."
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus; PLASMID=pIP501;
RX MEDLINE=94096867; PubMed=1461942;
RA Trieu-Cuot P., de Cespedes G., Horand F.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of

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RT the streptococcal plasmid pIP501.*;
RL Plasmid 28:272-275(1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M58515; AAA26612; .
CC EMBL: M58516; AAA16528; .
CC EMBL: X02872; CAA26530; .
CC EMBL: X60827; CAA43217; .
CC EMBL: X65462; CAA46454; .
CC PIR: B24362; B24362.
CC PIR: S30494; S30494.
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA: 1074 MW: 509CAH5AAB05B333 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KK 6
DB 2 KK 4
RESULT 47
NSKL_SARBU STANDARD; PRT; 9 AA.
AC P41492;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 01-FEB-1996 (rel. 33, Last annotation update)
DE Neosulfakinin; (NEB-SK-I)
OS Sarcophaga bullata (grey flesh fly) (Neobellieria bullata).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Eudopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Sarcophagidae; Sarcophaga.
CX NCBI_TaxID=7365;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083141; PubMed=1400667;
RA Fonagy A., Scholts L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata."
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -!- FUNCTION: MYOTROPIC PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Neuropeptide; Amidation; Sulfation.
FT MOD_RES 4 4 SULFATION (POTENTIAL).
FT MOD_RES 9 9 AMIDATION (POTENTIAL).
SQ SEQUENCE 9 AA: 1187 MW: 8B0A0691E86B5AAA CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MR 10
DB 7 MR 8
RESULT 48
SAMP_MUSCA STANDARD; PRT; 9 AA.
ID SAMP_MUSCA
AC P19095;

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01 NOV 1990 (Rel. 16, Created)  
 02-NOV 1990 (Rel. 16, Last sequence update)  
 03-FEB 2003 (Rel. 41, Last annotation update)  
 04 SERUM amyloid P-component (SAP) (Fragment)  
 05 Mustelus carls (Smooth doufin)  
 06 Eukaryote, Metazoa; Chordata; Vertebrata; Chondrichthyes  
 07 Elasmobranchii; Galeomorphii; Galeorhinidae; Chondrichthyes; Trachidae  
 08 Mustelus  
 09 NCBI\_TaxID 7812;  
 10 RN  
 11  
 12 SEQUENCE  
 13 MEDLINE=43160942; PubMed 43160942;  
 14 Kosey F.A., Takao T., Liu F.-Y.,  
 15 "Isolation and characterization of 14 major serum proteins from the  
 16 dogfish, Mustelus carls, C-reactive protein and amyloid P  
 17 component";  
 18 J. Biol. Chem. 258:3889-3894 (1983).  
 19 CC  
 20 1- SEROIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISO ID  
 21 ARRAKEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 22  
 23 1- SUBCELLULAR LOCATION: SECRETED.  
 24  
 25 1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPLEXES WHICH IS FOUND  
 26 IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 27  
 28 1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 29  
 30 1- INTERPRO: IPR001759; PENTAXIN.  
 31 PROSITE: PS0289; PENTAXIN; PARTIAL  
 32 Location: Amyloid; glycoprotein; plasma; pentaxin  
 33 DOMAIN 1 59  
 34 NUMBER 5  
 35 SEQUENCE 9 AA: 965 MW: 60567.80 Da; 59 (8-96)  
 36  
 37 Query Match: 18.2%, Score 2, DB 1, Length 9;  
 38 Best Local Similarity: 100.0%, Pred. No. 1,3e+05;  
 39 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 40  
 41 4 GK 5  
 42 11  
 43 4 GK 5

01 NOV 1990 (Rel. 16, Created)  
 02-NOV 1990 (Rel. 16, Last sequence update)  
 03-FEB 2003 (Rel. 41, Last annotation update)  
 04 SERUM amyloid P-component (SAP) (Fragment)  
 05 Mustelus carls (Smooth doufin)  
 06 Eukaryote, Metazoa; Chordata; Vertebrata; Chondrichthyes  
 07 Elasmobranchii; Galeomorphii; Galeorhinidae; Chondrichthyes; Trachidae  
 08 Mustelus  
 09 NCBI\_TaxID 7812;  
 10 RN  
 11  
 12 SEQUENCE  
 13 MEDLINE=43160942; PubMed 43160942;  
 14 Kosey F.A., Takao T., Liu F.-Y.,  
 15 "Isolation and characterization of 14 major serum proteins from the  
 16 dogfish, Mustelus carls, C-reactive protein and amyloid P  
 17 component";  
 18 J. Biol. Chem. 258:3889-3894 (1983).  
 19 CC  
 20 1- SEROIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISO ID  
 21 ARRAKEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 22  
 23 1- SUBCELLULAR LOCATION: SECRETED.  
 24  
 25 1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPLEXES WHICH IS FOUND  
 26 IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 27  
 28 1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 29  
 30 1- INTERPRO: IPR001759; PENTAXIN.  
 31 PROSITE: PS0289; PENTAXIN; PARTIAL  
 32 Location: Amyloid; glycoprotein; plasma; pentaxin  
 33 DOMAIN 1 59  
 34 NUMBER 5  
 35 SEQUENCE 9 AA: 965 MW: 60567.80 Da; 59 (8-96)  
 36  
 37 Query Match: 18.2%, Score 2, DB 1, Length 9;  
 38 Best Local Similarity: 100.0%, Pred. No. 1,3e+05;  
 39 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 39 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 40  
 41 4 GK 5  
 42 11  
 43 4 GK 5

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 30, 2003, 10:22:04 : Search time 31.6577 seconds  
(with local acceleration)  
64,669 Million cell updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: 1 AEGCKKKMRA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 25805464 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4659

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Prod. No. is the number of results produced for the query. In this case, the number is higher than or equal to the score. The results listed are sorted by score and are derived by analysis of the total set of distributions.

#### SUMMARY

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	3	27.3	9	2	Q4392	Q4392
2	3	27.3	9	2	P2149	P2149
3	3	27.3	9	4	Q9H18	Q9H18
4	3	27.3	9	11	Q99M34	Q99M34
5	3	27.3	10	6	Q7F542	Q7F542
6	3	27.3	10	6	Q7113	Q7113
7	3	27.3	10	9	Q8217	Q8217
8	3	27.3	10	12	P90476	P90476
9	3	27.3	11	2	Q8K81	Q8K81
10	3	27.3	11	12	Q8S428	Q8S428
11	3	27.3	11	14	Q9P522	Q9P522
12	3	27.3	12	6	Q8BQ7	Q8BQ7
13	3	27.3	12	6	Q9N258	Q9N258
14	3	27.3	12	15	Q75729	Q75729
15	3	27.3	12	15	Q4161	Q4161
16	3	27.3	12	16	Q25177	Q25177

17	3	27.3	13	4	Q5NR93	Q5NR93
18	3	27.3	13	8	Q9T569	Q9T569
19	3	27.3	13	10	Q39380	Q39380
20	3	27.3	13	11	Q62355	Q62355
21	3	27.3	14	4	Q9NY40	Q9NY40
22	3	27.3	14	4	Q96050	Q96050
23	3	27.3	14	4	O15222	O15222
24	3	27.3	14	4	Q81VK4	Q81VK4
25	3	27.3	14	6	Q9TR83	Q9TR83
26	3	27.3	14	15	O8UT17	O8UT17
27	3	27.3	15	4	Q9UC07	Q9UC07
28	3	27.3	15	6	Q9TR45	Q9TR45
29	3	27.3	15	6	Q9GLJ0	Q9GLJ0
30	3	27.3	15	10	Q9SQ16	Q9SQ16
31	3	27.3	15	10	Q9FYV6	Q9FYV6
32	3	27.3	15	10	P82431	P82431
33	3	27.3	15	10	P82439	P82439
34	3	27.3	15	15	Q8USK4	Q8USK4
35	3	27.3	15	15	Q8UM88	Q8UM88
36	2	18.2	8	2	Q9S6D5	Q9S6D5
37	2	18.2	8	2	P72279	P72279
38	2	18.2	8	2	Q9R712	Q9R712
39	2	18.2	8	2	Q9AGP4	Q9AGP4
40	2	18.2	8	2	Q68485	Q68485
41	2	18.2	8	2	Q93SR0	Q93SR0
42	2	18.2	8	2	Q44463	Q44463
43	2	18.2	8	2	Q32560	Q32560
44	2	18.2	8	2	Q92558	Q92558
45	2	18.2	8	2	Q56429	Q56429
46	2	18.2	8	2	Q9R9E0	Q9R9E0
47	2	18.2	8	2	Q9SR0	Q9SR0
48	2	18.2	8	2	P72221	P72221
49	2	18.2	8	2	Q9R517	Q9R517
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52	2	18.2	8	4	Q60773	Q60773
53	2	18.2	8	5	Q9TWH6	Q9TWH6
54	2	18.2	8	5	Q8MUN6	Q8MUN6
55	2	18.2	8	5	Q94655	Q94655
56	2	18.2	8	6	Q9BFA7	Q9BFA7
57	2	18.2	8	6	Q9BF82	Q9BF82
58	2	18.2	8	6	Q9BEC2	Q9BEC2
59	2	18.2	8	6	Q9HF90	Q9HF90
60	2	18.2	8	6	Q9BFA1	Q9BFA1
61	2	18.2	8	6	Q9BFA1	Q9BFA1
62	2	18.2	8	6	Q9BF87	Q9BF87
63	2	18.2	8	6	Q8WNS1	Q8WNS1
64	2	18.2	8	6	Q9BF89	Q9BF89
65	2	18.2	8	6	Q9BF88	Q9BF88
66	2	18.2	8	6	Q9BFA8	Q9BFA8
67	2	18.2	8	6	Q9BFA9	Q9BFA9
68	2	18.2	8	6	Q9BFA2	Q9BFA2
69	2	18.2	8	6	Q9BFA5	Q9BFA5
70	2	18.2	8	6	Q9BFA6	Q9BFA6
71	2	18.2	8	6	Q9BFB3	Q9BFB3
72	2	18.2	8	6	Q9BFB8	Q9BFB8
73	2	18.2	8	6	Q9BF95	Q9BF95
74	2	18.2	8	6	Q9BF84	Q9BF84
75	2	18.2	8	6	Q9BFC3	Q9BFC3
76	2	18.2	8	6	Q9BFA4	Q9BFA4
77	2	18.2	8	6	Q9BFA2	Q9BFA2
78	2	18.2	8	6	Q9BFC5	Q9BFC5
79	2	18.2	8	6	Q9BFC1	Q9BFC1
80	2	18.2	8	6	Q9BF89	Q9BF89
81	2	18.2	8	6	Q9BF96	Q9BF96
82	2	18.2	8	6	Q9BF80	Q9BF80
83	2	18.2	8	6	Q9BF86	Q9BF86
84	2	18.2	8	6	Q9BF92	Q9BF92
85	2	18.2	8	6	Q9BF87	Q9BF87
86	2	18.2	8	6	Q9BF91	Q9BF91
87	2	18.2	8	6	Q9BFA4	Q9BFA4
88	2	18.2	8	6	Q9BFC0	Q9BFC0
89	2	18.2	8	6	Q9BF98	Q9BF98

Q9nr93 homo sapien  
Q9t569 zea mays (m  
Q39380 brassica ol  
Q62355 mus musculu  
Q9ny40 homo sapien  
Q96050 homo sapien  
O15222 homo sapien  
Q81vk4 homo sapien  
Q9tr83 sus scrofa  
Q8ut17 human immun  
Q9uc07 homo sapien  
Q9tr45 bos taurus  
Q9glj0 sus scrofa  
Q9sq16 oryza sativ  
Q9fyv6 gossypium h  
P82431 nicotiana t  
P82439 nicotiana t  
Q8usk4 human immun  
Q8um88 human immun  
Q9s6d5 escherichia  
P72279 rhodococcus  
Q9r712 escherichia  
Q9agp4 arthrobacte  
Q68485 klebsiella  
Q93sr0 staphylococ  
Q44463 rhizobiales  
Q32560 escherichia  
Q92558 synecococc  
Q56429 thermus the  
Q9r9e0 bacillus su  
Q9r5r0 shigella dy  
P72221 pseudomonas  
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Q15900 homo sapien  
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Q60773 homo sapien  
Q9twh6 perineuris  
Q8mun6 heliconius  
Q94655 physarum po  
Q9bfa7 macroscelid  
Q9bf82 ursus arcto  
Q9bfc2 macropus eu  
Q9bf90 tragelaphus  
Q9bf81 echinops te  
Q9bfa1 ateles fusc  
Q9bf87 tapirus ind  
Q8wns1 bos taurus  
Q9bf89 euphractus  
Q9bf88 chaetophrac  
Q9bfa8 loxodonta a  
Q9bfa9 procavia ca  
Q9bf82 sorex arane  
Q9bf85 erinaceus c  
Q9bf86 myrmecophag  
Q9bfb3 condylura c  
Q9bf88 equus cabal  
Q9bf95 roussetus l  
Q9bf84 panthera on  
Q9bfc3 didelphis m  
Q9bfa4 tupia mino  
Q9bfa2 tarsius ban  
Q9bf85 leopardus p  
Q9bf81 chooleopus h  
Q9bf89 akapia john  
Q9bf96 pteropus gl  
Q9bf80 trichechus  
Q9bf86 felis silve  
Q9bf92 tursiops tr  
Q9bf87 hippopotamu  
Q9bf91 tamandua te  
Q9bf84 talpa alta  
Q9bf80 chooleopus d  
Q9bf98 callimico q

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91	2	18.2	8	6	Q9BKA6	Q9BKA6 cryptotopas	164	2	18.2	9	8	Q31653	Q31653 anser caeru
92	2	18.2	8	6	Q9BKA8	Q9BKA8 canis famli	165	2	18.2	9	10	Q940K4	Q940K4 arabisopris
93	2	18.2	8	6	Q9BKA9	Q9BKA9 artibeus ja	166	2	18.2	9	11	Q8R514	Q8R514 rattus norv
94	2	18.2	8	6	Q9BKA5	Q9BKA5 cynoccephalu	167	2	18.2	9	11	Q9QZA7	Q9qza7 mus musculu
95	2	18.2	8	6	Q9BKA4	Q9BKA4 nycterus te	168	2	18.2	9	11	Q9QVH9	Q9qv19 mus sp. sup
96	2	18.2	8	6	Q9BKA2	Q9BKA2 saccharomye	169	2	18.2	9	12	Q86545	Q86545 human herpe
97	2	18.2	8	9	Q8BKA4	Q8BKA4 alcedinara f	170	2	18.2	9	12	Q82622	Q82622 avian infec
98	2	18.2	8	9	Q8BKA4	Q8BKA4 bacteriopho	171	2	18.2	9	12	Q89100	Q89100 herpes simp
99	2	18.2	8	9	Q8BKA9	Q8BKA9 bacteriopho	172	2	18.2	9	13	Q92009	Q92009 gallus gall
100	2	18.2	8	9	Q8BKA7	Q8BKA7 bacteriopho	173	2	18.2	10	2	Q9R791	Q9r791 borrelia af
101	2	18.2	8	9	Q8BKA5	Q8BKA5 bacteriopho	174	2	18.2	10	2	Q9XBH3	Q9xbh3 bacillus ce
102	2	18.2	8	9	Q8BKA3	Q8BKA3 bacteriopho	175	2	18.2	10	2	Q50032	Q50032 mycobacteri
103	2	18.2	8	9	Q8BKA1	Q8BKA1 bacteriopho	176	2	18.2	10	2	Q8VN85	Q8vn85 helicobacte
104	2	18.2	8	9	Q8BKA4	Q8BKA4 bacteriopho	177	2	18.2	10	2	Q52837	Q52837 rhizobium 1
105	2	18.2	8	9	Q8BKA18	Q8BKA18 bacteriopho	178	2	18.2	10	2	Q60194	Q60194 spiroplasma
106	2	18.2	8	9	Q8BKA16	Q8BKA16 bacteriopho	179	2	18.2	10	2	Q60192	Q60192 spiroplasma
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108	2	18.2	8	9	Q8BKA13	Q8BKA13 bacteriopho	181	2	18.2	10	2	Q51812	Q51812 escherichia
109	2	18.2	8	9	Q8BKA12	Q8BKA12 bacteriopho	182	2	18.2	10	2	Q52762	Q52762 rhizobium s
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123	2	18.2	8	11	Q9EAL2	Q9EAL2 mus musculu	196	2	18.2	10	5	Q8WPL6	Q8wpl6 oikopleura
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130	2	18.2	8	11	Q9QV94	Q9QV94 capra hircu	203	2	18.2	10	8	Q9TKF5	Q9tkf5 agonis spat
131	2	18.2	8	13	Q9QVZV	Q9QVZV rattus norv	204	2	18.2	10	8	Q9TKF1	Q9tkf1 homalosperm
132	2	18.2	8	13	Q9QVZV	Q9QVZV fulica leuc	205	2	18.2	10	8	Q9TKF4	Q9tkf4 anasomyrtu
133	2	18.2	8	13	Q8JFNE	Q8JFNE gallus gall	206	2	18.2	10	8	Q9TKF3	Q9tkf3 asteromyrtu
134	2	18.2	8	15	Q9NKK9	Q9NKK9 human immun	207	2	18.2	10	8	Q9TKF0	Q9tkf0 neofabricia
135	2	18.2	9	2	Q9BKA2	Q9BKA2 metanasece	208	2	18.2	10	8	Q9TKF0	Q9tkf0 kunzea amb
136	2	18.2	9	2	Q9BKA1	Q9BKA1 borrelia af	209	2	18.2	10	8	Q9TKF6	Q9tkf6 agonis obtu
137	2	18.2	9	2	Q50034	Q50034 streptomyce	210	2	18.2	10	8	Q9THM7	Q9thm7 leptospermu
138	2	18.2	9	2	Q9BKA1	Q9BKA1 shigella dy	211	2	18.2	10	8	Q9TKE2	Q9tke2 leptospermu
139	2	18.2	9	2	Q40002	Q40002 el shigellum	212	2	18.2	10	8	Q9TKE3	Q9tke3 leptospermu
140	2	18.2	9	2	Q40002	Q40002 lactococcus	213	2	18.2	10	8	Q9TKE7	Q9tke7 kunzea pulc
141	2	18.2	9	2	Q40002	Q40002 borrelia af	214	2	18.2	10	8	Q9THM6	Q9thm6 leptospermu
142	2	18.2	9	2	Q40002	Q40002 lactobacilli	215	2	18.2	10	8	Q9TKE6	Q9tke6 leptospermu
143	2	18.2	9	2	Q9BKA3	Q9BKA3 pseudomonas	216	2	18.2	10	8	Q9TKE8	Q9tke8 kunzea eric
144	2	18.2	9	2	Q9BKA2	Q9BKA2 borrelia af	217	2	18.2	10	8	Q9TKE9	Q9tke9 kunzea baxt
145	2	18.2	9	2	Q9BKA2	Q9BKA2 streptococ	218	2	18.2	10	8	Q9TKE1	Q9tkel neofabricia
146	2	18.2	9	4	Q9BKA2	Q9BKA2 homo sapien	219	2	18.2	10	8	Q9TKE4	Q9tkel leptospermu
147	2	18.2	9	4	Q9BKA2	Q9BKA2 homo sapien	220	2	18.2	10	10	Q94119	Q94119 zea mays (m
148	2	18.2	9	4	Q9BKA2	Q9BKA2 homo sapien	221	2	18.2	10	10	Q8L7F5	Q8L7F5 hevea bras
149	2	18.2	9	4	Q9BKA14	Q9BKA14 homo sapien	222	2	18.2	10	10	P82938	P82938 hordeum vul
150	2	18.2	9	4	Q15892	Q15892 homo sapien	223	2	18.2	10	11	Q08622	Q08622 rattus norv
151	2	18.2	9	4	Q16625	Q16625 homo sapien	224	2	18.2	10	11	Q9QVJ7	Q9qv17 mus sp. mep
152	2	18.2	9	5	Q8W119	Q8W119 drosophila	225	2	18.2	10	11	Q91W23	Q91w23 rattus sp.
153	2	18.2	9	5	Q27356	Q27356 baobab boy	226	2	18.2	10	11	Q9QVFO	Q9qv10 mus sp. pro
154	2	18.2	9	6	Q8M1T7	Q8M1T7 eulemur ful	227	2	18.2	10	11	Q9QVFI	Q9qv11 mus sp. pro
155	2	18.2	9	6	Q8M1T8	Q8M1T8 eulemur ful	228	2	18.2	10	12	Q9Q0M9	Q9q0m9 polymaviru
156	2	18.2	9	6	Q9XSL9	Q9XSL9 capra hircu	229	2	18.2	10	12	Q8JW7C	Q8jw7c polymaviru
157	2	18.2	9	8	Q9TKD9	Q9TKD9 perialgynma	230	2	18.2	10	12	Q9Q0W1	Q9q0w1 polymaviru
158	2	18.2	9	8	Q9Y6N1	Q9Y6N1 perialgynum	231	2	18.2	10	12	Q8JW68	Q8jw68 polymaviru
159	2	18.2	9	8	Q9T200	Q9T200 sp. nacia ol	232	2	18.2	10	12	Q9J1G8	Q9j1g8 tt virus. o
160	2	18.2	9	8	Q9TKF2	Q9TKF2 asteromyrtu	233	2	18.2	10	12	Q69347	Q69347 herpes simp
161	2	18.2	9	8	Q9T2M7	Q9T2M7 lautereria v	234	2	18.2	10	12	Q9Q0V9	Q9q0v9 polymaviru
162	2	18.2	9	8	Q9T2T1	Q9T2T1 st. bacilla ol	235	2	18.2	10	12	Q6JW84	Q6jw84 polymaviru

236	2	18.2	10	12	Q930W7	Q930W7 polyomavirus	409	2	18.2	11	13	Q8UUP1	Q8UUP1 xenopus lae
237	2	18.2	10	12	Q8JW66	Q8JW66 polyomavirus	310	2	18.2	11	13	Q8JW68	Q8JW68 ticedula al
238	2	18.2	10	12	Q930V7	Q930V7 polyomavirus	311	2	18.2	11	13	Q90735	Q90735 gallus gall
239	2	18.2	10	12	Q8JW76	Q8JW76 polyomavirus	312	2	18.2	11	15	Q98Y53	Q98Y53 human immun
240	2	18.2	10	12	Q8JW76	Q8JW76 polyomavirus	313	2	18.2	11	15	P88018	P88018 human immun
241	2	18.2	10	12	Q8JW74	Q8JW74 polyomavirus	314	2	18.2	12	2	Q56442	Q56442 escherichia
242	2	18.2	10	12	Q8JW74	Q8JW74 polyomavirus	315	2	18.2	12	2	Q8KH47	Q8KH47 enterococcus
243	2	18.2	10	12	Q930X7	Q930X7 polyomavirus	316	2	18.2	12	2	Q50342	Q50342 mycoplasma
244	2	18.2	10	12	Q8JW76	Q8JW76 polyomavirus	317	2	18.2	12	2	Q93208	Q93208 acinetobact
245	2	18.2	10	12	Q930W5	Q930W5 polyomavirus	318	2	18.2	12	2	Q46712	Q46712 escherichia
246	2	18.2	10	12	Q930X3	Q930X3 polyomavirus	319	2	18.2	12	2	Q53183	Q53183 rhodococcus
247	2	18.2	10	12	Q930X5	Q930X5 polyomavirus	320	2	18.2	12	2	Q54226	Q54226 saccharopol
248	2	18.2	10	12	Q930W3	Q930W3 polyomavirus	321	2	18.2	12	2	Q8KT49	Q8KT49 fischerella
249	2	18.2	10	12	Q8JW80	Q8JW80 polyomavirus	322	2	18.2	12	2	Q8VIX8	Q8VIX8 thermus the
250	2	18.2	10	12	Q930X1	Q930X1 polyomavirus	323	2	18.2	12	2	Q8KH15	Q8KH15 campylobact
251	2	18.2	10	12	Q930X4	Q930X4 polyomavirus	324	2	18.2	12	2	Q9X6Y0	Q9X6Y0 aquifex pyr
252	2	18.2	10	12	Q8JW72	Q8JW72 polyomavirus	325	2	18.2	12	2	Q9K3H3	Q9K3H3 helicobacte
253	2	18.2	10	13	Q8JW72	Q8JW72 polyomavirus	326	2	18.2	12	2	Q52112	Q52112 acinetobact
254	2	18.2	10	15	Q8JW72	Q8JW72 polyomavirus	327	2	18.2	12	2	Q8GMV1	Q8GMV1 acinetobact
255	2	18.2	10	15	Q90K10	Q90K10 human immun	328	2	18.2	12	2	Q8GMT8	Q8GMT8 acinetobact
256	2	18.2	11	2	Q9R759	Q9R759 borrelia ga	329	2	18.2	12	2	Q8OML2	Q8OML2 acinetobact
257	2	18.2	11	2	Q924F7	Q924F7 bacillus ce	330	2	18.2	12	3	Q01275	Q01275 neurospora
258	2	18.2	11	2	Q9X956	Q9X956 streptomyce	331	2	18.2	12	4	Q9UMR0	Q9UMR0 homo sapien
259	2	18.2	11	2	Q9S618	Q9S618 prochloroc	332	2	18.2	12	4	Q9H126	Q9H126 homo sapien
260	2	18.2	11	2	Q87882	Q87882 mycobacteri	333	2	18.2	12	4	Q9UC37	Q9UC37 homo sapien
261	2	18.2	11	2	Q8KTW1	Q8KTW1 candidatus	334	2	18.2	12	4	Q16452	Q16452 homo sapien
262	2	18.2	11	2	Q93MI7	Q93MI7 escherichia	335	2	18.2	12	4	Q9UMQ9	Q9UMQ9 homo sapien
263	2	18.2	11	2	Q9RF72	Q9RF72 mycoplasma	336	2	18.2	12	4	Q9UC29	Q9UC29 homo sapien
264	2	18.2	11	2	Q95514	Q95514 pasteurella	337	2	18.2	12	4	Q9H3W2	Q9H3W2 homo sapien
265	2	18.2	11	2	Q47420	Q47420 escherichia	338	2	18.2	12	4	Q96PK0	Q96PK0 homo sapien
266	2	18.2	11	2	Q44090	Q44090 acholeplasm	339	2	18.2	12	4	Q13865	Q13865 homo sapien
267	2	18.2	11	2	Q8GMU3	Q8GMU3 acinetobact	340	2	18.2	12	4	Q9UGS1	Q9UGS1 homo sapien
268	2	18.2	11	3	Q9URV5	Q9URV5 pichia anqu	341	2	18.2	12	4	Q9H4X3	Q9H4X3 homo sapien
269	2	18.2	11	3	Q9URG3	Q9URG3 neurospora	342	2	18.2	12	4	Q9NTQ2	Q9NTQ2 homo sapien
270	2	18.2	11	3	Q96V15	Q96V15 cryptorectu	343	2	18.2	12	4	Q9BR06	Q9BR06 homo sapien
271	2	18.2	11	4	Q14759	Q14759 homo sapien	344	2	18.2	12	5	Q8MUN4	Q8MUN4 heliciconis
272	2	18.2	11	4	Q60761	Q60761 homo sapien	345	2	18.2	12	5	Q9U7R8	Q9U7R8 conus querc
273	2	18.2	11	4	Q75811	Q75811 homo sapien	346	2	18.2	12	5	Q8MUN9	Q8MUN9 heliciconis
274	2	18.2	11	4	Q9H4H5	Q9H4H5 homo sapien	347	2	18.2	12	5	Q61574	Q61574 osteria
275	2	18.2	11	4	Q15997	Q15997 homo sapien	348	2	18.2	12	5	Q9TWY0	Q9TWY0 fasciola he
276	2	18.2	11	4	Q8NFN9	Q8NFN9 homo sapien	349	2	18.2	12	6	Q46664	Q46664 macropus ro
277	2	18.2	11	4	Q9UC46	Q9UC46 homo sapien	350	2	18.2	12	6	Q9N2B9	Q9N2B9 gorilla gor
278	2	18.2	11	4	Q9JCH1	Q9JCH1 homo sapien	351	2	18.2	12	6	Q9TQW3	Q9TQW3 bos taurus
279	2	18.2	11	4	Q4UH72	Q4UH72 homo sapien	352	2	18.2	12	6	Q9TRV6	Q9TRV6 bos taurus
280	2	18.2	11	5	Q260V2	Q260V2 pisaster oc	353	2	18.2	12	6	Q9N2C0	Q9N2C0 pan troglod
281	2	18.2	11	5	Q9TWX6	Q9TWX6 manduca sex	354	2	18.2	12	8	Q9G196	Q9G196 sargassum p
282	2	18.2	11	5	Q92232	Q92232 drosophila	355	2	18.2	12	8	P92454	P92454 cycas revol
283	2	18.2	11	5	Q95PX6	Q95PX6 caenorhabdi	356	2	18.2	12	8	P82164	P82164 spinacia ol
284	2	18.2	11	5	Q9TWH2	Q9TWH2 eplasia cal	357	2	18.2	12	8	Q8HB27	Q8HB27 picea glauc
285	2	18.2	11	5	Q6MKH8	Q6MKH8 heliciconis	358	2	18.2	12	8	Q8HB26	Q8HB26 picea maria
286	2	18.2	11	5	Q9FW65	Q9FW65 bos taurus	359	2	18.2	12	8	Q8HB25	Q8HB25 picea ruben
287	2	18.2	11	6	Q91BX2	Q91BX2 bos taurus	360	2	18.2	12	10	Q8SAS2	Q8SAS2 pinus sylve
288	2	18.2	11	6	Q91Q59	Q91Q59 equus cabal	361	2	18.2	12	10	Q93X21	Q93X21 zea mays (m
289	2	18.2	11	7	Q77B42	Q77B42 oreochromis	362	2	18.2	12	10	Q41744	Q41744 zea mays (m
290	2	18.2	11	7	Q77B60	Q77B60 oreochromis	363	2	18.2	12	10	Q02320	Q02320 pinus sylve
291	2	18.2	11	7	Q77906	Q77906 oreochromis	364	2	18.2	12	10	Q9SQF8	Q9SQF8 pinus taeda
292	2	18.2	11	7	Q77893	Q77893 oreochromis	365	2	18.2	12	10	Q38715	Q38715 arachis hyp
293	2	18.2	11	7	Q77907	Q77907 oreochromis	366	2	18.2	12	10	Q02319	Q02319 pinus sylve
294	2	18.2	11	8	Q9G3Y0	Q9G3Y0 pseudotrapi	367	2	18.2	12	10	Q94011	Q94011 arabidopsis
295	2	18.2	11	8	Q9G3Y6	Q9G3Y6 aquana atra	368	2	18.2	12	10	Q8HEE6	Q8HEE6 hordeum vul
296	2	18.2	11	9	Q38415	Q38415 bacterioph	369	2	18.2	12	11	Q35868	Q35868 mus musculu
297	2	18.2	11	9	Q37925	Q37925 bacterioph	370	2	18.2	12	11	Q64313	Q64313 rattus norv
298	2	18.2	11	10	Q95784	Q95784 gossypium h	371	2	18.2	12	11	Q9WUX1	Q9WUX1 rattus norv
299	2	18.2	11	10	Q8RU67	Q8RU67 zea mays (m	372	2	18.2	12	11	Q61331	Q61331 mus musculu
300	2	18.2	11	10	Q04131	Q04131 lycopersico	373	2	18.2	12	11	Q91YF5	Q91YF5 mus musculu
301	2	18.2	11	10	P82336	P82336 pisum sativ	374	2	18.2	12	11	Q8CJ30	Q8CJ30 mus musculu
302	2	18.2	11	11	Q9Y981	Q9Y981 mus musculu	375	2	18.2	12	12	Q91F00	Q91F00 human adeno
303	2	18.2	11	11	Q9RLN6	Q9RLN6 mus musculu	376	2	18.2	12	12	Q84268	Q84268 human papil
304	2	18.2	11	11	Q921H5	Q921H5 mus musculu	377	2	18.2	12	12	Q86570	Q86570 hepatitis d
305	2	18.2	11	11	P81075	P81075 mus musculu	378	2	18.2	12	12	Q91E29	Q91E29 human adeno
306	2	18.2	11	12	Q83083	Q83083 leucania se	379	2	18.2	12	13	Q9PVC2	Q9PVC2 gadus morhu
307	2	18.2	11	12	Q9J1G3	Q9J1G3 tt virus, o	380	2	18.2	12	13	Q9PVC3	Q9PVC3 lampris sp.
308	2	18.2	11	12	Q40974	Q40974 cauliflowe	381	2	18.2	12	13	Q9PVC0	Q9PVC0 mugil cepha

482	2	18.2	12	13	Q9PVC1	Q9PVC1 aphidius sp.	455	2	18.2	13	11	Q14804	Q14804 mus musculus
483	2	18.2	12	13	Q9PVB9	Q9PVB9 aphidius lat.	456	2	18.2	13	11	Q97944	Q97944 mus musculus
484	2	18.2	12	13	Q9PVC6	Q9PVC6 pleocionessu	457	2	18.2	13	11	Q9QW04	Q9QW04 mus sp. pi
485	2	18.2	12	13	Q9PVB8	Q9PVB8 nemirephas	458	2	18.2	13	11	Q8CJ33	Q8CJ33 mus musculus
486	2	18.2	12	13	Q9PVB8	Q9PVB8 nemirephas	459	2	18.2	13	11	Q8CFN7	Q8CFN7 mus musculus
487	2	18.2	12	13	Q9PVC7	Q9PVC7 esox lucius	460	2	18.2	13	12	Q9PXB5	Q9PXB5 duck hepatic
488	2	18.2	12	13	Q9PVC4	Q9PVC4 harpador sp.	461	2	18.2	13	12	Q81171	Q81171 cauliflower
489	2	18.2	12	13	Q9PVB7	Q9PVB7 gallus gall.	462	2	18.2	13	12	Q8Y394	Q8Y394 pseudorale
490	2	18.2	12	13	Q9PVB5	Q9PVB5 gallus gall.	463	2	18.2	13	13	Q9PVA0	Q9PVA0 colisa lali
491	2	18.2	12	13	Q9PVB3	Q9PVB3 xenopus lae	464	2	18.2	13	13	Q9PVB1	Q9PVB1 dendrochiru
492	2	18.2	12	13	Q9PVB3	Q9PVB3 rana catesb	465	2	18.2	13	13	Q9PVB5	Q9PVB5 mola mola (
493	2	18.2	12	13	Q9PVB3	Q9PVB3 salmo trutt	466	2	18.2	13	13	Q9PVB7	Q9PVB7 dissostichu
494	2	18.2	12	13	Q9PVB3	Q9PVB3 salmo salar	467	2	18.2	13	13	Q9PVB3	Q9PVB3 hippocampus
495	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	468	2	18.2	13	13	Q9PVB8	Q9PVB8 pettodes s
496	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	469	2	18.2	13	13	Q9PVB7	Q9PVB7 ballistes sp
497	2	18.2	12	13	Q9PVB6	Q9PVB6 avian carc	470	2	18.2	13	13	Q9PVB2	Q9PVB2 mastacembel
498	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	471	2	18.2	13	13	Q9PVB2	Q9PVB2 thunnus sp.
499	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	472	2	18.2	13	13	Q9PVB0	Q9PVB0 dicentrarch
500	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	473	2	18.2	13	13	Q9PVB4	Q9PVB4 zeus faber
501	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	474	2	18.2	13	13	Q9PVB9	Q9PVB9 channa sp.
502	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	475	2	18.2	13	13	Q9PVB5	Q9PVB5 cryptocentr
503	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	476	2	18.2	13	13	Q9PVB3	Q9PVB3 acanthurus
504	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	477	2	18.2	13	13	Q9PVB9	Q9PVB9 epinephelus
505	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	478	2	18.2	13	13	Q9PVB5	Q9PVB5 galaxias ma
506	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	479	2	18.2	13	13	Q8QZ55	Q8QZ55 fugu rubrip
507	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	480	2	18.2	13	13	Q9PVB4	Q9PVB4 siganous sp.
508	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	481	2	18.2	13	13	Q9PVB1	Q9PVB1 stromateus
509	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	482	2	18.2	13	13	Q9PVB9	Q9PVB9 ostracion s
510	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	483	2	18.2	13	13	Q9PVB5	Q9PVB5 sargocentro
511	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	484	2	18.2	13	13	Q9PVB7	Q9PVB7 fundulus he
512	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	485	2	18.2	13	13	Q9PVB6	Q9PVB6 poecilia la
513	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	486	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
514	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	487	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
515	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	488	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
516	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	489	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
517	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	490	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
518	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	491	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
519	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	492	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
520	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	493	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
521	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	494	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
522	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	495	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
523	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	496	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
524	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	497	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
525	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	498	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
526	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	499	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
527	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun	500	2	18.2	13	13	Q9PVB6	Q9PVB6 salarias sp
528	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
529	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
530	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
531	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
532	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
533	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
534	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
535	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
536	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
537	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
538	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
539	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
540	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
541	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
542	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
543	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
544	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
545	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
546	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
547	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
548	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
549	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
550	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
551	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
552	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
553	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
554	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
555	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
556	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
557	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
558	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
559	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
560	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
561	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
562	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
563	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
564	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
565	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
566	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
567	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
568	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
569	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
570	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
571	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
572	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
573	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
574	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
575	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
576	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
577	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
578	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
579	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
580	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
581	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
582	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
583	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
584	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
585	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
586	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
587	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
588	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
589	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
590	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
591	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
592	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
593	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
594	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
595	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							
596	2	18.2	12	13	Q9PVB6	Q9PVB6 human immun							



FT NNN\_TER 9 9 1904 MW: EF421126/4506/9411 CRC64;  
 SQ SEQUENCE 9 AA: 27.3% Score 3; DB 2; Length 9;  
 Query Match: Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
 II  
 7 AEG 9

RESULT 2  
 Q99M33 PRELIMINARY: PRI: 9 AA.  
 ID P72149  
 AC P72149  
 DT 01-FEB-1997 (TREMBLrel, 02, Created)  
 DI 01-FEB-1997 (TREMBLrel, 02, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel, 19, Last annotation update)  
 OE Putative glucokinase (Fragment).  
 GN GLK.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 CX NCBI\_taxid:287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:PA01;  
 RX MELLING-96427344; PubMed:4840719;  
 RA Sage A.E., Proctor W.D., Phillips P.V. Jr.  
 RT "A two-component response regulator, glkR, is located for glucose  
 transport activity in Pseudomonas aeruginosa PA01".  
 RL J. Bacteriol. 178:6064-6066(1996)  
 DR EMBL: U50932; AAC44474.1;  
 KW Kinase.  
 FT NNN\_TER 1 1  
 SQ SEQUENCE 9 AA: 944 MW: 140716.66/230676 CRC64;

Query Match: 27.3% Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
 II  
 7 AEG 9

RESULT 3  
 Q99M33 PRELIMINARY: PRI: 9 AA.  
 ID P72149  
 AC P72149  
 DT 01-MAR-2001 (TREMBLrel, 16, Created)  
 DI 01-MAR-2001 (TREMBLrel, 16, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel, 19, Last annotation update)  
 OE Putative protein with a similarity to the protein of the  
 inhibitor domain and WAP-type (Wey and Wey) (Fragment).  
 GN 24461P7.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartiodactyla; Hominidae; Homo.  
 CX NCBI\_taxid:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Lloyd D.;  
 RX Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AL121778; CAB76844.1;  
 FT NNN\_TER 9 9  
 SQ SEQUENCE 9 AA: 1036 MW: 254120.66/210676 CRC64;

Query Match: 27.3% Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
 II  
 7 EGG 9

RESULT 4  
 Q99M33 PRELIMINARY: PRI: 9 AA.  
 ID Q99M33  
 AC Q99M33  
 DT 01-JUN-2001 (TREMBLrel, 17, Created)  
 DI 01-JUN-2001 (TREMBLrel, 17, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel, 17, Last annotation update)  
 OE NCAM protein (Fragment).  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_taxid:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA More M.L., Kirsch F.P., Rathjen F.G.;  
 RT "Targeted deletion of NCAM and ankyrin-B results in disorganized lens  
 RT fibres leading to cataract formation".  
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF146472; AAK25814.1;  
 FT NNN\_TER 9 9  
 SQ SEQUENCE 9 AA: 1039 MW: 328272.18/333327 CRC64;

Query Match: 27.3% Score 3; DB 11; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 II  
 3 KKK 9

RESULT 5  
 Q9TS42 PRELIMINARY: PRI: 10 AA.  
 ID Q9TS42  
 AC Q9TS42  
 DT 01-MAY-2000 (TREMBLrel, 13, Created)  
 DI 01-MAY-2000 (TREMBLrel, 13, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel, 21, Last annotation update)  
 OE GSTRADIOL-RECEPTOR-P2 peptide (Fragment).  
 GN Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Artiodactyla; Suina; Suidae; Sus.  
 CX NCBI\_taxid:9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:9129128; PubMed:2064608;  
 RA Thiele H.H., Jungblut P.W., Jakob F.;  
 RT "The progesterone-driven dissociation of oestradiol-receptor dimers as a  
 RT preparative tool. Isolation of a 32 kDa fragment from porcine uteri  
 RT and assignment of C-terminal origin by partial sequencing".  
 RL Biochem. J. 276:709-714(1991).  
 FT NNN\_TER 1 1  
 SQ SEQUENCE 10 AA: 992 MW: D95E047B1451B76D CRC64;

Query Match: 27.3% Score 3; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
 II  
 7 EGG 9

RESULT 6  
 Q97J03 PRELIMINARY: PRI: 10 AA.  
 ID Q97J03

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AC Q37103;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 2.1 kDa protein
OS Saccharomyces cerevisiae (Baker's yeast)
GC Mitochondrion
RC Bakayoka; Fudai; Ascomycota; Saccharomycotina; Saccobasidiomycetes
OC Saccharomycetales; Saccharomycotinales; Sacchari; Fungi
OX NCBI_TaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:WILD TYPE STRAIN A;
RX MEDLINE:85155510; PubMed:6494346;
RA de Zambrano M., Fardoun-Farley G., Boudreau J., Goussard P.,
  Bernardi G.;
RT "The ori sequences of the retroviral, derived of a wild-type yeast
  RT strain: number, location, orientation and structure";
RL Gene 32:439-457(1984);
DR EMBL: K03305; AAA66858.1;
DR EMBL: K03290; AAA69852.1;
DR EMBL: K03297; AAA69853.1;
DR EMBL: K03300; AAA69854.1;
KW Hypothetical protein; Mitochondrion
SQ SEQUENCE 10 AA: 1141 MW: 11638.6569 kDa CRC64:

Query Match 27.3% Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KKR 9
DB 4 KKR 6

RESULT 7
Q38217 PRELIMINARY; PRI; 11 AA;
AC Q38217;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LE Bacteriophage HK5-T promoter P1 DNA (fragment)
OS Lactococcus phage HK5-T
GC Viruses; dsDNA viruses, no RNA stage; Bacteriophages; Siphoviridae
OX NCBI_TaxID=11754;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE:90254170; PubMed:11754;
RA Takshimova G., Davison A.E., Brierley J.E.;
RT "Molecular characterization of promoters of the Lactococcus lactis
  PT subsp. cremoris temperate bacteriophage HK5-T: identification of a
  RI phage gene implicated in the temperate lifestyle and virulence";
RL Appl. Environ. Microbiol. 56:544-542(1990);
DR EMBL: M14490; AAA32241.1;
FT NON_TER 10
SQ SEQUENCE 10 AA: 1203 MW: 9725.9436 kDa CRC64:

Query Match 27.3% Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 KKR 10
DB 7 KKR 9

RESULT 8
P46574 PRELIMINARY; PRI; 11 AA;
DI 01-MAY-1997 (TrEMBLrel. 01, Created)
DE 01-MAY-1997 (TrEMBLrel. 01, Last sequence update)
DI 01-MAY-1997 (TrEMBLrel. 01, Last annotation update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE QLS (Fragment);
OS Pseudorabies virus
GC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirinae;
OX NCBI_TaxID:10445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:Rock;
RA Pederson N.E., Casey D.L., Koslowski K.M.;
RT "Pseudorabies virus QLS Q16 and Q17 sequence";
RL Submitted (Aug. 1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U66824; AAA47266.1;
FT NON_TER 10
SQ SEQUENCE 10 AA: 859 MW: 92424.21000 kDa CRC64:

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AEG 3
DB 7 AEG 9

RESULT 9
Q38K61 PRELIMINARY; PRI; 11 AA;
AC Q38K61;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-lactamase CTX-M-9 (Fragment);
GN BLACTX-M-9;
OS Escherichia coli;
GC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:743 D;
RA Sabate M., Navarro F., Miro E., Campoy S., Barbe J.,
  Prats G.;
RT "A novel complex salivary integron in Escherichia coli carrying the
  RI bla(CTX-M-9) gene";
RL Submitted (Mar. 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY092038; AAM15718.1;
FT NON_TER 11
SQ SEQUENCE 11 AA: 1071 MW: 12684.18050 kDa CRC64:

Query Match 27.3% Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AEG 4
DB 8 AEG 10

RESULT 10
Q38Z8 PRELIMINARY; PRI; 11 AA;
AC Q38Z8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W2 peptide (fragment);
OS Psphocarpus tetrasolobus (Goa bean) (Asparagaceae);
GC Fungi; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots; Fabales; Papilionoideae; Phaseoleae;
OX NCBI_TaxID=5911;

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RN      SEQUENCE.
RX      MEDLINE=92232221; PubMed 1468037;
RQ      Hirano H., Kagawa H., Okubo K.;
RI      Phytochemistry 31:731-735(1992).
RT      NON_TER 1
FT      NON_TER 11
SQ      SEQUENCE 11 AA; 1165 MW; 40387E1BAA842A7 Cleaved

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY      3 GSK 5
DB      11
        9 GSK 11

RESULT 11
Q9N2B8
ID      Q9N2B8 PRELIMINARY: PRT; 12 AA.
AC      Q9N2B8;
DI      01-OCT-2000 (TREMBLrel_15, Created)
DT      01-OCT-2000 (TREMBLrel_15, Last sequence update)
DE      01-MAR-2002 (TREMBLrel_20, Last annotation update)
DR      Indolethylamine N-methyltransferase (Fragment).
GN      INMT.
OS      Pongo pygmaeus (orangutan).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
OX      NCBI_TaxID:9600;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-oran-Poli;
RA      Kitano T., Kobayakawa H., Saitou N.;
RT      "Silver Project";
RL      Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL: AB041365; FAF44454.1;
KW      Methyltransferase; Transferase.
FT      NON_TER 12
SQ      SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Query Match          27.3%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EGG 4
DB      111
        2 EGG 4

RESULT 14
Q75729
ID      Q75729 PRELIMINARY: PRT; 12 AA.
AC      Q75729;
DI      01-NOV-1996 (TREMBLrel_01, Created)
DT      01-NOV-1996 (TREMBLrel_01, Last sequence update)
DE      01-MAR-2003 (TREMBLrel_23, Last annotation update)
DR      Not known.
GN      NEF.
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID:11576;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN HP9411;
RA      Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RT      Destrois R.C., Skowronski J.;
RT      *High frequency of defective nef alleles in a long-term survivor with
RT      nonprogressive HIV-1 infection.*
RL      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR      EMBL: U61801; AAS04720.1;
DR      InterPro: IPR000583; GATASE_2.
DR      PROSITE: PS00443; GATASE_TYPE_II; 1.
SQ      SEQUENCE 12 AA; 1238 MW; 2B921E1187B325A3 CRC64;

Query Match          27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GSK 5
DB      11
        9 GSK 11

RESULT 12
Q9HQJ1
ID      Q9HQJ1 PRELIMINARY: PRT; 12 AA.
AC      Q9HQJ1;
DI      01-JEN-2001 (TREMBLrel_17, Created)
DT      01-JUN-2001 (TREMBLrel_17, Last sequence update)
DE      01-JUN-2001 (TREMBLrel_17, Last annotation update)
DR      BA28309.2.2 (Novel protein (Isotom 3)) (Fragment).
GN      Cj63IM1.3.5.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX      NCBI_TaxID:9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Lloyd D.;
RL      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL: AL121582; CAC36669.1;
FT      NON_TER 1
SQ      SEQUENCE 12 AA; 1017 MW; 4784672D8E787577 CRC64;

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RN      SEQUENCE.
RX      MEDLINE=92232221; PubMed 1468037;
RQ      Hirano H., Kagawa H., Okubo K.;
RI      Phytochemistry 31:731-735(1992).
RT      NON_TER 1
FT      NON_TER 11
SQ      SEQUENCE 11 AA; 1165 MW; 40437E1BAA442A7 Cleaved

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY      3 GCK 5
DB      11
        9 GCK 11

RESULT 11
Q9N2B8
ID      Q9N2B8 PRELIMINARY: PRT; 12 AA.
AC      Q9N2B8;
DI      01-OCT-2000 (TREMBlrel_15, Created)
DT      01-OCT-2000 (TREMBlrel_15, Last sequence update)
DE      01-MAR-2002 (TREMBlrel_20, Last annotation update)
DR      Indolethylamine N-methyltransferase (Fragment).
GN      INMT.
OS      Pongo pygmaeus (orangutan).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
OX      NCBI_TaxID:9600;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-oran-Poli;
RA      Kitano T., Kobayakawa H., Saitou N.;
RT      "Silver Project";
RL      Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL: AB041365; FAF44454.1;
KW      Methyltransferase; Transferase.
FT      NON_TER 12
SQ      SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Query Match          27.3%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EGG 4
DB      111
        2 EGG 4

RESULT 14
Q75729
ID      Q75729 PRELIMINARY: PRT; 12 AA.
AC      Q75729;
DI      01-NOV-1996 (TREMBlrel_01, Created)
DT      01-NOV-1996 (TREMBlrel_01, Last sequence update)
DE      01-MAR-2003 (TREMBlrel_23, Last annotation update)
DR      Not known.
GN      NEF.
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID:11576;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN HP9411;
RA      Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RT      Destrois R.C., Skowronski J.;
RT      *High frequency of defective nef alleles in a long-term survivor with
RT      nonprogressive HIV-1 infection.*
RL      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR      EMBL: U61801; AAS04720.1;
DR      InterPro: IPR000583; GATASE_2.
DR      PROSITE: PS00443; GATASE_TYPE_II; 1.
SQ      SEQUENCE 12 AA; 1238 MW; 2B921E1187B325A3 CRC64;

Query Match          27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCK 5
DB      11
        9 GCK 11

RESULT 12
Q9HQJ1
ID      Q9HQJ1 PRELIMINARY: PRT; 12 AA.
AC      Q9HQJ1;
DI      01-JEN-2001 (TREMBlrel_17, Created)
DT      01-JEN-2001 (TREMBlrel_17, Last sequence update)
DE      01-JUN-2001 (TREMBlrel_17, Last annotation update)
DR      BA28309.2.2 (Novel protein (Isotom 3)) (Fragment).
GN      Cj63IM1.3.5.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX      NCBI_TaxID:9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Lloyd D.;
RL      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL: AL121582; CAC36669.1;
FT      NON_TER 1
SQ      SEQUENCE 12 AA; 1017 MW; 4784672D8E787577 CRC64;

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RN 11
RX SEQUENCE:
RX MEDLINE:92432221; PubMed 1468037;
RA Hirano H., Kagawa H., Okubo K.:
RI Phytochemistry 31:731-735(1992).
RT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA: 1165 MW: 80437816;AAS44237; Cys11

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 11
Q9N2B8 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q9N2B8 PRELIMINARY: PRT: 11 AA.
AC Q9N2B8;
DI 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DI 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hydrix 17, VASOTOCINIL-GLY-HYS
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Musculofascicular Pipidae;
OC Xenopus;
CX NCBI_TaxID:8355;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:oran-Pol3;
RA Kitano T., Kobayakawa H., Saitou N.;
RI "Silver Project";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB041365; HAA44454.1;
KW Methyltransferase, Transferase.
FT NON_TER 12
SQ SEQUENCE 12 AA: 1290 MW: CF079554917861A9 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 111
2 EGG 4

RESULT 14
Q75729 27.3%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Not
OS Human immunodeficiency virus 1;
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
CX NCBI_TaxID:11576;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RA Desrosiers R.C., Skowronski J.;
RT *High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.*
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AAS04720.1;
DR InterPro: IPR000583; GATase_2;
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA: 1238 MW: 2B921E1187B325A3 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 14
Q75729 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Not
OS Human immunodeficiency virus 1;
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
CX NCBI_TaxID:11576;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RA Desrosiers R.C., Skowronski J.;
RT *High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.*
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AAS04720.1;
DR InterPro: IPR000583; GATase_2;
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA: 1238 MW: 2B921E1187B325A3 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 14
Q75729 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Not
OS Human immunodeficiency virus 1;
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
CX NCBI_TaxID:11576;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RA Desrosiers R.C., Skowronski J.;
RT *High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.*
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AAS04720.1;
DR InterPro: IPR000583; GATase_2;
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA: 1238 MW: 2B921E1187B325A3 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 14
Q75729 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Not
OS Human immunodeficiency virus 1;
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
CX NCBI_TaxID:11576;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RA Desrosiers R.C., Skowronski J.;
RT *High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.*
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AAS04720.1;
DR InterPro: IPR000583; GATase_2;
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA: 1238 MW: 2B921E1187B325A3 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 14
Q75729 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Not
OS Human immunodeficiency virus 1;
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
CX NCBI_TaxID:11576;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RA Desrosiers R.C., Skowronski J.;
RT *High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.*
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AAS04720.1;
DR InterPro: IPR000583; GATase_2;
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA: 1238 MW: 2B921E1187B325A3 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 14
Q75729 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Not
OS Human immunodeficiency virus 1;
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
CX NCBI_TaxID:11576;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN:HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.;
RA Desrosiers R.C., Skowronski J.;
RT *High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.*
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AAS04720.1;
DR InterPro: IPR000583; GATase_2;
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA: 1238 MW: 2B921E1187B325A3 CRC64;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 14
Q75729 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q75729 PRELIMINARY: PRT: 12 AA.
AC Q75729;
DI 01-NOV-1996 (TREMBlrel.
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DB          2 GKK 4

RESULT 15
Q41611
ID Q41611 PRELIMINARY: PRT: 12 AA.
AC Q41611
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DI 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Nei protein (Fragment).
GN NEI.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentiviruses
GX NCBI_TaxID:11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:M02;
RX MEDLINE:98105804; PubMed:9445059;
RA Connor R.L., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker R.D., Neumann A.U., Varmund S.R., Weststock J., Jackson S.,
RA Fendmore E., Cao Y., Gao F., Katsura S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wolfinsky S.M.,
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines";
RL J. Virol. 72:1552-1576(1998).
DR EMBL: U84854; AAC58899.1;
FT NON_TER 12 12
SQ SEQUENCE 12 AA: 1222 MW: 28921619; P: 55% AA: CR 64;

Query Match 27.3%; Score 3; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5
DB 2 GKK 4

RESULT 16
Q25179
ID Q25179 PRELIMINARY: PRT: 12 AA.
AC Q25179;
DT 01 JAN 1998 (TrEMBLrel. 05, Created)
DI 01 JAN 1998 (TrEMBLrel. 05, Last sequence update)
DE 01 MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein HP0429
GN HP0429
OS Helicobacter pylori (Campylobacter pylori)
OC Bacterial Proteobacteria; Epsilonproteobacteria; Campylobacteres;
OC Helicobacteraceae; Helicobacter
GX NCBI_TaxID:210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:26695 / ATCC 700392;
RX MEDLINE:97394467; PubMed:9252145;
RA Tomb J.F., White O., Kerlavage A.R., Fleischman R.A., Sutton G.G.,
RA Fleischman R.D., Ketchum K.A., Kleck H., Gill S., Gonsky B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson J., Adams B.D., Glodek A.,
RA McKenney K., Fitzgerald L.M., De N. Adams R.D., Hickey E.K.,
RA Holt D.E., Gorayue J.D., Uffordback J.B., Peterson J.D., Kelley C.M.,
RA Cotton M.D., Weidman J.M., Eddy M.R., Bowman C., Wooley M., Wallis E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.C., Fraser C.M.,
RA Venter J.S.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori";
RL Nature 388:539-547(1997).
DR EMBL: AE000559; AAD07512.1;
DI 11GR: HP0429;
KW Hypothetical protein; Complete proteome;
SQ SEQUENCE 12 AA: 1375 MW: 209994842; P: 53% AA: CR 64;

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Query Match 27.3%; Score 3; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6
DB 5 GKK 7

RESULT 17
Q2NR93
ID Q2NR93 PRELIMINARY: PRT: 13 AA.
AC Q2NR93;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ULIP (Fragment).
GN ULIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:20287517; PubMed:10748015;
RA Matsuo T., Stauffer J.K., Walker R.L., Melizer P., Thiele C.J.;
RT "Structure and promoter analysis of the human unc-33-like
RT phosphoprotein gene. E-box required for maximal expression in
RT neuroblastoma and myoblasts.";
RL J. Biol. Chem. 275:16560-16568(2000).
DR EMBL: AF246692; AAF76324.1;
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1536 MW: 5175F2CE06D4333 CRC64;

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Query Match 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GKK 6
DB 5 GKK 7

RESULT 18
Q9T569
ID Q9T569 PRELIMINARY: PRT: 13 AA.
AC Q9T569;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial plasmid S 2 DNA, 5' end (fragment).
OS Zea mays (Maize).
GX Mitochondrion
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
GX NCBI_TaxID:4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RA Traynor P.L., Levings C.S. III.;
RT "Transcription of the S-2 maize mitochondrial plasmid.";
RL Plant Mol. Biol. 7:255-263(1986).
DR EMBL: M16992; AAA70281.1;
KW Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1626 MW: 7B5E03673918A1F4 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 KKK 7  
DB 9 KKK 11

## RESULT 19

Q39380 Q39380 PRELIMINARY: PRT: 13 AA.  
AC Q39380;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE IFA binding protein (Sp10) (Fragment).  
OS Brassica oleracea (cauliflower).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudots; Rosidae;  
OC eurosids I; Brassicales; Brassicaceae; Brassica;  
OX NCBI\_TaxID=3712;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DOX; TISSUE=Curd surface;  
RA Willis G.;  
RI "An investigation of nuclear lamin homologies in plants: an apparently  
RI not intermediate filament sequence that bind a polyclonal anti-lamin  
RI antisera";  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RR EMBL: X97678; CAA66268.1;  
FT NON\_TER 1  
SQ SEQUENCE 13 AA: 1413 MW; D1D4EA126B42772 CRC64;

Query Match 27.3%; Score 4; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 9 EGG 11

## RESULT 20

Q62355 Q62355 PRELIMINARY: PRT: 13 AA.  
AC Q62355;  
DT 01-NOV-1995 (TREMBLrel. 01, Created)  
DT 01-NOV-1995 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Trypsin (Fragment).  
GN TRY4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Muridae; Mus.  
OC Mammalia; Eutheria; Rodentia; Muridae; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A2;  
RA Stevens B.J., Hagenbuchle G., Weisner R.K.;  
RE MEDLINE=67066713; PubMed=3641189;  
RT "Sequence organisation and transcriptional regulation of the mouse  
RT elastase II and trypsin genes."  
RL Nucleic Acids Res. 14:8307-8330(1986)  
DR EMBL: X04580; CAA28248.1;  
DR MGI: 102757; Try4.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA: 1346 MW; D0FF4200214D729 CRC64;

Query Match 27.3%; Score 4; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MRA 11  
DB 1 MRA 3

## RESULT 21

Q9NY40 Q9NY40 PRELIMINARY: PRT: 14 AA.  
AC Q9NY40;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE CH13L1 protein (Fragment).  
GN CH13L1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ammon C., Rehli M., Andreessen R., Krause S.W.;  
RT "Alternative splicing of the human cartilage gp-39 gene generates  
RT multiple mRNA transcripts encoding for at least four putative protein  
RT isoforms with distinct carboxyl termini";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ251847; CAB76473.1;  
FT NON\_TER 1  
SQ SEQUENCE 14 AA: 1431 MW; 9EFAACDE1A14A7C5 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 1 EGG 3

## RESULT 22

Q96050 Q96050 PRELIMINARY: PRT: 14 AA.  
AC Q96050;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Mitochondrial ribosomal protein L33 (Fragment).  
GN MRPL33.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=21429115; PubMed=11543634;  
RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.;  
RA Watanabe K., Tanaka T.;  
RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes  
RT to the chromosomes and implications for human disorders";  
RL Genomics 77:65-70(2001).  
DR EMBL: AB051623; BAB54951.1;  
KW Ribosomal protein.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA: 1744 MW; 64ED243E9AED663B CRC64;

Query Match 27.3%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
DB 8 KKK 10

## RESULT 23

O15222 O15222 PRELIMINARY: PRT: 14 AA.  
ID O15222  
AC O15222;

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DI 01-JAN-1998 (TrEMBLrel. 05, Created)
DI 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DI 01-DEC-2002 (TrEMBLrel. 19, Last annotation update)
DE HOXC9 protein (Fragment).
GN HOX9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homin.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96319011; PubMed:9457979;
RA Flaqueiro D., Gibaud A., Bétrancourt P., Legendre M.F., Kalfay B.
RT *Distinct patterns of all-trans retinoic acid-dependent expression of
RT the HOXB and HOXC homeogenes in human embryonal and small cell lung
RT carcinoma cell lines.*
RL FEBS Lett. 415:264-267(1997).
DR EMBL: X99682; CAA67998.1;
DR TRANSFAC; T03427;
FT NON_TER
FT 1
SQ SEQUENCE 14 AA; 1725 MW; 6C5672725499A48C9C644.

Query Match 27.38; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKK 5
DB 2 KKK 4

RESULT 24
Q91VK4 PRELIMINARY; PRT; 14 AA.
AC Q91VK4;
DI 01-MAR-2003 (TrEMBLrel. 23, Created)
DI 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Steerin2 protein (Fragment).
GN STEERIN2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homin.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Peeters P.J., Verhasselt P., Meekens J.W., Luyten W.H.B.,
RA Geyssels J.G.H.;
RT *Sensorineural defects in mice hypomorphic for a transcription homeodomain
RT gene.*
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: A348520; CAD32560.1;
FT NON_TER
FT 14
SQ SEQUENCE 14 AA; 1267 MW; C67BE24868465846584654;

Query Match 27.38; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 5
DB 12 GKK 14

RESULT 25
Q9TR83 PRELIMINARY; PRT; 14 AA.
AC Q9TR83;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 16, Last annotation update)
DE TRIMKINASE (EC 2.7.1.28) (Fragment).
GN S-S scrofa (P14).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE-95132498; PubMed-7831203;
RA Miwa I., Kito Y., Okada J.;
RL Prep. Biochem. 24:203-223(1994).
SQ SEQUENCE 14 AA; 1441 MW; C1F0CB1590001DD CRC64;

Query Match 27.38; Score 3; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKK 4
DB 4 EKK 5

RESULT 26
Q8UT17 PRELIMINARY; PRT; 14 AA.
AC Q8UT17;
DI 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein.
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-00BW2127.214;
RA Novitsky V.A., Smith D.R., Gilbert P., McLane M.F., Chigwedore P.,
RA Williamson C., Ndung'u T., Klein L., Chang S.-Y., Peter T., Thior L.,
RA Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RT *HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
RT vaccine design.*
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF443105; AAL34832.1;
SQ SEQUENCE 14 AA; 1486 MW; 1F8F11F22AA03E20 CRC64;

Query Match 27.38; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 5
DB 10 GKK 12

RESULT 27
Q9UCV7 PRELIMINARY; PRT; 15 AA.
AC Q9UCV7;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Midkine (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homin.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-94059521; PubMed-8241100;
RA Novotny W.F., Matfi T., Mehta R.L., Milner P.G.;
RT *Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.*
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA; 1527 MW; C34B6B97878474AC CRC64;

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Query Match 27.3%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 3 KKK 5

## RESULT 28

ID Q99145 PRELIMINARY: PRI: 15 AA  
 AC Q99145 (TEMBLREL, 14, Created)  
 DT 01-MAY-2000 (TEMBLREL, 14, Last sequence update)  
 LT 01-MAY-2000 (TEMBLREL, 14, Last annotation update)  
 LE Amphoterin homolog (Fragment).  
 OS Bos taurus (bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE: 96029571; PubMed 7592757.  
 RA Mori O., Brett J., Slattery T., Cai R., Zhang J., Chen J.X.,  
 RA Nishishima M., Lundh E.K., Vijay S., Nitschke J.  
 RA "The receptor for advanced glycation end products (RAGE) is a cellular  
 RI binding site for amphotericin. Mediation of neurite outgrowth and co-  
 RT expression of rage and amphotericin in the developing nervous system."  
 RL J. Biol. Chem. 270:25752-25761(1995).  
 SQ SEQUENCE 15 AA; 1757 MW; 390960780C9E20 C6064;

Query Match 27.3%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 11 KKK 13

## RESULT 29

ID Q99146 PRELIMINARY: PRI: 15 AA  
 AC Q99146 (TEMBLREL, 16, Created)  
 DT 01-MAR-2001 (TEMBLREL, 16, Last sequence update)  
 LT 01-MAR-2001 (TEMBLREL, 16, Last annotation update)  
 LE Calpain II light chain-like protein (Fragment).  
 OS Sus scrofa (pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 CX NCBI\_TaxID=9923;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smith I.P.L., Fahrenkrug S.C., Rehner J.A., Simeoni P.A.,  
 RA Kexrood C.E. III, Keele J.W.  
 RA "Mapping of expressed sequence tags from a porcine early embryonic  
 RT cDNA library."  
 RL Submitted (MAY-2000) to the EMBL/Genbank/CCDS databases.  
 DR EMBL; AF267718; AAC25933.1;  
 FT NON-TER 1  
 SQ SEQUENCE 15 AA; 1825 MW; F9FE010ED0921E C6064;

Query Match 27.3%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6  
 DB 13 GKK 15

## RESULT 30

ID Q9SQ16 PRELIMINARY: PRI: 15 AA  
 AC Q9SQ16 (TEMBLREL, 14, Created)  
 DT 01-MAY-2000 (TEMBLREL, 14, Last sequence update)  
 LT 01-OCT-2002 (TEMBLREL, 22, Last annotation update)  
 LE Translation elongation factor (Fragment).  
 OS Gryza saliva (pig).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Ehrhartoideae; Oryzede; Gryza.  
 CX NCBI\_TaxID=4540;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li Z.-Y., Chen S.-Y.  
 RA "Inducible expression of translation elongation factor 1A gene in rice  
 RT seedlings in response to environmental stresses."  
 RL Acta Bot. Sin. 41:800-806(1999).  
 DR EMBL; AF067195; AAC75991.1;  
 CX Gramene; Q9SQ16;  
 KW Elongation factor.  
 FT NON-TER 1  
 SQ SEQUENCE 15 AA; 1514 MW; 95E5C46F069C9775 C6064;

Query Match 27.3%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 13 KKK 15

## RESULT 31

ID Q9FYV6 PRELIMINARY: PRI: 15 AA  
 AC Q9FYV6 (TEMBLREL, 16, Created)  
 DT 01-MAR-2001 (TEMBLREL, 16, Last sequence update)  
 LT 01-MAR-2001 (TEMBLREL, 16, Last annotation update)  
 LE Alcohol dehydrogenase E (EC 1.1.1.1) (Fragment).  
 GN ADHE.  
 OS Gossypium herbaceum.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC Eurosid; Malvales; Malvaceae; Malvoideae; Gossypium.  
 CX NCBI\_TaxID=4274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 20384599; PubMed:10924485;  
 RA Small R.L., Wendel J.F.  
 RA "Copy number variability and evolutionary dynamics of the Adh gene family  
 RT in diploid and tetraploid cotton (Gossypium)."  
 RL Genetics 155:1913-1926(2000).  
 DR EMBL; AF250211; AAF94553.1;  
 KW Oxidoreductase.  
 FT NON-TER 1  
 SQ SEQUENCE 15 AA; 1298 MW; 7C8D379B78E4067E C6064;

Query Match 27.3%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGC 3  
 DB 7 AGC 9

## RESULT 32

162431  
 ID P62431 PRELIMINARY: PRT: 15 AA.  
 AC P62431:  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DI 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DE 100 kDa cell wall protein (Fragment)  
 OS Nicotiana glauca (Common tobacco)  
 NC Nicotiana glauca: Streptococcus  
 CC Eukaryota: Viridiplantae: Streptococcus  
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 CC Asteroideae: lamiales: Solanales: Solanaceae: Nicotiana  
 NCBI\_TaxID: 4097;  
 RN 11  
 RP SEQUENCE  
 RC STRAIN: cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Janderhede D., Sluts A.P.,  
 RA Wojtaszek P., Solwell G.P.  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture."  
 RL Planta 200-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 FT NON-TER  
 SQ SEQUENCE 15 AA: 1694 MW: 5F4B62E346187626 (5964)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 111  
 4 KKK 6

RESULT 35  
 ID P62431 PRELIMINARY: PRT: 15 AA.  
 AC P62431:  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DI 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DE 100 kDa cell wall protein (Fragment)  
 OS Nicotiana glauca (Common tobacco)  
 NC Nicotiana glauca: Streptococcus  
 CC Eukaryota: Viridiplantae: Streptococcus  
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 CC Asteroideae: lamiales: Solanales: Solanaceae: Nicotiana  
 NCBI\_TaxID: 4097;  
 RN 11  
 RP SEQUENCE  
 RC STRAIN: cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Janderhede D., Sluts A.P.,  
 RA Wojtaszek P., Solwell G.P.  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture."  
 RL Planta 200-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 FT NON-TER  
 SQ SEQUENCE 15 AA: 1694 MW: 5F4B62E346187626 (5964)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 111  
 4 KKK 6

RESULT 35  
 ID P62431 PRELIMINARY: PRT: 15 AA.  
 AC P62431:  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DI 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DE 100 kDa cell wall protein (Fragment)  
 OS Nicotiana glauca (Common tobacco)  
 NC Nicotiana glauca: Streptococcus  
 CC Eukaryota: Viridiplantae: Streptococcus  
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 CC Asteroideae: lamiales: Solanales: Solanaceae: Nicotiana  
 NCBI\_TaxID: 4097;  
 RN 11  
 RP SEQUENCE  
 RC STRAIN: cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Janderhede D., Sluts A.P.,  
 RA Wojtaszek P., Solwell G.P.  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture."  
 RL Planta 200-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 FT NON-TER  
 SQ SEQUENCE 15 AA: 1694 MW: 5F4B62E346187626 (5964)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 111  
 4 KKK 6

RESULT 34  
 ID Q95605 PRELIMINARY: PRT: 8 AA.  
 AC Q95605:  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DE 01 MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q8USK4  
 ID Q8USK4 PRELIMINARY: PRT: 15 AA.  
 AC Q8USK4:  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DI 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Truncated net protein.  
 OS Human immunodeficiency virus 1.  
 CC Viruses: Retroviruses: Retroviridae: Lentivirus.  
 NCBI\_TaxID: 11676;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: LTS 700;  
 RA Ashton D., Rhodes D., Solomon A., Deacon N., Satchell C., Carr A.,  
 RA Cooper D., Hill R., Stewart G., Kaldor J.  
 RT "Viral diversity in the net/ltk region of the HIV-1 genome:  
 RI associations with long-term nonprogression."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC EMBL: AF219816; AAL65348.1;  
 CC EMBL: AF219817; AAL65349.1;  
 CC EMBL: AF219818; AAL65350.1;  
 CC EMBL: AF219819; AAL65351.1;  
 CC EMBL: AF219820; AAL65352.1;  
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 CC EMBL: AF219979; AAL65511.1;  
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 CC EMBL: AF219999; AAL65531.1;  
 CC EMBL: AF220000; AAL65532.1;  
 CC EMBL: AF220001; AAL65533.1;  
 CC EMBL: AF220002; AAL65534.1;  
 CC EMBL: AF220003; AAL65535.1;  
 CC EMBL: AF220004; AAL65536.1;  
 CC EMBL: AF220005; AAL65537.1;  
 CC EMBL: AF220006; AAL65538.1;  
 CC EMBL: AF220007; AAL65539.1;  
 CC EMBL: AF220008; AAL65540.1;  
 CC EMBL: AF220009; AAL65541.1;  
 CC EMBL: AF220010; AAL65542.1;  
 CC EMBL: AF220011; AAL65543.1;  
 CC EMBL: AF220012; AAL65544.1;  
 CC EMBL: AF220013; AAL65545.1;  
 CC EMBL: AF220014; AAL65546.1;  
 CC EMBL: AF220015; AAL65547.1;  
 CC EMBL: AF220016; AAL65548.1;  
 CC EMBL: AF220017; AAL65549.1;  
 CC EMBL: AF220018; AAL65550.1;  
 CC EMBL: AF220019; AAL65551.1;  
 CC EMBL: AF220020; AAL65552.1;  
 CC EMBL: AF220021; AAL65553.1;  
 CC EMBL: AF220022; AAL65554.1;  
 CC EMBL: AF220023; AAL65555.1;  
 CC EMBL: AF220024; AAL65556.1;  
 CC EMBL: AF220025; AAL65557.1;  
 CC EMBL: AF220026; AAL65558.1;  
 CC EMBL: AF220027; AAL65559.1;  
 CC EMBL: AF220028; AAL65560.1;  
 CC EMBL: AF220029; AAL65561.1;  
 CC EMBL: AF220030; AAL65562.1;  
 CC EMBL: AF220031; AAL65563.1;  
 CC EMBL: AF220032; AAL65564.1;  
 CC EMBL: AF220033; AAL65565.1;  
 CC EMBL: AF220034; AAL65566.1;  
 CC EMBL: AF220035; AAL65567.1;  
 CC EMBL: AF220036; AAL65568.1;  
 CC EMBL: AF220037; AAL65569.1;  
 CC EMBL: AF220038; AAL65570.1;  
 CC EMBL: AF220039; AAL65571.1;  
 CC EMBL: AF220040; AAL65572.1;  
 CC EMBL: AF220041; AAL65573.1;  
 CC EMBL: AF220042; AAL65574.1;  
 CC EMBL: AF220043; AAL65575.1;  
 CC EMBL: AF220044; AAL65576.1;  
 CC EMBL: AF220045; AAL65577.1;  
 CC EMBL: AF220046; AAL65578.1;  
 CC EMBL: AF220047; AAL65579.1;  
 CC EMBL: AF220048; AAL65580.1;  
 CC EMBL: AF220049; AAL65581.1;  
 CC EMBL: AF220050; AAL65582.1;  
 CC EMBL: AF220051; AAL65583.1;  
 CC EMBL: AF220052; AAL65584.1;  
 CC EMBL: AF220053; AAL65585.1;  
 CC EMBL: AF220054; AAL65586.1;  
 CC EMBL: AF220055; AAL65587.1;  
 CC EMBL: AF220056; AAL65588.1;  
 CC EMBL: AF220057; AAL65589.1;  
 CC EMBL: AF220058; AAL65590.1;  
 CC EMBL: AF220059; AAL65591.1;  
 CC EMBL: AF220060; AAL65592.1;  
 CC EMBL: AF220061; AAL65593.1;  
 CC EMBL: AF220062; AAL65594.1;  
 CC EMBL: AF220063; AAL65595.1;  
 CC EMBL: AF220064; AAL65596.1;  
 CC EMBL: AF220065; AAL65597.1;  
 CC EMBL: AF220066; AAL65598.1;  
 CC EMBL: AF220067; AAL65599.1;  
 CC EMBL: AF220068; AAL65600.1;  
 CC EMBL: AF220069; AAL65601.1;  
 CC EMBL: AF220070; AAL65602.1;  
 CC EMBL: AF220071; AAL65603.1;  
 CC EMBL: AF220072; AAL65604.1;  
 CC EMBL: AF220073; AAL65605.1;  
 CC EMBL: AF220074; AAL65606.1;  
 CC EMBL: AF220075; AAL65607.1;  
 CC EMBL: AF220076; AAL65608.1;  
 CC EMBL: AF220077; AAL65609.1;  
 CC EMBL: AF220078; AAL65610.1;  
 CC EMBL: AF220079; AAL65611.1;  
 CC EMBL: AF220080; AAL65612.1;  
 CC EMBL: AF220081; AAL65613.1;  
 CC EMBL: AF220082; AAL65614.1;  
 CC EMBL: AF220083; AAL65615.1;  
 CC EMBL: AF220084; AAL65616.1;  
 CC EMBL: AF220085; AAL65617.1;  
 CC EMBL: AF220086; AAL65618.1;  
 CC EMBL: AF220087; AAL65619.1;  
 CC EMBL: AF220088; AAL65620.1;  
 CC EMBL: AF220089; AAL65621.1;  
 CC EMBL: AF220090; AAL65622.1;  
 CC EMBL: AF220091; AAL65623.1;  
 CC EMBL: AF220092; AAL65624.1;  
 CC EMBL: AF220093; AAL65625.1;  
 CC EMBL: AF220094; AAL65626.1;  
 CC EMBL: AF220095; AAL65627.1;  
 CC EMBL: AF220096; AAL65628.1;  
 CC EMBL: AF220097; AAL65629.1;  
 CC EMBL: AF220098; AAL65630.1;  
 CC EMBL: AF220099; AAL65631.1;  
 CC EMBL: AF220100; AAL65632.1;  
 CC EMBL: AF220101; AAL65633.1;  
 CC EMBL: AF220102; AAL65634.1;  
 CC EMBL: AF220103; AAL65635.1;  
 CC EMBL: AF220104; AAL65636.1;  
 CC EMBL: AF220105; AAL65637.1;  
 CC EMBL: AF220106; AAL65638.1;  
 CC EMBL: AF220107; AAL65639.1;  
 CC EMBL: AF220108; AAL65640.1;  
 CC EMBL: AF220109; AAL65641.1;  
 CC EMBL: AF220110; AAL65642.1;  
 CC EMBL: AF220111; AAL65643.1;  
 CC EMBL: AF220112; AAL65644.1;  
 CC EMBL: AF220113; AAL65645.1;  
 CC EMBL: AF220114; AAL65646.1;  
 CC EMBL: AF220115; AAL65647.1;  
 CC EMBL: AF220116; AAL65648.1;  
 CC EMBL: AF220117; AAL65649.1;  
 CC EMBL: AF220118; AAL65650.1;  
 CC EMBL: AF220119; AAL65651.1;  
 CC EMBL: AF220120; AAL65652.1;  
 CC EMBL: AF220121; AAL65653.1;  
 CC EMBL: AF220122; AAL65654.1;  
 CC EMBL: AF220123; AAL65655.1;  
 CC EMBL: AF220124; AAL65656.1;  
 CC EMBL: AF220125; AAL65657.1;  
 CC EMBL: AF220126; AAL65658.1;  
 CC EMBL: AF220127; AAL65659.1;  
 CC EMBL: AF220128; AAL65660.1;  
 CC EMBL: AF220129; AAL65661.1;  
 CC EMBL: AF220130; AAL65662.1;  
 CC EMBL: AF220131; AAL65663.1;  
 CC EMBL: AF220132; AAL65664.1;  
 CC EMBL: AF220133; AAL65665.1;  
 CC EMBL: AF220134; AAL65666.1;  
 CC EMBL: AF220135; AAL65667.1;  
 CC EMBL: AF220136; AAL65668.1;  
 CC EMBL: AF220137; AAL65669.1;  
 CC EMBL: AF220138; AAL65670.1;  
 CC EMBL: AF220139; AAL65671.1;  
 CC EMBL: AF220140; AAL65672.1;  
 CC EMBL: AF220141; AAL65673.1;  
 CC EMBL: AF220142; AAL65674.1;  
 CC EMBL: AF220143; AAL65675.1;  
 CC EMBL: AF220144; AAL65676.1;  
 CC EMBL: AF220145; AAL65677.1;  
 CC EMBL: AF220146; AAL65678.1;  
 CC EMBL: AF220147; AAL65679.1;  
 CC EMBL: AF220148; AAL65680.1;  
 CC EMBL: AF220149; AAL65681.1;  
 CC EMBL: AF220150; AAL65682.1;  
 CC EMBL: AF220151; AAL65683.1;  
 CC EMBL: AF220152; AAL65684.1;  
 CC EMBL: AF220153; AAL65685.1;  
 CC EMBL: AF220154; AAL65686.1;  
 CC EMBL: AF220155; AAL65687.1;  
 CC EMBL: AF220156; AAL65688.1;  
 CC EMBL: AF220157; AAL65689.1;  
 CC EMBL: AF220158; AAL65690.1;  
 CC EMBL: AF220159; AAL65691.1;  
 CC EMBL: AF220160; AAL65692.1;  
 CC EMBL: AF220161; AAL65693.1;  
 CC EMBL: AF220162; AAL65694.1;  
 CC EMBL: AF220163; AAL65695.1;  
 CC EMBL: AF220164; AAL65696.1;  
 CC EMBL: AF220165; AAL65697.1;  
 CC EMBL: AF220166; AAL65698.1;  
 CC EMBL: AF220167; AAL65699.1;  
 CC EMBL: AF220168; AAL65700.1;  
 CC EMBL: AF220169; AAL65701.1;  
 CC EMBL: AF220170; AAL65702.1;  
 CC EMBL: AF220171; AAL65703.1;  
 CC EMBL: AF220172; AAL65704.1;  
 CC EMBL: AF220173; AAL65705.1;  
 CC EMBL: AF220174; AAL65706.1;  
 CC EMBL: AF220175; AAL65707.1;  
 CC EMBL: AF220176; AAL65708.1;  
 CC EMBL: AF220177; AAL65709.1;  
 CC EMBL: AF220178; AAL65710.1;  
 CC EMBL: AF220179; AAL65711.1;  
 CC EMBL: AF220180; AAL65712.1;  
 CC EMBL: AF220181; AAL65713.1;  
 CC EMBL: AF220182; AAL65714.1;  
 CC EMBL: AF22018



DT 01-MAY-2002 (TrEMBLrel. 13, last annotation update)  
 DE Putative 1530 transposase (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OX Enterobacteriaceae; Escherichia.  
 RN NCBI\_TaxID=562;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=99194747; PubMed=10094716;  
 RA Kato A., Brumme-Smith J., Whitfield G.  
 RI "Conserved organization in the cps gene clusters for expression of  
 Escherichia coli group 1 K antigens: relationship to the colanic acid  
 biosynthesis locus and the cps genes from Klebsiella pneumoniae."  
 RJ J. Bacteriol. 181:2307-2313(1999).  
 RL EMBL; AF118251; AAD30008.1; .  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1011 MW; F21D01A9D1B41406 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AE 2  
 DB 7 AE 8

RESULT 39  
 Q9AGP4 PRELIMINARY; PRI: 8 AA  
 ID Q9AGP4  
 AC Q9AGP4; PRI: 8 AA  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)  
 DE Biphenyl dioxygenase (Fragment).  
 GN BPHB  
 OS Rhodococcus globulus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OX Corynebacterineae; Nocardiaceae; Rhodococcus  
 RN NCBI\_TaxID=13008;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255652; PubMed=7737502;  
 RA Asturias J.A., Diaz E., Timmis K.N.;  
 RI "Evolutionary relationship of the biphenyl dioxygenase of the gram-  
 positive bacterium Rhodococcus globulus to multicompone  
 dioxygenases of gram-negative bacteria".  
 RL Gene 156:111-18(1995).  
 DR EMBL; X80041; CAA56350.1; .  
 KW Dioxygenase.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 989 MW; FB2D761A0E074406 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 MR 10  
 DB 1 MR 2

RESULT 39  
 Q9R712 PRELIMINARY; PRI: 8 AA  
 ID Q9R712  
 AC Q9R712  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)  
 DE Hypothetical 1.0 kDa protein (Fragment).  
 GN YQFQ.  
 OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OX Enterobacteriaceae; Escherichia.  
 RN NCBI\_TaxID=562;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,  
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RI "A 718-kb DNA sequence of Escherichia coli K-12 Genome Corresponding  
 to the 12.7-28.0 min Region on the Linkage Map."  
 RJ DNA Res. 3:147-155(1996).  
 RL EMBL; D90705; HAA95310.1; .  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 964 MW; DF133BLDD04B476A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AE 2  
 DB 5 AE 6

RESULT 39  
 Q9AGP4 PRELIMINARY; PRI: 8 AA  
 ID Q9AGP4  
 AC Q9AGP4; PRI: 8 AA  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)  
 DE Serine hydroxymethyltransferase (Fragment).  
 GN GUYA.  
 OS Arthrobacter sp. lin.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OX Micrococciaceae; Micrococcaceae; Arthrobacter.  
 RN NCBI\_TaxID=153502;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=lin;  
 RA Meskys R., Harris R.J., Casalte V., Basran J., Scrutton N.S.;  
 RI "Genetic organization of the genes involved in dimethylglycine and  
 sarcosine degradation in Arthrobacter spp.: implications for glycine  
 betaine catabolism".  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF329478; AAK16486.1; .  
 KW Methyltransferase; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 898 MW; 6B1870533372457 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KK 6  
 DB 4 KK 5

RESULT 40  
 O68485 PRELIMINARY; PRI: 8 AA  
 ID O68485  
 AC O68485; PRI: 8 AA  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)  
 DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).

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GN AAPAL.
OS Klebsiella pneumoniae.
GC Plasmid pAQ3000.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Klebsiella.
CX NCBI_TaxID=573;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=N.C.1;
RX MEDLINE=98287600; PubMed 9624504;
KA Cotton D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
RT aac(6)-Ib from the integron of a natural multi-resistance plasmid.";
BL Antimicrob. Agents Chemother. 42:1506-1518(1998).
DR EMBL: AF047556; AAC25501.1;
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA: 878 MW: 87865A2B15A556 CRC64;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 3 AE 4

RESULT 4;
ID Q93SK0 PRELIMINARY; PRT; 8 AA.
AC Q93SK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-lactamase repressor Blal (Fragment).
GN BLAL.
OS Staphylococcus epidermidis.
GC Plasmid pS16.
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
CX NCBI_TaxID=1282;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=N.A.
KA Sidhu M.S., Hair E., Sorum H., Holtek A.L.;
RT "Genetic linkage between quaternary ammonium compound and beta lactam
RT resistance in Staphylococci isolated from band 2."
PL Submitted (MAR-2001) to the EMBL/GenBank/DBJ Databases.
DR EMBL: AY028779; AAK38453.1;
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA: 930 MW: 451250AA142A27A7A1

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 7 KK 8

RESULT 4;
ID Q44463 PRELIMINARY; PRT; 8 AA.
AC Q44463;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Archaeobacterium tumerfaciens T1 plasmid 9110A and vir24 genes
DE (Fragment).
OS Rhizobiales (rhizobacteria).
GC Plasmid T1.

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OC Bacteria; Proteobacteria; Alphaproteobacteria.
CX NCBI_TaxID=356;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=88015611; PubMed=4658701;
RA Portner S.G., Yancofsky M.F., Nester E.W.;
RT "molecular characterization of the vird operon from Agrobacterium
RT tumefaciens.";
RL Nucleic Acids Res. 15:7503-7517(1987).
DR EMBL: X06045; CAA29439.1;
KW Plasmid.
FT NON_TER 8
SQ SEQUENCE 8 AA: 857 MW: 8572C325B33861A6 CRC64;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CK 5
DB 3 CK 4

RESULT 4;
ID Q32560 PRELIMINARY; PRT; 8 AA.
AC Q32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Propionate kinase (Fragment).
GN TKCD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hessleringer G., Sawers G.;
RT "The tdcE gene in Escherichia coli W3110 is separated from the rest of
RT the tdc operon by insertion of 155 elements.";
RL DNA Seq. 9:183-188(1998).
DR EMBL: AJ001620; CAA04875.1;
KW Kinase.
FT NON_TER 1
SQ SEQUENCE 6 AA: 1000 MW: 3A505EB04140DC4 CRC64;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RA 11
DB 1 RA 2

RESULT 4;
ID Q09258 PRELIMINARY; PRT; 8 AA.
AC Q09258;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NifH (Fragment).
GN NIFH.
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
CX NCBI_TaxID=41431;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;

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RX MEDLINE-99231861; PubMed-10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.:
RT "Organization and expression of nitrogen fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RT RF-1."
RL Microbiology 145:743-753(1999).
DR EMBL: AF001760; AAC33369.1;
FT NON_TER 8
SQ SEQUENCE 8 AA; 965 MW; F16B59D13846C436 70%
Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 1 MR 2

RESULT 45
Q56425 PRELIMINARY: PRT: 8 AA.
AC Q56425;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAPDH (Fragment).
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococcus; Thermobacterales; Thermaceae;
CX NCBI_TaxID:274;
FN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-Hrc8;
RA MEDLINE-99025722; PubMed-3052437;
RX Bowen D., Littlechild J.A., Forthright J.E., Watson R.C., Hall L.:
RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
RT extreme thermophile, Thermus thermophilus 8.7."
RL Biochem. J. 254:509-517(1989).
DR EMBL: X12464; CAA31005.1;
FT NON_TER 1
SQ SEQUENCE 8 AA; 885 MW; 33CB743A712724B 6%

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 1 MR 2

RESULT 46
Q9R9E0 PRELIMINARY: PRT: 8 AA.
AC Q9R9E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
CX NCBI_TaxID:1423;
FN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA MEDLINE-94003529; PubMed-7391053;
RX Henriques A.O., de Lencastre H., Plagiot I.:
RT "A Bacillus subtilis morphotype cluster that includes SPOVE is
RT homologous to the mra region of Escherichia coli."
RL Biochimie 74:735-748(1992).
DR EMBL: X64258; CAA45556.1;

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FT NON_TER 8
SQ SEQUENCE 8 AA; 893 MW; FE75A1A3321B1A6 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 4 KK 5

RESULT 47
Q9R5R0 PRELIMINARY: PRT: 8 AA.
AC Q9R5R0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11,500 bp product of ORF4 (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CX NCBI_TaxID:622;
FN 1;
RP SEQUENCE.
RX MEDLINE-92085268; PubMed-1560923;
RA Polard P., Piere M.F., Chandler M., Fayet O.:
RT "Programmed translational frameshifting and initiation at an AUU codon
RT in gene expression of bacterial insertion sequence IS911."
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

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QY 5 KK 6
DB 2 KK 3

RESULT 48
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AC P72221;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Arginate lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria
CX NCBI_TaxID:H6038;
FN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-OS-ALG-9;
RA Fujiyama K.:
KL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN-OS-ALG-9;
RX MEDLINE-93329366; PubMed-8336113;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.:
RT "Cloning, sequence analysis and expression in Escherichia coli of a
RT gene encoding an arginate lyase from Pseudomonas sp. OS-ALG-9."
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL: D38469; BAA21704.1;
KW Lyase.
FT NON_TER 1
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 DT 01 MAY 2000 (TRENBLER, 14, Created)  
 DT 01 MAY 2000 (TRENBLER, 14, Last sequence update)  
 DT 01 JUN 2000 (TRENBLER, 14, Last annotation update)  
 DE 1,4-beta-D-glucan glucanohydrolase (EC 3.2.1.4) (Fragment)  
 OS Clostridium thermocellum  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium  
 CC NCBI\_TaxID 1515  
 GN [1]  
 RP SEQUENCE  
 RX MEDLINE-94211850; PubMed-1667839  
 RA Kozminski M.P., Fauth U., Kobayashi T., Buskisson N.S., Barker P.,  
 RA Gaudin A.L.  
 FT "Purification and characterization of a new endoglucanase from  
 FT Clostridium thermocellum."  
 RG Biochem J 283:69-73(1992)  
 SQ SEQUENCE 8 AA: 823 MW: 82144.00pI: 5.56

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 DT 01 NOV 1996 (TRENBLER, 61, Created)  
 DT 01 NOV 1996 (TRENBLER, 61, Last sequence update)  
 DT 01 DEC 2001 (TRENBLER, 19, Last annotation update)  
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 RA FISHER-PLACENTIA  
 RA Lee C., G. Vardoulakis, A. Wehnert M., Bercy J., Chirault G.A., Xu J.,  
 RA Chirault G.A., Chirault G.A., Bercy J., Chirault G.A., Xu J.,  
 RA Cuskey C.P.  
 RT "Isolation of chromosome-specific probes for the human gene  
 RT arrayed cDNAs and cosmid libraries."  
 RI Hum Mol Genet 4:100-105(1995)  
 DR EMBL: U32579; AAA73890.1  
 FT NON-TER 1  
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QY 10 RA 11

GenCore version 5.1.6  
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DM protein protein search, using sw model

Run on: September 30, 2003, 10:07:00 : Search time 11m43s Seconds  
(without alignment)  
42.55: Million cell updates/sec

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Scoring table: X1G0

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 7859

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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8	6	54.5	9	3	US-08-135-9045-12	Sequence 12, Appl
9	6	54.5	9	3	US-08-135-9045-13	Sequence 13, Appl
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11	6	54.5	9	3	US-08-135-9045-15	Sequence 15, Appl
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17	6	54.5	10	3	US-08-135-9045-21	Sequence 21, Appl
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19	6	54.5	10	3	US-08-135-9045-23	Sequence 23, Appl
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25	6	54.5	10	3	US-08-135-9045-29	Sequence 29, Appl
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249	3	27.3	8	2	US-08-350-260A-520	Sequence 520, App	322	3	27.3	9	1	US-08-215-805A-60	Sequence 60, Appl
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## ALIGNMENTS

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RESULT 1
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: Sequence 5, Application US/08105904B
: Patent No. 6001364
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cocley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/105,904B
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Neeley, Richard L.
: REGISTRATION NUMBER: 30,092

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1 REFERENCE/DOCKET NUMBER: ABIC-001/020S
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4 TELEFAX: (415)857-0663
5 TELE: 390816 COOLEYPA
6 INFORMATION FOR SEQ ID NO: 5:
7 SEQUENCE CHARACTERISTICS:
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10 TOPOLOGY: linear
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50 Patent No. 6001364
51 GENERAL INFORMATION:
52 APPLICANT: Rose, Keith
53 TITLE OF INVENTION: HETERO-POLYXIME COMPOUNDS AND THEIR
54 PREPARATION BY PARALLEL ASSEMBLY
55 NUMBER OF SEQUENCES: 24
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
58 STREET: 5 Palo Alto Square, 4000 El Camino Real
59 CITY: Palo Alto
60 STATE: California
61 COUNTRY: U.S.A.
62 ZIP: 94306
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 OPERATING SYSTEM: IBM PC compatible
66 SOFTWARE: PatentIn Release #1.0, Version #1.0
67 CURRENT APPLICATION DATA:
68 APPLICATION NUMBER: US/08/105-904B
69 FILING DATE: 31-AUG-1993
70 CLASSIFICATION: 424

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 08/057,594
3 FILING DATE: 05-MAY-1993
4 CLASSIFICATION: 424
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Neeley, Richard L.
7 REGISTRATION NUMBER: 50,092
8 REFERENCE/DOCKET NUMBER: ABIC-001/020S
9 TELECOMMUNICATION INFORMATION:
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11 TELEFAX: (415)857-0663
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13 INFORMATION FOR SEQ ID NO: 6:
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17 TOPOLOGY: linear
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61 PREPARATION BY PARALLEL ASSEMBLY
62 NUMBER OF SEQUENCES: 24
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1  COMPUTER: IBM PC compatible
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6  FILING DATE: 31-AUG-1993
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10 FILING DATE: 05-MAY-1994
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14 REGISTRATION NUMBER: 30,042
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57 QY 3 GKKKK 8
58 IIIII
59 DB 2 GKKKK 7
60
61 RESULT: 4
62 US-08-105-904B-20
63 Sequence 20: Application US/08/057594B
64 Patent No. 6001364
65 GENERAL INFORMATION:
66 APPLICANT: Rose, Keith
67 APPLICANT: Offord, Robin
68 TITLE OF INVENTION: HETERO-POLYMER COMPOUNDS AND ASSEMBLIES
69 NUMBER OF SEQUENCES: 24
70 CORRESPONDENCE ADDRESS:
71 ADDRESSEE: Cooley Godward Castro Roddenberry P.C. 500

```

```

1  STREET: 5 Palo Alto Square, 3000 El Camino Real
2  CITY: Palo Alto
3  STATE: California
4  COUNTRY: U.S.A.
5  ZIP: 94306
6  COMPUTER READABLE FORM:
7  MEDIUM TYPE: Floppy disk
8  COMPUTER: IBM PC compatible
9  OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/105-904B
13 FILING DATE: 31-AUG-1993
14 CLASSIFICATION: 424
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/057,594
17 FILING DATE: 05-MAY-1994
18 CLASSIFICATION: 424
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Neeley, Richard L.
21 REGISTRATION NUMBER: 30,042
22 REFERENCE/DOCKET NUMBER: ABIC-001/020S
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (415)843-5000
25 TELEFAX: (415)857-0663
26 TELEX: 380816 CooleyPA
27 INFORMATION FOR SEQ ID NO: 20:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 9 amino acids
30 TYPE: amino acid
31 TOPOLOGY: linear
32 MOLECULE TYPE: peptide
33 HYPOTHETICAL: NO
34 FEATURE:
35 NAME/KEY: Modified-site
36 LOCATION: 4
37 OTHER INFORMATION: Lys-BAC
38 FEATURE:
39 NAME/KEY: Modified-site
40 LOCATION: 5
41 OTHER INFORMATION: Lys-BAC
42 FEATURE:
43 NAME/KEY: Modified-site
44 LOCATION: 6
45 OTHER INFORMATION: Lys-BAC
46 FEATURE:
47 NAME/KEY: Modified-site
48 LOCATION: 7
49 OTHER INFORMATION: Lys-BAC
50 FEATURE:
51 NAME/KEY: Modified-site
52 LOCATION: 8
53 OTHER INFORMATION: Lys-BAC
54 US-08-105-904B-20
55
56 Query Match: 54.5% Score 6: DB 3: Length 9:
57 Best Local Similarity 100.0% Pred. No. 2.5e-05;
58 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
59
60 QY 3 GKKKK 8
61 IIIII
62 DB 2 GKKKK 7
63
64 RESULT: 5
65 US-08-105-904B-22
66 Sequence 22: Application US/08/057594B
67 Patent No. 6001364
68 GENERAL INFORMATION:

```

```

: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HETERO-POLYXIME COMPOUNDS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/105,904B
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: ABIC 001/020US
: TELEPHONE: (415)843-5000
: TELEFAX: (415)857-0663
: TELEX: 380816 CooleyPA
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-Boc-Ser(Leu-yl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-Boc-Ser(Leu-yl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: Lys-Boc-Ser(Leu-yl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-Boc-Ser(Leu-yl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-Boc-Ser(Leu-yl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 9
: OTHER INFORMATION: Gly-PAM
: US-08 105-904B-23

```

```

Query Match          54.5%  Score 6: 0b 4: Length 9:
Best Local Similarity 100.0%  Prod No. 2.5e+05
Matches 6: Conservative 0: Mismatches 0: Indexes 0:

```

```

QY      3 GKKKK 8
DB      2 GKKKK 7

```

```

: RESULT 6
: US-08-105-904B-23
: Sequence 23, Application US/08105904B
: Patent No.: 6001304
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HETERO-POLYXIME COMPOUNDS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/105,904B
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: ABIC-001/020US
: TELEPHONE: (415)843-5000
: TELEFAX: (415)857-0663
: TELEX: 380816 CooleyPA
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: bromoacetyl-Gly
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified site
: LOCATION: 6
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-Boc-Ser
: US-08-105-904B-23

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Query Match 54.5%; Score 6; Db 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCKKKK 8  
 Db 2 GCKKKK 7

## RESULT 7

US-08-114-877A 5  
 : Sequence 5, Application US/08114877A

Patent No. 6174530  
 : GENERAL INFORMATION:  
 : APPLICANT: Rose, Keith  
 : APPLICANT: Offord, Robin  
 : TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR  
 : PREPARATION BY PARALLEL ASSEMBLY  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 : STREET: 5 Palo Alto Square  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: U.S.A.  
 : ZIP: 94036

COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/114,877A  
 : FILING DATE: 31-AUG-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/057,594  
 : FILING DATE: 05-MAY-1993  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Nectley, Richard L.  
 : REGISTRATION NUMBER: 30,092  
 : REFERENCE/DOCKET NUMBER: ABIC 0.1/01US

TELEPHONE: (415) 843 5070  
 : TELEFAX: (415) 857-0663  
 : TELEX: 380816 CooleyCA  
 : INFORMATION FOR SEQ ID NO: 5:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear

MOLECULE TYPE: peptide  
 : HYPOTHEICAL: NO  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 1

OTHER INFORMATION: ACA-Gly  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 4

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 5

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 6

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 7

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 8

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 9

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 10

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 11

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 12

OTHER INFORMATION: Lys-A/A  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 9  
 : OTHER INFORMATION: Lys A/A  
 : US-08-114-877A-5

Query Match 54.5%; Score 6; Db 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCKKKK 8  
 Db 2 GCKKKK 7

## RESULT 6

US-08-114-877A 6  
 : Sequence 6, Application US/08114877A

Patent No. 6174530  
 : GENERAL INFORMATION:  
 : APPLICANT: Rose, Keith  
 : APPLICANT: Offord, Robin  
 : TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR  
 : PREPARATION BY PARALLEL ASSEMBLY  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 : STREET: 5 Palo Alto Square  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: U.S.A.  
 : ZIP: 94036

COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/114,877A  
 : FILING DATE: 31-AUG-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/057,594  
 : FILING DATE: 05-MAY-1993  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Nectley, Richard L.  
 : REGISTRATION NUMBER: 30,092  
 : REFERENCE/DOCKET NUMBER: ABIC-G01/01US

TELEPHONE: (415) 843 5070  
 : TELEFAX: (415) 857-0663  
 : TELEX: 380816 CooleyCA  
 : INFORMATION FOR SEQ ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear

MOLECULE TYPE: peptide  
 : HYPOTHEICAL: NO  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 1

OTHER INFORMATION: GXL-Gly  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 4

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 5

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 6

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 7

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 8

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 9

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 10

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 11

OTHER INFORMATION: Lys-GXL  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 12

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FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Lys-GXL
US-08-114-877A-6

```

```

Query Match: 54.5%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GGKKKK 8
    IIIII
DB 2 GGKKKK 7

```

```

RESULT 9
US-08-114-877A-8
: Sequence 8, Application US/08114877A
: Patent No. 6174530
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/SOCKET NUMBER: ABIC-001/0105
: TELEPHONE: (415) 843 5070
: TELEFAX: (415) 857-0663
: TELEX: 380816 CooleyPA
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: Lys-GXL
FEATURE:

```

```

FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Lys-GXL
US-08-114-877A-8

```

```

Query Match: 54.5%; Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GGKKKK 8
    IIIII
DB 2 GGKKKK 7

```

```

RESULT 10
US-08-114-877A-13
: Sequence 13, Application US/08114877A
: Patent No. 6174530
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/114,877A
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/SOCKET NUMBER: ABIC-001/0105
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 843 5070
: TELEFAX: (415) 857-0663
: TELEX: 380816 CooleyPA
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
NAME/KEY: Modified-site

```



1 REFERENCE/DOCKET NUMBER: ABIC 001/0105  
 2 TELECOMMUNICATION INFORMATION:  
 3 TELEPHONE: (415)843-5000  
 4 TELEFAX: (415)857-0663  
 5 TELEFAX: 380916 CooleyPA  
 6 INFORMATION FOR SEQ ID NO: 7:  
 7 SEQUENCE CHARACTERISTICS:  
 8 LENGTH: 10 amino acids  
 9 TYPE: amino acid  
 10 TOPOLOGY: linear  
 11 MOLECULE TYPE: peptide  
 12 HYPOTHETICAL: NO  
 13 FEATURE:  
 14 NAME/KEY: Modified site  
 15 LOCATION: 5  
 16 OTHER INFORMATION: Lys-Serine  
 17 FEATURE:  
 18 NAME/KEY: Modified site  
 19 LOCATION: 6  
 20 OTHER INFORMATION: Lys-Serine  
 21 FEATURE:  
 22 NAME/KEY: Modified site  
 23 LOCATION: 7  
 24 OTHER INFORMATION: Lys-Serine  
 25 FEATURE:  
 26 NAME/KEY: Modified site  
 27 LOCATION: 8  
 28 OTHER INFORMATION: Lys-Serine  
 29 FEATURE:  
 30 NAME/KEY: Modified site  
 31 LOCATION: 9  
 32 OTHER INFORMATION: Lys-Serine  
 33 US 08-105-904B-7

Query Match 54.5%: Score 6: DB 3: Length 10:  
 Best Local Similarity 100.0%: Prod. No. 2.8:  
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 3 GKKKK 8  
 Db 3 GKKKK 8

RESULT 14  
 US-08-114-877A-7  
 ? Sequence 7: Application US/08114877A  
 ? Patent No. 6174530  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Rose, Keith  
 ? TITLE OF INVENTION: HOMOCENES POLYMERIZATION IN ANIS AND THEIR  
 ? TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY  
 ? NUMBER OF SEQUENCES: 15  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 ? STREET: 5 Palo Alto Square  
 ? CITY: Palo Alto  
 ? STATE: California  
 ? COUNTRY: U.S.A.  
 ? ZIP: 94306  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.2  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/114,877A  
 ? FILING DATE: 31-AUG-1993  
 ? CLASSIFICATION: 424  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 08/057,154  
 ? FILING DATE: 05-MAY-1993  
 ? CLASSIFICATION: 424

1 ATTORNEY/AGENT INFORMATION:  
 2 NAME: Neeley, Richard L.  
 3 REGISTRATION NUMBER: 30,092  
 4 REFERENCE/DOCKET NUMBER: ABIC-001/0105  
 5 TELECOMMUNICATION INFORMATION:  
 6 TELEPHONE: (415) 843 5070  
 7 TELEFAX: (415) 857-0663  
 8 TELEFAX: 380916 CooleyPA  
 9 INFORMATION FOR SEQ ID NO: 7:  
 10 SEQUENCE CHARACTERISTICS:  
 11 LENGTH: 10 amino acids  
 12 TYPE: amino acid  
 13 TOPOLOGY: linear  
 14 MOLECULE TYPE: peptide  
 15 HYPOTHETICAL: NO  
 16 FEATURE:  
 17 NAME/KEY: Modified site  
 18 LOCATION: 5  
 19 OTHER INFORMATION: Lys-Serine  
 20 FEATURE:  
 21 NAME/KEY: Modified site  
 22 LOCATION: 6  
 23 OTHER INFORMATION: Lys-Serine  
 24 FEATURE:  
 25 NAME/KEY: Modified site  
 26 LOCATION: 7  
 27 OTHER INFORMATION: Lys-Serine  
 28 FEATURE:  
 29 NAME/KEY: Modified site  
 30 LOCATION: 8  
 31 OTHER INFORMATION: Lys-Serine  
 32 FEATURE:  
 33 NAME/KEY: Modified site  
 34 LOCATION: 9  
 35 OTHER INFORMATION: Lys-Serine  
 36 US-08-114-877A-7  
 37  
 38 Query Match 54.5%: Score 6: DB 3: Length 10:  
 39 Best Local Similarity 100.0%: Prod. No. 2.8:  
 40 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 41  
 42 Qy 3 GKKKK 8  
 43 Db 3 GKKKK 8  
 44  
 45 RESULT 14  
 46 US-08-105-904B-9  
 47 ? Sequence 9: Application US/08105904B  
 48 ? Patent No. 6001364  
 49 ? GENERAL INFORMATION:  
 50 APPLICANT: Rose, Keith  
 51 APPLICANT: Gifford, Robin  
 52 TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR  
 53 TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY  
 54 NUMBER OF SEQUENCES: 24  
 55 CORRESPONDENCE ADDRESS:  
 56 ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 57 STREET: 5 Palo Alto Square, 3000 El Camino Real  
 58 CITY: Palo Alto  
 59 STATE: California  
 60 COUNTRY: U.S.A.  
 61 ZIP: 94306  
 62 COMPUTER READABLE FORM:  
 63 MEDIUM TYPE: Floppy disk  
 64 COMPUTER: IBM PC compatible  
 65 OPERATING SYSTEM: PC-DOS/MS-DOS  
 66 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 67 CURRENT APPLICATION DATA:  
 68 APPLICATION NUMBER: US/08/105,904B  
 69 FILING DATE: 31-AUG-1993  
 70 CLASSIFICATION: 424  
 71 PRIOR APPLICATION DATA:

```

1  APPLICATION NUMBER: US 08/057,594
2  FILING DATE: 05-MAY-1993
3  CLASSIFICATION: 424
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Neeley, Richard L.
6  REGISTRATION NUMBER: 30,094
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: (415)843-5000
9  TELEFAX: (415)857-0663
10  INFORMATION FOR SEQ ID NO. 1:
11  SEQUENCE CHARACTERISTICS:
12  LENGTH: 11 amino acids
13  TYPE: amino acid
14  TOPOLOGY: linear
15  MOLECULE TYPE: peptide
16  HYPOTHEetical: NO
17  FEATURE:
18  NAME/KEY: Modified-site
19  LOCATION: 1
20  OTHER INFORMATION: GXL-Gly
21  FEATURE:
22  NAME/KEY: Modified-site
23  LOCATION: 4
24  OTHER INFORMATION: Lys-GXL
25  FEATURE:
26  NAME/KEY: Modified-site
27  LOCATION: 5
28  OTHER INFORMATION: Lys-GXL
29  FEATURE:
30  NAME/KEY: Modified-site
31  LOCATION: 6
32  OTHER INFORMATION: Lys-GXL
33  FEATURE:
34  NAME/KEY: Modified-site
35  LOCATION: 7
36  OTHER INFORMATION: Lys-GXL
37  FEATURE:
38  NAME/KEY: Modified-site
39  LOCATION: 8
40  OTHER INFORMATION: Lys-GXL
41  FEATURE:
42  NAME/KEY: Modified-site
43  LOCATION: 9
44  OTHER INFORMATION: Lys-GXL
45  FEATURE:
46  NAME/KEY: Modified-site
47  LOCATION: 10
48  OTHER INFORMATION: Lys-GXL
49  US 08/105-904B-21

```

```

Query Match 54.5% Score 6 10 10 10 10 10
Best Local Similarity 100.0% Pred. No. 3
Matches 6: Conservative 0: Mismatches 0: Gaps 0:

```

```

QY 3 GKKKK 8
   1111
BB 2 GKKKK 7

```

```

RESULT 15
US-08-105-904B-21
1 Sequence 21, Application 05/04/05/04B
2 Patent No. 6001364
3 GENERAL INFORMATION:
4 APPLICANT: Rose, Keith
5 APPLICANT: Orford, Robin
6 TITLE OF INVENTION: HETERO POLYXIME COMPOUNDS AND THEIR
7 PREPARATION BY RAPIDLY ASSEMBLY
8 NUMBER OF SEQUENCES: 24
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Cooley Godward Kasriel P.A.

```

```

1  STREET: 5 Palo Alto Square, 3000 El Camino Real
2  CITY: Palo Alto
3  STATE: California
4  COUNTRY: U.S.A.
5  ZIP: 94306
6  COMPUTER READABLE FORM:
7  MEDIUM TYPE: Floppy disk
8  COMPUTER: IBM PC compatible
9  OPERATING SYSTEM: PC DOS/MS-DOS
10  SOFTWARE: Patent In Release #1.0, Version #1.25
11  CURRENT APPLICATION DATA:
12  APPLICATION NUMBER: US/08/105,904B
13  FILING DATE: 31 AUG 1993
14  CLASSIFICATION: 424
15  PRIOR APPLICATION DATA:
16  APPLICATION NUMBER: US 08/057,594
17  FILING DATE: 05-MAY-1993
18  CLASSIFICATION: 424
19  ATTORNEY/AGENT INFORMATION:
20  NAME: Neeley, Richard L.
21  REGISTRATION NUMBER: 30,094
22  REFERENCE/DOCKET NUMBER: AB-C-001/020S
23  TELECOMMUNICATION INFORMATION:
24  TELEPHONE: (415)843-5000
25  TELEFAX: (415)857-0663
26  TELEX: 460816 CooleyPA
27  INFORMATION FOR SEQ ID NO. 21:
28  SEQUENCE CHARACTERISTICS:
29  LENGTH: 11 amino acids
30  TYPE: amino acid
31  TOPOLOGY: linear
32  MOLECULE TYPE: peptide
33  HYPOTHEtical: NO
34  FEATURE:
35  NAME/KEY: Modified-site
36  LOCATION: 4
37  OTHER INFORMATION: Lys-Boc
38  FEATURE:
39  NAME/KEY: Modified-site
40  LOCATION: 5
41  OTHER INFORMATION: Lys-Boc
42  FEATURE:
43  NAME/KEY: Modified-site
44  LOCATION: 6
45  OTHER INFORMATION: Lys-Boc
46  FEATURE:
47  NAME/KEY: Modified-site
48  LOCATION: 7
49  OTHER INFORMATION: Lys-Boc
50  FEATURE:
51  NAME/KEY: Modified-site
52  LOCATION: 8
53  OTHER INFORMATION: Lys-Boc
54  FEATURE:
55  NAME/KEY: Modified-site
56  LOCATION: 9
57  OTHER INFORMATION: Lys-Boc
58  FEATURE:
59  NAME/KEY: Modified-site
60  LOCATION: 10
61  OTHER INFORMATION: Lys-Boc
62  FEATURE:
63  NAME/KEY: Modified-site
64  LOCATION: 11
65  OTHER INFORMATION: Gly-PAM
66  US-08-105-904B-21

```

```

Query Match 54.5% Score 6: DB 3: Length 11:
Best Local Similarity 100.0% Pred. No. 3:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 GKKKK 8
   1111

```



2 GSKKKK 7  
 RESULT 16  
 US-08-114-877A-9  
 : Sequence 9, Application US/08114877A  
 : Patent No. 6174530  
 : GENERAL INFORMATION:  
 : APPLICANT: Rose, Keith  
 : APPLICANT: Offord, Robin  
 : TITLE OF INVENTION: HOMOGENOUS POLYOXINE COMPOSITIONS AND THEIR  
 : PREPARATION BY PARALLEL ASSEMBLY  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 : STREET: 5 Palo Alto Square  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: U.S.A.  
 : ZIP: 94036  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC Compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/114.877A  
 : FILING DATE: 31-AUG-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/057,594  
 : FILING DATE: 05-MAY-1993  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Neeley, Richard L.  
 : REGISTRATION NUMBER: 30,092  
 : REFERENCE/DOCKET NUMBER: ABIC-061/010US  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 843 5070  
 : TELEFAX: (415) 857-0663  
 : TELEX: 380816 CooleyPA  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 11 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : HYPOTHETICAL: NO  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 1  
 : OTHER INFORMATION: GLX Gly  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 4  
 : OTHER INFORMATION: Lys-GLX  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 5  
 : OTHER INFORMATION: Lys-GLX  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 6  
 : OTHER INFORMATION: Lys-GLX  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 7  
 : OTHER INFORMATION: Lys-GLX  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 8  
 : OTHER INFORMATION: Lys-GLX  
 : FEATURE:

: NAME/KEY: Modified-site  
 : LOCATION: 9  
 : OTHER INFORMATION: Lys-GLX  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 10  
 : OTHER INFORMATION: Lys-GLX  
 : US-08-114-877A-9  
 Query Match 54.5% Score 6; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GSKKKK 8  
 Db 2 GSKKKK 7  
 RESULT 17  
 US-08-114-877A 14  
 : Sequence 14, Application US/08114877A  
 : Patent No. 6174530  
 : GENERAL INFORMATION:  
 : APPLICANT: Rose, Keith  
 : APPLICANT: Offord, Robin  
 : TITLE OF INVENTION: HOMOGENOUS POLYOXINE COMPOSITIONS AND THEIR  
 : PREPARATION BY PARALLEL ASSEMBLY  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 : STREET: 5 Palo Alto Square  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: U.S.A.  
 : ZIP: 94036  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC Compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/114.877A  
 : FILING DATE: 31-AUG-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/057,594  
 : FILING DATE: 05-MAY-1993  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Neeley, Richard L.  
 : REGISTRATION NUMBER: 30,092  
 : REFERENCE/DOCKET NUMBER: ABIC-061/010US  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 843 5070  
 : TELEFAX: (415) 857-0663  
 : TELEX: 380816 CooleyPA  
 : INFORMATION FOR SEQ ID NO: 14:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 11 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : HYPOTHETICAL: NO  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 4  
 : OTHER INFORMATION: Lys-BOC  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 5  
 : OTHER INFORMATION: Lys-b-X  
 : FEATURE:  
 : NAME/KEY: Modified-site

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: LOCATION: 6
: OTHER INFORMATION: Lys-BUC
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-BUC
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-BUC
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 9
: OTHER INFORMATION: Lys-BUC
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: Lys-BUC
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 11
: OTHER INFORMATION: Gly-PAM
: US-08-114-877A-14

Query Match 54.5%; Score 6; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8
DB 2 GKKKK 7

RESULT 18
US-08-615-181-67
: Sequence 67, Application US/08615181
: Patent No. 5756666
: GENERAL INFORMATION:
: APPLICANT: MASAFUMI, TAKIUCHI
: TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
: TITLE OF INVENTION: RESPONSE TO HIV AND AID1 AIDS AGENT FOR PREVENTING AND
: NUMBER OF SEQUENCES: 115
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MOULLELAND, HAER & NEUSTADT,
: STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.00
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/615-181
: FILING DATE: 04-APR-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP94/01756
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 261302/1993
: FILING DATE: 19-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLON, NORMAN F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 10-756-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000

```

```

: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
: US-08-615-181-67

Query Match 45.5%; Score 5; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7
DB 1 GKKKK 5

RESULT 19
US-09-389-390-7
: Sequence 7, Application US/09389390
: Patent No. 6558961
: GENERAL INFORMATION:
: APPLICANT: SAKPHIE
: TITLE OF INVENTION: IMMUNODIAGNOSTICS USING PARTICLE DELIVERY METHODS
: FID REFERENCE: OPF1620
: CURRENT APPLICATION NUMBER: US/09/389,390
: PRIOR FILING DATE: 1999-09-03
: PRIOR APPLICATION NUMBER: 60/099,261
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 60/139,045
: PRIOR FILING DATE: 1999-06-10
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:synthetic
: US-09-389-390-7

Query Match 45.5%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7
DB 1 GKKKK 5

RESULT 20
US-08-159-339A-1163
: Sequence 1163, Application US/08159339A
: Patent No. 6037135
: GENERAL INFORMATION:
: APPLICANT: Kubo, Ralph T.
: APPLICANT: Grey, Howard M.
: APPLICANT: Settle, Alessandro
: APPLICANT: Celis, Esteban
: TITLE OF INVENTION: HLA Binding peptides and Their
: TITLE OF INVENTION: Uses
: NUMBER OF SEQUENCES: 1254
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA

```

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastISO for Windows Version: 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,454A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,596  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/03,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 1163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-1163

Query Match: 45.5%; Score 5; DB 3; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
DB 5 GKKKK 9

RESULT 2:  
US-08-197-484-30  
Sequence 30, Application US/08197484  
Patent No. 6419931  
GENERAL INFORMATION:  
APPLICANT: VITIELLO, Maria A.  
APPLICANT: CHESTNUT, Robert W.  
APPLICANT: SETTE, Alessandro D.  
APPLICANT: CELIS, Esteban  
APPLICANT: GRAY, Howard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Koorntje and Crew  
Street: Stewart Street Tower, One Market Plaza  
City: San Francisco  
State: California  
Country: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,484  
FILING DATE: 16-FEB-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (206) 623-6794  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-197-484-30

Query Match: 45.5%; Score 5; DB 4; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
DB 1 GKKKK 5

RESULT 22  
PCT US95-02121-30  
Sequence 30, Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
NUMBER OF SEQUENCES: 153  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,484  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600  
 TELEFAX: (415) 543-5043  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 ECT-US95-02121-10

Query Match 45.5%, Score 5, DR 2, Length 12;  
 Best Local Similarity 100.0%, Pred. No. 31;  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 3 GKKKK 7  
 DB 1111  
 6 KKKKK 5

RESULT 24  
 US-08-928-958 16  
 Sequence 16, Application US/08928-958  
 Patent No. 5877282  
 GENERAL INFORMATION:  
 APPLICANT: NADLER, STEVEN S.  
 APPLICANT: CLEVELAND, JEFFREY S.  
 APPLICANT: BLAKE, JAMES K.  
 APPLICANT: HAEFAR, OMAR K.  
 TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
 TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
 TITLE OF INVENTION: METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ROBINS & ASSOCIATES  
 STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
 CITY: MENLO PARK  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/928-958  
 FILING DATE: 12-SEP-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/928-958  
 FILING DATE: 20-SEP-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: F. HENS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/AGENT NUMBER: 5998 0013  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 325-7812  
 TELEFAX: (650) 325-7823  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-928-958 16

Query Match 45.5%, Score 5, DR 2, Length 12;  
 Best Local Similarity 100.0%, Pred. No. 31;  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 3 GKKKK 9

DB 1111  
 6 KKKKK 10

RESULT 24  
 US-09-072-429-16  
 Sequence 16, Application US/09072429  
 Patent No. 5962415  
 GENERAL INFORMATION:  
 APPLICANT: NADLER, STEVEN S.  
 TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
 TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLATION AND AN  
 TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bristol Myers Squibb Company  
 STREET: P.O. Box 4000  
 CITY: Princeton  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 08543-4000  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/072-429  
 FILING DATE: 04 MAY-1998  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Klein, Christopher A.  
 REGISTRATION NUMBER: 34,484  
 REFERENCE/AGENT NUMBER: 0901410  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (609) 252-3714  
 TELEFAX: (609) 252-4526  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-072-429-16

Query Match 45.5%, Score 5, DR 2, Length 12;  
 Best Local Similarity 100.0%, Pred. No. 31;  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 KKKKK 9  
 DB 1111  
 6 KKKKK 10

RESULT 25  
 US-08-970-833 9  
 Sequence 9, Application US/08970833  
 Patent No. 6520859  
 GENERAL INFORMATION:  
 APPLICANT: Kessling, Linda L.  
 APPLICANT: Murphy, Robert M.  
 TITLE OF INVENTION: INHIBITORS OF BETA AMYLOID TOXICITY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quarles & Brady  
 STREET: 411 East Wisconsin Avenue  
 CITY: Milwaukee  
 STATE: Wisconsin  
 COUNTRY: U.S.A.  
 ZIP: 53202-4307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/975,833
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Baker, Jean C.
: REGISTRATION NUMBER: 35,433
: REFERENCE/DOCKET NUMBER: 960296, 34291
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (414) 277-5769
: TELEFAX: (414) 271-3552
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-970-833-9

Query Match 45.5%: Score 5; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8
DL 6 GKKKK 10

RESULT 26
: Sequence 11, Application US/07854629
: Patent No. 5480667
: GENERAL INFORMATION:
: APPLICANT: MICHAEL, ANDREW J.
: APPLICANT: NIXON, DOUGLAS F.
: APPLICANT: TOWNSEND, ALAIN R. M.
: APPLICANT: GUTCH, FRANCES M.
: TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTAEDT,
: STREET: 1755 S. Jefferson Davis Highway, Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/854,629
: FILING DATE: 19920706
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9004287.4
: FILING DATE: 05-JAN-1990
: APPLICATION NUMBER: GB 9003577.5
: FILING DATE: 16-FEB-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLON, NO. 548067man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 3077-003-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Human immunodeficiency virus
: US-08-474-008 11

```

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: TELEX: 248855 OPAT UR
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Human immunodeficiency virus
: US-07-854-629-11

Query Match 45.5%: Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7
DL 4 GKKKK 5

RESULT 27
: Sequence 11, Application US/08474008
: Patent No. 5700469
: GENERAL INFORMATION:
: APPLICANT: MICHAEL, ANDREW J.
: APPLICANT: NIXON, DOUGLAS F.
: APPLICANT: TOWNSEND, ALAIN R. M.
: APPLICANT: GUTCH, FRANCES M.
: TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTAEDT,
: STREET: 1755 S. Jefferson Davis Highway, Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,008
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/854,629
: FILING DATE: 06-JUL-1992
: APPLICATION NUMBER: GB 900287.4
: FILING DATE: 05-JAN-1990
: APPLICATION NUMBER: GB 9003577.5
: FILING DATE: 16-FEB-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLON, NO. 5700469man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 3077-003-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Human immunodeficiency virus
: US-08-474-008 11

```

1. TITLE OF INVENTION: TRANSFERASE

1 CURRENT APPLICATION DATA:  
2 APPLICATION NUMBER: US/08/985,320A  
3 FILING DATE:  
4 CLASSIFICATION: 514  
5 PRIOR APPLICATION DATA:  
6 APPLICATION NUMBER: 60/032,579  
7 FILING DATE: 05-DEC-1996  
8 ATTORNEY/AGENT INFORMATION:  
9 NAME: Muthard, David A.  
10 REGISTRATION NUMBER: 35,297  
11 REFERENCE/DOCKET NUMBER: 19850Y  
12 TELECOMMUNICATION INFORMATION:  
13 TELEPHONE: 908-594-3903  
14 TELEFAX: 908-594-4720  
15 TELEX:

16 INFORMATION FOR SEQ ID NO: 1:

17 SEQUENCE CHARACTERISTICS:

18 LENGTH: 15 amino acids

19 TYPE: amino acid

20 STRANDEDNESS: single

21 TOPOLOGY: linear

22 MOLECULE TYPE: protein

23 US 08-985-320A-1

Query Match 45.5% Score 5; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

|||||

Db 1 GKKKK 5

RESULT 3:

US-08-984,732A-1

Sequence 1, Application US/08484732A

Patent No. 6015417

GENERAL INFORMATION:

APPLICANT: Halczenko, Wasyli

APPLICANT: Slump, Craig A.

TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN

TITLE OF INVENTION: TRANSFERASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000, 126 E. Lincoln Ave.

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/984,732A

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,126

FILING DATE: 05-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Muthard, David A.

REGISTRATION NUMBER: 35,297

REFERENCE/DOCKET NUMBER: 19849Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3903

TELEFAX: 908-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

1 TYPE: amino acid  
2 STRANDEDNESS: single  
3 TOPOLOGY: linear  
4 MOLECULE TYPE: protein  
5 US-08-984-732A-1

Query Match 45.5% Score 5; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

|||||

Db 1 GKKKK 5

RESULT 32

US-09-195-578-13

Sequence 13, Application US/09195578

Patent No. 6054466

GENERAL INFORMATION:

APPLICANT: Ciccarone, Terrence M.

APPLICANT: deSolms, Jane S. J.

APPLICANT: Merck & Co., Inc.

TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN

TITLE OF INVENTION: TRANSFERASE

FILE REFERENCE: 20121Y

CURRENT APPLICATION NUMBER: US/09/195,578

CURRENT FILING DATE: 1998-11-18

EARLIER APPLICATION NUMBER: 60/067,552

EARLIER FILING DATE: 1997-12-04

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-195-578-13

Query Match 45.5% Score 5; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

|||||

Db 1 GKKKK 5

RESULT 33

US-09-140-557-13

Sequence 13, Application US/09140557A

Patent No. 6103487

GENERAL INFORMATION:

APPLICANT: Merck & Co., Inc.

APPLICANT: Barnett, Stanley F.

APPLICANT: Heimbrook, David C.

APPLICANT: Huber, Hans E.

APPLICANT: Patrick, Denis R.

TITLE OF INVENTION: A METHOD OF TREATING CANCER

FILE REFERENCE: 20034Y

CURRENT APPLICATION NUMBER: US/09/140,557A

CURRENT FILING DATE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/057,340

EARLIER FILING DATE: 1997-08-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthesized peptide substrate for

OTHER INFORMATION: geranylgeranyl-protein transferase type I

US-09-140-557-13

Query Match 45.5% Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
DB 1 GKKKK 5

## RESULT 14

US-09-170-951-13

Sequence 13, Application US/05170951

Patent No. 6104723

GENERAL INFORMATION:

APPLICANT: Bergman, Jeffrey M.

APPLICANT: Dismore, Christopher J.

APPLICANT: Graham, Samuel L.

APPLICANT: Merck & Co., Inc.

TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN

FILE REFERENCE: 19867Y

CURRENT APPLICATION NUMBER: US/09/170-951

CURRENT FILING DATE: 1998-10-13

EARLIER APPLICATION NUMBER: 60/364,342

EARLIER FILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-170-951-13

Query Match 45.5% Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
DB 1 GKKKK 5

## RESULT 15

US-09-154-482-13

Sequence 13, Application US/09104442A

Patent No. 6127490

GENERAL INFORMATION:

APPLICANT: Merck & Co., Inc.

APPLICANT: deSoums, S. Jane

APPLICANT: Lema, William P.

APPLICANT: Shaw, Anthony W.

APPLICANT: Susko, John T.

APPLICANT: Tucker, Thomas J.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

FILE REFERENCE: 20025Y

CURRENT APPLICATION NUMBER: US/09/154-482A

CURRENT FILING DATE: 1998-10-01

EARLIER APPLICATION NUMBER: 60/660,871

EARLIER FILING DATE: 1997-10-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthesized peptide substrate for

OTHER INFORMATION: geranylgeranyl-protein transferase type 1

US-09-154-482-13

Query Match 45.5% Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 37;

QY 4 GKKKK 8  
DB 1 GKKKK 5

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
DB 1 GKKKK 5

## RESULT 36

US-09-332-769-2

Sequence 2, Application US/09332769

Patent No. 6172076

GENERAL INFORMATION:

APPLICANT: Embrey, Mark W.

APPLICANT: Perlow, David S.

APPLICANT: Wai, Colin S.

APPLICANT: Hoffman, Jacob M.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN

FILE REFERENCE: 19982Y

CURRENT APPLICATION NUMBER: US/09/332,769

CURRENT FILING DATE: 1999-06-14

EARLIER APPLICATION NUMBER: US 60/089,311

EARLIER FILING DATE: 1998-06-15

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-332-769-2

Query Match 45.5% Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
DB 1 GKKKK 5

## RESULT 37

US-09-456-153-2

Sequence 2, Application US/09456153

Patent No. 6284755

GENERAL INFORMATION:

APPLICANT: deSoums, S. Jane

APPLICANT: Graham, Samuel L.

APPLICANT: Shaw, Anthony W.

APPLICANT: Ciccarone, Terrence M.

APPLICANT: Stokker, Gerald E.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN

FILE REFERENCE: 20312Y

CURRENT APPLICATION NUMBER: US/09/456,153

CURRENT FILING DATE: 1999-12-07

EARLIER APPLICATION NUMBER: US 60/111,416

EARLIER FILING DATE: 1998-12-08

EARLIER APPLICATION NUMBER: US 60/129,282

EARLIER FILING DATE: 1999-04-14

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-456-153-2

Query Match 45.5% Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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db      1 GKKKK 5

RESULT 38
US 09-157-180 14
: Sequence 13, Application US/09157180
: Patent No. 6297239
: GENERAL INFORMATION:
: APPLICANT: deSolms, S. Jane
: APPLICANT: Hutchinsch, John H.
: APPLICANT: Shaw, Anthony W.
: APPLICANT: Graham, Samuel L.
: APPLICANT: Citardone, Terrence M.
: APPLICANT: Merck & Co., Inc.
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
: FILE REFERENCE: 19928Y
: CURRENT APPLICATION NUMBER: US/09157180
: CURRENT FILING DATE: 1998-10-06
: EARLIER APPLICATION NUMBER: 62/862,535
: EARLIER FILING DATE: 1997-10-08
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 13
: LENGTH: 15
: TYPE: PRI
: ORGANISM: Homosapien
US 09-167-180-13
: Query Match      45.5%, Score 5; DB 13; Length 15;
: Best Local Similarity 100.0%; Pred. No. 37;
: Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GKKKK 8
DB      1 GKKKK 5

RESULT 39
US-09-455-627-2
: Sequence 2, Application US/09455627
: Patent No. 6316476
: GENERAL INFORMATION:
: APPLICANT: deSolms, S. Jane
: APPLICANT: Shaw, Anthony W.
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
: FILE REFERENCE: 20325
: CURRENT APPLICATION NUMBER: US/09455627
: CURRENT FILING DATE: 1999-12-07
: EARLIER APPLICATION NUMBER: US 62/31162
: EARLIER FILING DATE: 1998-12-08
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 15
: TYPE: PRI
: ORGANISM: Homosapien
US 09-455-627 2
: Query Match      45.5%, Score 5; DB 4; Length 15;
: Best Local Similarity 100.0%; Pred. No. 37;
: Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GKKKK 8
DB      1 GKKKK 5

RESULT 40
US 09-426-533-2
: Sequence 2, Application US/09426533
: Patent No. 6359376
: GENERAL INFORMATION:

```

```

: APPLICANT: Bergman, Jeffrey M.
: TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase
: FILE REFERENCE: 2028Y
: CURRENT APPLICATION NUMBER: US/09/426.533
: CURRENT FILING DATE: 1999-10-26
: EARLIER APPLICATION NUMBER: 60/101,177
: EARLIER FILING DATE: 1998-10-29
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 15
: TYPE: PRI
: ORGANISM: Homosapien
US 09-426-533-2
: Query Match      45.5%, Score 5; DB 4; Length 15;
: Best Local Similarity 100.0%; Pred. No. 37;
: Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GKKKK 8
DB      1 GKKKK 5

RESULT 41
US-09-609-205-2
: Sequence 2, Application US/09609205
: Patent No. 6335325
: GENERAL INFORMATION:
: APPLICANT: Merck & Co., Inc.
: APPLICANT: Dinsmore, Christopher J.
: APPLICANT: Graham, Samuel L.
: APPLICANT: Williams, Theresa M.
: TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
: FILE REFERENCE: 20488
: CURRENT APPLICATION NUMBER: US/09/609,205
: CURRENT FILING DATE: 2000-05-30
: PRIOR APPLICATION NUMBER: 60/145,331
: PRIOR FILING DATE: 1999-07-23
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 15
: TYPE: PRI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: completely synthetic sequence
US 09-609-205-2
: Query Match      45.5%, Score 5; DB 4; Length 15;
: Best Local Similarity 100.0%; Pred. No. 37;
: Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GKKKK 8
DB      1 GKKKK 5

RESULT 42
US 09-516-945 2
: Sequence 2, Application US/09516945
: Patent No. 6355345
: GENERAL INFORMATION:
: APPLICANT: Merck & Co., Inc.
: APPLICANT: Lema, William G. Jr.
: APPLICANT: Smith, Anthony M.
: APPLICANT: Sisko, John T.
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
: FILE REFERENCE: 20435Y
: CURRENT APPLICATION NUMBER: US/09/516,945
: CURRENT FILING DATE: 2000-03-01
: EARLIER APPLICATION NUMBER: 60/122,970
: EARLIER FILING DATE: 1998-05-03

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: EARLIER APPLICATION NUMBER: 60/127,259  
 : EARLIER FILING DATE: 1999-03-31  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-516-757-2

Query Match 45.5% Score 5: 14.4 Length 15  
 Best Local Similarity 100.0% Pred. No. 37  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 1 GKKKK 5

RESULT 44  
 US-09-757-218-3  
 : Sequence 2: Application US/095757-18  
 : Patent No. 6350755  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Luzzo, William C. Jr.  
 : APPLICANT: Sisk, John T.  
 : APPLICANT: Smith, Anthony M.  
 : APPLICANT: Tucker, Thomas J.  
 : APPLICANT: Dinsmore, Christopher J.  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20399Y  
 : CURRENT APPLICATION NUMBER: US/09/516,750  
 : PRIOR APPLICATION NUMBER: 60/175,253  
 : PRIOR FILING DATE: 2000-01-12  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 3  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely synthetic sequence  
 US-09-757-218-3

Query Match 45.5% Score 5: 14.4 Length 15  
 Best Local Similarity 100.0% Pred. No. 37  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 1 GKKKK 5

RESULT 44  
 US-09-516-757-2  
 : Sequence 2: Application US/09516757  
 : Patent No. 6358956  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Luzzo, William C. Jr.  
 : APPLICANT: Sisk, John T.  
 : APPLICANT: Smith, Anthony M.  
 : APPLICANT: Tucker, Thomas J.  
 : APPLICANT: Berkman, Jeffrey M.  
 : APPLICANT: Dinsmore, Christopher J.  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20399Y  
 : CURRENT APPLICATION NUMBER: US/09/516,750  
 : PRIOR APPLICATION NUMBER: 60/122,768  
 : PRIOR FILING DATE: 1998-03-31  
 : EARLIER APPLICATION NUMBER: 60/127,253  
 : EARLIER FILING DATE: 1999-03-31

: EARLIER FILING DATE: 1999-03-31  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-516-757-2

Query Match 45.5% Score 5: 14.4 Length 15  
 Best Local Similarity 100.0% Pred. No. 37  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 1 GKKKK 5

RESULT 45  
 US-09-516-750-2  
 : Sequence 2: Application US/09516750  
 : Patent No. 6358956  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Luzzo, William C. Jr.  
 : APPLICANT: Sisk, John T.  
 : APPLICANT: Smith, Anthony M.  
 : APPLICANT: Stokker, Gerald E.  
 : APPLICANT: Tucker, Thomas J.  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20399Y  
 : CURRENT APPLICATION NUMBER: US/09/516,750  
 : CURRENT FILING DATE: 2000-03-01  
 : EARLIER APPLICATION NUMBER: 60/122,768  
 : EARLIER FILING DATE: 1998-03-31  
 : EARLIER APPLICATION NUMBER: 60/127,253  
 : EARLIER FILING DATE: 1999-03-31  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely synthetic sequence  
 US-09-516-750-2

Query Match 45.5% Score 5: 14.4 Length 15  
 Best Local Similarity 100.0% Pred. No. 37  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 1 GKKKK 5

RESULT 45  
 US-09-516-757-2  
 : Sequence 2: Application US/0942577  
 : Patent No. 6358956  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Anthony, Neville J.  
 : APPLICANT: Bell, Ian M.  
 : APPLICANT: Beshore, Douglas C.  
 : APPLICANT: Ciccatone, Terrence M.  
 : APPLICANT: Desolms, S. Jane  
 : APPLICANT: Dinsmore, Christopher J.  
 : APPLICANT: Stokker, Gerald E.  
 : TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN

; TITLE OF INVENTION: TRANSFERASE  
 ; FILE REFERENCE: 202751  
 ; CURRENT APPLICATION NUMBER: US/09/342,577  
 ; CURRENT FILING DATE: 1999-06-29  
 ; EARLIER APPLICATION NUMBER: 60/591,513  
 ; EARLIER FILING DATE: 1998-07-02  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 15  
 ; TYPE: PR1  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: completely synthetic sequence  
 US-09-342-577-3

Query Match 45.5% Score 5; DB 4; Length 15;  
 Best Local Similarity 100.0% Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
 DB 1 GKKKK 5

RESULT 47  
 US-09-516-756-2  
 ; Sequence 2; Application US/09516756  
 ; Patent No. 6475496  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Battman, George D.  
 ; APPLICANT: Lamma, William C. Jr.  
 ; APPLICANT: Smith, Anthony M.  
 ; APPLICANT: Tucker, Thomas J.  
 ; APPLICANT: Reimold, Jeffrey M.  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20288Y  
 ; CURRENT APPLICATION NUMBER: US/09/516,756  
 ; CURRENT FILING DATE: 2000-03-01  
 ; EARLIER APPLICATION NUMBER: 60/122,478  
 ; EARLIER FILING DATE: 1998-03-03  
 ; EARLIER APPLICATION NUMBER: 60/122,142  
 ; EARLIER FILING DATE: 1999-03-31  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 15  
 ; TYPE: PR1  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: completely synthetic sequence  
 US-09-516-756-2

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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
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 ; Sequence 3; Application US/09628061A  
 ; Patent No. 6480228  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Craig A. Stump  
 ; APPLICANT: Theresa M. Williams  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20635Y  
 ; CURRENT APPLICATION NUMBER: US/09/828,061A  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/196,231  
 ; PRIOR FILING DATE: 2000-04-10  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 15  
 ; TYPE: PR1  
 ; ORGANISM: Artificial Sequence  
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 ; OTHER INFORMATION: Completely Synthetic Amino Acid  
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QY 4 GKKKK 8  
 IIII  
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RESULT 49  
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 ; Sequence 2; Application US/09463917  
 ; Patent No. 6387904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Dinsmore, Christopher J.  
 ; APPLICANT: Hutchinson, John H.  
 ; APPLICANT: Williams, Theresa M.  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20040Y  
 ; CURRENT APPLICATION NUMBER: US/09/463,917  
 ; CURRENT FILING DATE: 2000-02-01  
 ; PRIOR APPLICATION NUMBER: 60/057,080  
 ; PRIOR FILING DATE: 1997-06-27  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 15  
 ; TYPE: PR1  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthesized peptide substrate for  
 ; OTHER INFORMATION: qcratylquanyl-prtoein transferase type I  
 US-09-463-917-2

Query Match 45.5% Score 5; DB 4; Length 15;  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
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 ; Sequence 3; Application US/09347673  
 ; Patent No. 6410544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Dinsmore, Christopher J.  
 ; APPLICANT: Reil, Ian M.  
 ; APPLICANT: Reshore, Douglas C.  
 ; APPLICANT: Williams, Theresa M.  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20236Y  
 ; CURRENT APPLICATION NUMBER: US/09/347,673  
 ; CURRENT FILING DATE: 1999-06-29

! EARLIER APPLICATION NUMBER: 60/091,596  
! EARLIER FILING DATE: 1998-07-02  
! NUMBER OF SEQ ID NOS: 25  
! SOFTWARE: FastSeq for Windows Version 3.0  
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! TYPE: PRT  
! ORGANISM: Artificial Sequence  
! FEATURE:  
! OTHER INFORMATION: completely synthetic sequence  
US 09-347-673-3

Query Match: 45.58; Score 5; DB 4; Length 15;  
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Matches 5; Conservative 0; Mismatches 0; Gaps 0;

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Job time : 15.9.67 secs

GenCore version 5.1.6  
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OLM protein - protein search, using sw model

Run on: September 30, 2004, 10:13:03 : Search time 21.5 seconds  
(without alignments)  
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Title: US-09-787-443-19

Perfect score: 11

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Scoring table: Gapop 60.0, Gapext 60.0

Searched: 566894 seqs, 151307093 residues

Word size: 0

Total number of hits satisfying chosen parameters: 65887

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

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Prod. No. is the number of results produced by chance to have a score greater than or equal to the score of the best hit below printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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7	5	45.5	9	12	US-10-206-156-13
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33	4	36.4	8	10	US-09-945-249-82	Sequence 82, Appl1
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102	4	36.4	10	15	US-10-133-230-21	Sequence 21, Appl	175	4	36.4	14	11	US-09-876-904A-91	Sequence 91, Appl
103	4	36.4	10	15	US-10-075-869-45	Sequence 55, Appl	176	4	36.4	14	11	US-09-876-904A-330	Sequence 330, App
104	4	36.4	11	10	US-09-846-442-1	Sequence 1, Appl	177	4	36.4	14	12	US-10-133-973-51	Sequence 51, Appl
105	4	36.4	11	10	US-09-835-501-5	Sequence 5, Appl	178	4	36.4	14	12	US-10-264-672-13	Sequence 13, Appl
106	4	36.4	11	10	US-09-835-501-43	Sequence 43, Appl	179	4	36.4	14	12	US-10-226-629A-280	Sequence 280, App
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141	4	36.4	13	10	US-09-746-176-5	Sequence 40, Appl	214	3	27.3	8	9	US-09-765-527-237	Sequence 237, App
142	4	36.4	13	10	US-09-805-431-7	Sequence 7, Appl	215	3	27.3	8	9	US-09-796-264-6	Sequence 6, Appl
143	4	36.4	13	10	US-09-805-431-11	Sequence 45, Appl	216	3	27.3	8	9	US-09-796-264-9	Sequence 9, Appl
144	4	36.4	13	10	US-09-805-431-11	Sequence 50, Appl	217	3	27.3	8	9	US-09-949-780-7	Sequence 7, Appl
145	4	36.4	13	11	US-09-862-291-52	Sequence 101, App	218	3	27.3	8	9	US-09-847-712-3	Sequence 3, Appl
146	4	36.4	13	11	US-09-876-904A-38	Sequence 88, Appl	219	3	27.3	8	9	US-09-898-461-1	Sequence 1, Appl
147	4	36.4	13	11	US-09-876-904A-59	Sequence 89, Appl	220	3	27.3	8	10	US-09-845-226-6	Sequence 6, Appl
148	4	36.4	13	11	US-09-876-904A-590	Sequence 595, App	221	3	27.3	8	10	US-09-845-226-9	Sequence 9, Appl
149	4	36.4	13	11	US-09-876-904A-600	Sequence 600, App	222	3	27.3	8	10	US-09-984-056-69	Sequence 69, Appl
150	4	36.4	13	11	US-09-876-904A-620	Sequence 420, App	223	3	27.3	8	10	US-09-984-056-79	Sequence 79, Appl
151	4	36.4	13	11	US-09-013-077A-6	Sequence 6, Appl	224	3	27.3	8	10	US-09-864-866-30	Sequence 30, Appl
152	4	36.4	13	11	US-09-922-666-23	Sequence 27, Appl	225	3	27.3	8	10	US-09-985-157-10	Sequence 10, Appl
153	4	36.4	13	11	US-09-948-783-422	Sequence 422, App	226	3	27.3	8	10	US-09-883-825-2	Sequence 2, Appl
154	4	36.4	13	12	US-09-741-524-24	Sequence 24, Appl	227	3	27.3	8	10	US-09-969-192-1	Sequence 1, Appl
155	4	36.4	13	12	US-09-741-524-136	Sequence 136, Appl	228	3	27.3	8	10	US-09-984-057-69	Sequence 69, Appl
156	4	36.4	13	12	US-10-153-243-75	Sequence 75, Appl	229	3	27.3	8	10	US-09-984-057-79	Sequence 79, Appl
157	4	36.4	13	12	US-10-153-243-75	Sequence 138, Appl	230	3	27.3	8	10	US-09-967-772-8	Sequence 8, Appl
158	4	36.4	13	12	US-10-153-243-185	Sequence 188, App	231	3	27.3	8	10	US-09-795-903A-6	Sequence 6, Appl
159	4	36.4	13	12	US-10-153-243-248	Sequence 248, App	232	3	27.3	8	10	US-09-795-903A-9	Sequence 9, Appl
160	4	36.4	13	12	US-10-153-243-248	Sequence 4, Appl	233	3	27.3	8	10	US-09-840-277-3	Sequence 3, Appl
161	4	36.4	13	15	US-10-267-849-45	Sequence 45, Appl	234	3	27.3	8	11	US-09-999-724-74	Sequence 74, Appl

235	8	11	US-09-847-724-94	Sequence 94, Appl	308	3	27.3	9	9	US-09-879-936-24	Sequence 24, Appl
236	8	11	US-09-847-249A-8	Sequence 6, Appl	309	3	27.3	9	9	US-09-916-109-9	Sequence 9, Appl
237	8	11	US-09-843-241A-6	Sequence 3, Appl	310	3	27.3	9	10	US-09-850-351A-95	Sequence 95, Appl
238	8	11	US-09-840-669B-3	Sequence 3, Appl	311	3	27.3	9	10	US-09-780-053-56	Sequence 56, Appl
239	8	11	US-09-840-748-3-42	Sequence 412, Ap	312	3	27.3	9	10	US-09-780-053-255	Sequence 255, App
240	8	11	US-09-876-924A-84	Sequence 84, Appl	313	3	27.3	9	10	US-09-780-053-260	Sequence 260, App
241	8	11	US-09-876-904A-263	Sequence 263, App	314	3	27.3	9	10	US-09-780-053-333	Sequence 333, App
242	8	11	US-09-876-904A-263	Sequence 452, App	315	3	27.3	9	10	US-09-780-053-334	Sequence 334, App
243	8	11	US-09-876-904A-263	Sequence 456, App	316	3	27.3	9	10	US-09-894-018-224	Sequence 224, App
244	8	11	US-09-876-904A-263	Sequence 456, App	317	3	27.3	9	10	US-09-971-067-1	Sequence 1, Appl
245	8	11	US-09-876-904A-263	Sequence 456, App	318	3	27.3	9	10	US-09-888-721-30	Sequence 30, Appl
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247	8	11	US-09-876-904A-263	Sequence 456, App	320	3	27.3	9	10	US-09-753-831-10	Sequence 10, Appl
248	8	11	US-09-876-904A-263	Sequence 456, App	321	3	27.3	9	10	US-09-753-831-11	Sequence 11, Appl
249	8	11	US-09-876-904A-263	Sequence 456, App	322	3	27.3	9	10	US-09-753-831-27	Sequence 27, Appl
250	8	11	US-09-876-904A-263	Sequence 506, App	323	3	27.3	9	10	US-09-753-831-28	Sequence 28, Appl
251	8	11	US-09-876-904A-263	Sequence 506, App	324	3	27.3	9	10	US-09-753-831-33	Sequence 33, Appl
252	8	11	US-09-876-904A-263	Sequence 574, App	325	3	27.3	9	10	US-09-739-068-5	Sequence 5, Appl
253	8	11	US-09-876-904A-263	Sequence 612, App	326	3	27.3	9	10	US-09-791-378-125	Sequence 125, App
254	8	11	US-09-932-613-13	Sequence 13, Appl	327	3	27.3	9	10	US-09-780-668A-24	Sequence 24, Appl
255	8	11	US-09-855-588A-94	Sequence 94, Appl	328	3	27.3	9	10	US-09-920-174-26	Sequence 26, Appl
256	8	12	US-10-073-33A-22	Sequence 21, Appl	329	3	27.3	9	10	US-09-919-048-95	Sequence 95, Appl
257	8	12	US-10-158-825-146	Sequence 146, App	330	3	27.3	9	10	US-09-919-048-173	Sequence 173, App
258	8	12	US-10-348-504-60	Sequence 60, Appl	331	3	27.3	9	10	US-09-779-308-210	Sequence 210, App
259	8	12	US-10-348-504-60	Sequence 64, Appl	332	3	27.3	9	10	US-09-779-308-378	Sequence 378, App
260	8	12	US-10-348-504-72	Sequence 72, Appl	333	3	27.3	9	10	US-09-779-308-594	Sequence 594, App
261	8	12	US-10-348-504-72	Sequence 106, App	334	3	27.3	9	10	US-09-779-308-674	Sequence 674, App
262	8	12	US-09-815-455-42	Sequence 42, Appl	335	3	27.3	9	10	US-09-017-743C-112	Sequence 112, App
263	8	12	US-10-244-672-10	Sequence 10, Appl	336	3	27.3	9	11	US-09-799-250-558	Sequence 558, App
264	8	12	US-10-257-050-13	Sequence 13, Appl	337	3	27.3	9	11	US-09-799-250-630	Sequence 630, App
265	8	12	US-10-272-497-84	Sequence 84, Appl	338	3	27.3	9	11	US-09-791-393-52	Sequence 52, Appl
266	8	12	US-10-244-672A-96	Sequence 96, Appl	339	3	27.3	9	11	US-09-791-389-52	Sequence 52, Appl
267	8	12	US-10-244-672A-96	Sequence 224, App	340	3	27.3	9	11	US-09-809-391-626	Sequence 626, App
268	8	12	US-10-244-672A-96	Sequence 675, App	341	3	27.3	9	11	US-09-880-748-3137	Sequence 3137, Ap
269	8	14	US-10-067-761-19	Sequence 19, Appl	342	3	27.3	9	11	US-09-876-904A-360	Sequence 260, App
270	8	14	US-10-067-761-19	Sequence 6, Appl	343	3	27.3	9	11	US-09-876-904A-336	Sequence 336, App
271	8	14	US-10-067-761-19	Sequence 14, Appl	344	3	27.3	9	11	US-09-876-904A-543	Sequence 543, App
272	8	14	US-10-067-761-19	Sequence 15, Appl	345	3	27.3	9	11	US-09-876-904A-570	Sequence 570, App
273	8	14	US-10-067-761-19	Sequence 15, Appl	346	3	27.3	9	11	US-09-876-904A-588	Sequence 588, App
274	8	14	US-10-067-761-19	Sequence 17, Appl	347	3	27.3	9	11	US-09-876-904A-615	Sequence 615, App
275	8	14	US-10-067-761-19	Sequence 18, App	348	3	27.3	9	11	US-09-865-548A-77	Sequence 77, Appl
276	8	14	US-10-067-761-19	Sequence 19, App	349	3	27.3	9	11	US-09-978-309A-35	Sequence 35, Appl
277	8	14	US-10-067-761-19	Sequence 24, App	350	3	27.3	9	12	US-09-932-165-72	Sequence 72, Appl
278	8	14	US-10-067-761-22	Sequence 22, App	351	3	27.3	9	12	US-09-932-165-1201	Sequence 1201, Ap
279	8	14	US-10-067-761-25	Sequence 25, App	352	3	27.3	9	12	US-10-104-385-8	Sequence 8, Appl
280	8	14	US-10-067-761-26	Sequence 26, App	353	3	27.3	9	12	US-10-291-250-13	Sequence 13, Appl
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282	8	14	US-10-067-761-28	Sequence 28, Appl	355	3	27.3	9	12	US-10-292-418-13	Sequence 13, Appl
283	8	14	US-10-067-761-29	Sequence 30, App	356	3	27.3	9	12	US-10-190-082-529	Sequence 529, App
284	8	14	US-10-067-761-31	Sequence 31, App	357	3	27.3	9	12	US-10-251-805-2	Sequence 2, Appl
285	8	14	US-10-067-761-31	Sequence 42, App	358	3	27.3	9	12	US-10-375-992-177	Sequence 177, App
286	8	14	US-10-067-761-31	Sequence 44, App	359	3	27.3	9	12	US-09-908-100-2	Sequence 2, Appl
287	8	14	US-10-067-761-31	Sequence 44, App	360	3	27.3	9	12	US-09-935-384-112	Sequence 112, App
288	8	14	US-10-067-761-31	Sequence 8, Appl	361	3	27.3	9	12	US-09-935-384-140	Sequence 140, App
289	8	14	US-10-067-761-31	Sequence 10, Appl	362	3	27.3	9	12	US-09-935-384-207	Sequence 207, App
290	8	15	US-10-158-164-22	Sequence 22, Appl	363	3	27.3	9	12	US-09-935-384-312	Sequence 312, App
291	8	15	US-10-158-164-51	Sequence 51, Appl	364	3	27.3	9	12	US-09-935-384-550	Sequence 550, App
292	8	15	US-10-044-967-14	Sequence 12, Appl	365	3	27.3	9	12	US-09-935-384-642	Sequence 642, App
293	8	15	US-10-044-944-44	Sequence 74, Appl	366	3	27.3	9	12	US-09-935-384-643	Sequence 643, App
294	8	15	US-10-158-847-148	Sequence 148, App	367	3	27.3	9	12	US-10-062-109A-274	Sequence 274, App
295	8	15	US-10-042-818-9	Sequence 9, Appl	368	3	27.3	9	12	US-10-062-109A-365	Sequence 365, App
296	8	15	US-10-042-818-11	Sequence 11, Appl	369	3	27.3	9	12	US-10-062-109A-559	Sequence 559, App
297	8	15	US-10-158-212-140	Sequence 170, App	370	3	27.3	9	12	US-10-062-109A-558	Sequence 558, App
298	8	15	US-10-158-573A-6	Sequence 5, Appl	371	3	27.3	9	12	US-10-077-106-13	Sequence 13, Appl
299	8	15	US-10-158-573A-11	Sequence 11, Appl	372	3	27.3	9	12	US-10-077-106-15	Sequence 15, Appl
300	9	8	US-08-452-843A-19	Sequence 19, Appl	373	3	27.3	9	12	US-10-077-106-18	Sequence 18, Appl
301	9	8	US-08-805-814-7	Sequence 17, Appl	374	3	27.3	9	12	US-09-882-171-626	Sequence 626, Appl
302	9	9	US-09-118-944-6	Sequence 6, Appl	375	3	27.3	9	12	US-09-920-195A-26	Sequence 26, Appl
303	9	9	US-09-760-599-69	Sequence 39, Appl	376	3	27.3	9	12	US-10-138-434A-5	Sequence 5, Appl
304	9	9	US-09-760-599-41	Sequence 45, Appl	377	3	27.3	9	12	US-10-239-313A-540	Sequence 540, App
305	9	9	US-09-765-186-177	Sequence 177, App	378	3	27.3	9	12	US-10-239-313A-544	Sequence 544, App
306	9	9	US-09-844-813-12	Sequence 12, App	379	3	27.3	9	12	US-10-353-929-138	Sequence 138, App
307	9	9	US-09-879-946-13	Sequence 13, App	380	3	27.3	9	12	US 10-153-929-145	Sequence 145, App

381	9	12	US-10-353-929-149	Sequence 149, App	454	10	11	US-09-572-404B-72	Sequence 72, Appl
382	3	27.3	US-10-353-929-149	Sequence 149, App	455	3	27.3	US-09-572-404B-74	Sequence 74, Appl
383	9	14	US-10-613-322-4	Sequence 4, Appl	456	3	27.3	US-09-572-404B-112	Sequence 112, App
384	3	27.3	US-10-613-322-4	Sequence 4, Appl	457	3	27.3	US-09-572-404B-136	Sequence 136, App
385	9	14	US-10-613-322-4	Sequence 4, Appl	458	3	27.3	US-09-572-404B-227	Sequence 227, App
386	3	27.3	US-10-211-207-15	Sequence 15, Appl	459	3	27.3	US-09-572-404B-412	Sequence 412, App
387	9	15	US-10-211-207-15	Sequence 15, Appl	460	3	27.3	US-09-572-404B-626	Sequence 626, App
388	3	27.3	US-10-211-207-15	Sequence 15, Appl	461	3	27.3	US-09-572-404B-633	Sequence 633, App
389	9	15	US-10-394-285-45	Sequence 95, Appl	462	3	27.3	US-09-572-404B-636	Sequence 636, App
390	3	27.3	US-10-394-285-45	Sequence 95, Appl	463	3	27.3	US-09-572-404B-682	Sequence 682, App
391	9	15	US-10-091-158-11	Sequence 11, Appl	464	3	27.3	US-09-572-404B-770	Sequence 770, App
392	3	27.3	US-10-091-158-11	Sequence 11, Appl	465	3	27.3	US-09-572-404B-772	Sequence 772, App
393	9	15	US-10-335-795-173	Sequence 95, Appl	466	3	27.3	US-09-572-404B-774	Sequence 774, App
394	3	27.3	US-10-335-795-173	Sequence 95, Appl	467	3	27.3	US-09-572-404B-787	Sequence 787, App
395	9	15	US-10-041-862-842	Sequence 842, App	468	3	27.3	US-09-572-404B-842	Sequence 842, App
396	3	27.3	US-10-041-862-842	Sequence 842, App	469	3	27.3	US-09-572-404B-990	Sequence 990, App
397	9	15	US-10-041-862-842	Sequence 842, App	470	3	27.3	US-09-572-404B-992	Sequence 992, App
398	3	27.3	US-10-041-862-842	Sequence 842, App	471	3	27.3	US-09-572-404B-1078	Sequence 1078, App
399	9	15	US-10-041-862-1011	Sequence 1011, A	472	3	27.3	US-09-572-404B-1094	Sequence 1094, App
400	3	27.3	US-10-041-862-1011	Sequence 1011, A	473	3	27.3	US-09-572-404B-1120	Sequence 1120, App
401	9	15	US-10-041-862-1011	Sequence 1011, A	474	3	27.3	US-09-572-404B-1142	Sequence 1142, App
402	3	27.3	US-10-041-862-1011	Sequence 1011, A	475	3	27.3	US-09-572-404B-1158	Sequence 1158, App
403	9	15	US-10-041-862-1011	Sequence 1011, A	476	3	27.3	US-09-572-404B-1162	Sequence 1162, App
404	3	27.3	US-10-041-862-1011	Sequence 1011, A	477	3	27.3	US-09-572-404B-1237	Sequence 1237, App
405	9	15	US-10-133-211-74	Sequence 74, App	478	3	27.3	US-09-572-404B-1511	Sequence 1511, App
406	3	27.3	US-10-133-211-74	Sequence 74, App	479	3	27.3	US-09-572-404B-1619	Sequence 1619, App
407	9	15	US-10-211-207-15	Sequence 15, App	480	3	27.3	US-09-572-404B-1629	Sequence 1629, App
408	3	27.3	US-10-211-207-15	Sequence 15, App	481	3	27.3	US-09-572-404B-1632	Sequence 1632, App
409	9	15	US-10-091-124-5	Sequence 50, Appl	482	3	27.3	US-09-572-404B-1635	Sequence 1635, App
410	3	27.3	US-10-091-124-5	Sequence 50, Appl	483	3	27.3	US-09-572-404B-1640	Sequence 1640, App
411	9	15	US-09-731-395-14	Sequence 33, Appl	484	3	27.3	US-09-572-404B-1694	Sequence 1694, App
412	3	27.3	US-09-731-395-14	Sequence 33, Appl	485	3	27.3	US-09-572-404B-1696	Sequence 1696, App
413	9	15	US-09-731-395-14	Sequence 33, Appl	486	3	27.3	US-09-572-404B-1891	Sequence 1891, App
414	3	27.3	US-09-731-395-14	Sequence 33, Appl	487	3	27.3	US-09-572-404B-1896	Sequence 1896, App
415	9	15	US-09-731-395-14	Sequence 33, Appl	488	3	27.3	US-09-572-404B-1898	Sequence 1898, App
416	3	27.3	US-09-731-395-14	Sequence 33, Appl	489	3	27.3	US-09-572-404B-1947	Sequence 1947, App
417	9	15	US-09-731-395-14	Sequence 33, Appl	490	3	27.3	US-09-572-404B-2016	Sequence 2016, App
418	3	27.3	US-09-731-395-14	Sequence 33, Appl	491	3	27.3	US-09-572-404B-2018	Sequence 2018, App
419	9	15	US-09-731-395-14	Sequence 33, Appl	492	3	27.3	US-09-572-404B-2066	Sequence 2066, App
420	3	27.3	US-09-731-395-14	Sequence 33, Appl	493	3	27.3	US-09-572-404B-2146	Sequence 2146, App
421	9	15	US-09-731-395-14	Sequence 33, Appl	494	3	27.3	US-09-572-404B-2149	Sequence 2149, App
422	3	27.3	US-09-731-395-14	Sequence 33, Appl	495	3	27.3	US-09-572-404B-2481	Sequence 2481, App
423	9	15	US-09-731-395-14	Sequence 33, Appl	496	3	27.3	US-09-572-404B-2524	Sequence 2524, App
424	3	27.3	US-09-731-395-14	Sequence 33, Appl	497	3	27.3	US-09-572-404B-2535	Sequence 2535, App
425	9	15	US-09-731-395-14	Sequence 33, Appl	498	3	27.3	US-09-572-404B-2547	Sequence 2547, App
426	3	27.3	US-09-731-395-14	Sequence 33, Appl	499	3	27.3	US-09-572-404B-2648	Sequence 2648, App
427	9	15	US-09-731-395-14	Sequence 33, Appl	500	3	27.3	US-09-572-404B-2706	Sequence 2706, App
428	3	27.3	US-09-731-395-14	Sequence 33, Appl					
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## ALIGNMENTS

## RESULT 1

US-09-876-904A-212  
Sequence 262, Application US/09876904A  
Publication No. US20030072734A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, IENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
FILE REFERENCE: TB 2002-00  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIORITY FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 262  
LENGTH: 13  
TYPE: PRI  
ORGANISM: Bos sp.  
FEATURE:



OTHER INFORMATION: Calf thymus HMG 1  
US-09-876-904A-262

Query Match 63.6%; Score 7; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EGKKKK 8  
DB 3 EGKKKK 9

## RESULT 2

US-09-876-904A-617  
Sequence 617, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMI DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 617  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Bos sp.  
FEATURE:  
OTHER INFORMATION: Calf thymus HMG 2 (256 aa);  
US-09-876-904A-517

Query Match 63.6%; Score 7; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EGKKKK 8  
DB 3 EGKKKK 9

## RESULT 3

US-09-876-904A-623  
Sequence 620, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMI DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 620  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Bos sp.  
FEATURE:  
OTHER INFORMATION: Calf thymus HMG 2 (256 aa);  
US-09-876-904A-620

Query Match 54.5%; Score 6; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GKKKK 8  
DB 6 GKKKK 11

## RESULT 4

US-10-024-918-10  
Sequence 10, Application US/10024918  
Publication No. US20020168718A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey  
APPLICANT: Schense, Jason  
APPLICANT: Zisch, Andreas  
APPLICANT: Hall, Heike  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING  
FILE REFERENCE: CIT 2606 CIP  
CURRENT APPLICATION NUMBER: US/10/024,918  
CURRENT FILING DATE: 2001-12-18  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 8  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: random coupling polylysine peptide attached to active peptic  
NAME/KEY: MOD\_RES  
LOCATION: (1)-(11)  
OTHER INFORMATION: dansylated leucine  
US-10-024-918-10

Query Match 45.5%; Score 5; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5; le-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GKKKK 8  
DB 3 GKKKK 7

## RESULT 5

US-08-344-824-35  
Sequence 35, Application US/0844824  
Publication No. US20030152580A1  
GENERAL INFORMATION:  
APPLICANT: SEITE, Alessandro  
APPLICANT: SIDNEY, John  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower, 20th  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1

```

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (415) 543-9600
3 TELEFAX: (415) 543-5043
4 INFORMATION FOR SEQ ID NO: 35:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 9 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: single
9 TOPOLOGY: linear
10 MOLECULE TYPE: DNA (genomic)
11 US-08-344 824-35

```

```

Query Match      45.5%: Score 5; DB 1; Length 9;
Best Local Similarity 100.0%: Pred. No. 5; Len-5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 GGKKK 7
      ||| 1
      : GGKKK 5

```

```

RESULT 5
2S-09-898 451-5
1 Sequence 5; Application US/09898461
2 Patent No. US2002090709A1
3 GENERAL INFORMATION:
4 APPLICANT: Bequet, Richard HJ
5 APPLICANT: Chester, Kerry
6 APPLICANT: Milton, Nigel P
7 APPLICANT: Rees, Anthony K
8 APPLICANT: Sharma, Surinder K
9 APPLICANT: Spencer, Daniel IR
10 TITLE OF INVENTION: Modified carboxypeptidase enzymes and their use
11 FILE REFERENCE: 620-150
12 CURRENT APPLICATION NUMBER: US/09/898 461
13 PRIOR FILING DATE: 2001-07-05
14 PRIOR APPLICATION NUMBER: US 60/226,689
15 PRIOR FILING DATE: 2000-07-07
16 NUMBER OF SEQ ID NOS: 21
17 SOFTWARE: PatentIn Ver. 2.1
18 SEQ ID NO 5
19 LENGTH: 9
20 TYPE: PRT
21 ORGANISM: Pseudomonas sp.
22 US-09-898 461-5

```

```

Query Match      45.5%: Score 5; DB 1; Length 9;
Best Local Similarity 100.0%: Pred. No. 5; Len-5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 EGGKK 6
      ||| 1
      1 EGGKK 5

```

```

RESULT 7
US-10-206-155-13
1 Sequence 13; Application US/10206155
2 Publication No. US20030157135A1
3 GENERAL INFORMATION:
4 APPLICANT: Tsuji, Moriya
5 APPLICANT: Gonzalez-Asequinolaza, Gloria
6 APPLICANT: Nussenzeig, Ruth S.
7 APPLICANT: Koetuka, Yasuhiko
8 TITLE OF INVENTION: USE OF GLYCOSYLCEFAZOLIDES AS ADJUVANTS
9 FILE REFERENCE: 5986/1H9590S1
10 CURRENT APPLICATION NUMBER: US/10/206.155
11 PRIOR FILING DATE: 2002-07-25
12 PRIOR APPLICATION NUMBER: 60/308,056
13 PRIOR FILING DATE: 2001-07-25
14 NUMBER OF SEQ ID NOS: 19
15 SOFTWARE: FastSPQ for Windows Version 3.0

```

```

1 SEQ ID NO 13
2 LENGTH: 9
3 TYPE: PRT
4 ORGANISM: HIV-1
5 US-10-206-155-13

```

```

Query Match      45.5%: Score 5; DB 12; Length 9;
Best Local Similarity 100.0%: Pred. No. 5; Len-5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 GGKKK 7
      ||| 1
      5 GGKKK 9

```

```

RESULT 6
US-10-128-711-43
1 Sequence 30; Application US/10128711
2 Publication No. US20030099644A1
3 GENERAL INFORMATION:
4 APPLICANT: VITIELLO, Maria A.
5 CHESTNUT, Robert W.
6 SETTE, Alessandro D.
7 CELIS, Esteban
8 GRAY, Howard
9 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
10 NUMBER OF SEQUENCES: 153
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Townsend and Townsend Kourie and Crew
13 STREET: Stewart Street Tower, One Market Plaza
14 CITY: San Francisco
15 STATE: California
16 COUNTRY: US
17 ZIP: 94105-1493
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: PatentIn Release #1.0, Version #1.25
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/10/128,711
25 FILING DATE: 22-Apr-2002
26 CLASSIFICATION: <Unknown>
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US/08/197,484
29 FILING DATE: 15-FEB-1994
30 APPLICATION NUMBER: US 07/935,811
31 FILING DATE: 26-AUG-1992
32 APPLICATION NUMBER: US 07/874,491
33 FILING DATE: 27-APR-1992
34 APPLICATION NUMBER: US 07/827,682
35 FILING DATE: 29-JAN-1992
36 APPLICATION NUMBER: US 07/749,568
37 FILING DATE: 26-AUG-1991
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Parmelee, Steven W.
40 REGISTRATION NUMBER: 31,990
41 REFERENCE/DOCKET NUMBER: 14137-26-4
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (206) 467-9600
44 TELEFAX: (206) 623-6793
45 INFORMATION FOR SEQ ID NO: 30:
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 9 amino acids
48 TYPE: amino acid
49 STRANDEDNESS: unknown
50 TOPOLOGY: unknown
51 MOLECULE TYPE: peptide
52 SEQUENCE DESCRIPTION: SEQ ID NO: 30:
53 US-10-128-711-30

```

```

Query Match      45.5%: Score 5; DB 15; Length 9;

```

```

Best Local Similarity 100.0%; Score 5; DB 11; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GKKKK 7
DB 1 GKKKK 5

RESULT 9
US-09-876-904A-362
: Sequence 362, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 362
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: Murine DEF-1.
US-09-876-904A-362

Query Match 45.5%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8
DB 1 GKKKK 5

RESULT 10
US-09-876-904A-363
: Sequence 363, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 363
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Human TGF-1 alpha.
US-09-876-904A-363

Query Match 45.5%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8
DB 1 GKKKK 5

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```

RESULT 11
US-09-876-904A-51
: Sequence 51, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 51
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Murine c-abl (
US-09-876-904A-51

```

```

Query Match 45.5%; Score 5; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 5 KKKKK 5
DB 6 KKKKK 10

```

```

RESULT 12
US-10-315-920-13
: Sequence 13, Application US/10315920
: Publication No. US20030175809A1
: GENERAL INFORMATION:
: APPLICANT: FIADKOV, Aleksey
: TITLE OF INVENTION: FLUORESCENT TUMOR PROTEINS AND METHODS
: TITLE OF INVENTION: FOR THEIR USE
: FILE REFERENCE: CIGN-077C:P
: CURRENT APPLICATION NUMBER: US/10/315,920
: CURRENT FILING DATE: 2002-12-09
: PRIOR APPLICATION NUMBER: 60/211,607
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: PCT/US01/10097
: PRIOR FILING DATE: 2001-06-13
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: nuclear localization signal
US-10-315-920-13

```

```

Query Match 45.5%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 5 KKKKK 9
DB 6 KKKKK 10

```

```

RESULT 13
US-10-156-570A-12
: Sequence 12, Application US/10156570A

```

```

1 PUBLIC:om No. US2004012524A1
2 GENERAL INFORMATION:
3 APPLICANT: ROSENBERG, JOSEPH
4 APPLICANT: RITTER, WOLFGANG
5 APPLICANT: KUDOLPH, CARSTEN
6 APPLICANT: PLANK, CHRISTIAN
7 TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIPLES OF NUCLEAR
8 TITLE OF INVENTION: LOCALIZATION SIGNALS OF A PROTEIN TRANSDUCTION DOMAINS
9 TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
10 TITLE OF INVENTION: INTO CELLS
11 FILE REFERENCE: WO-05-45
12 CURRENT APPLICATION NUMBER: US/09/156,522
13 PRIOR FILING DATE: 2002-05-24
14 PRIOR APPLICATION NUMBER: PCT/EP/01/060
15 NUMBER OF SEQ ID NOS: 32
16 SOFTWARE: PatentIn Ver. 2.1
17 SEQ ID NO 1
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Description of Artificial Sequences and/or Gene IV
22 OTHER INFORMATION: nuclear localization sequence
23 US 10-156-570A 12
24
25 Query Match 45.5% Score 5: DB 15: Length 12:
26 Best Local Similarity 100.0%: Pct. No. 76:
27 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
28
29 CY 5 KKKKK 9
30 DB 5 KKKKK 10
31
32 RESULT 14
33 US 09-770-467-2
34 Sequence 2: Application US/09770-067
35 Patent No. US2002010184A1
36 GENERAL INFORMATION:
37 APPLICANT: Merck & Co., Inc.
38 APPLICANT: Teismore, Christopher J.
39 APPLICANT: Bequith, Jeffrey M.
40 TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferrase
41 FILE REFERENCE: 20495
42 CURRENT APPLICATION NUMBER: US/09/770-067
43 PRIOR FILING DATE: 2001-01-26
44 PRIOR APPLICATION NUMBER: 09/180,000
45 NUMBER OF SEQ ID NOS: 21
46 SOFTWARE: FastSeq for Windows Version 4.0
47 SEQ ID NO 1
48 LENGTH: 15
49 TYPE: PRT
50 ORGANISM: Homosapien
51 US 09-770-467-2
52
53 Query Match 45.5% Score 5: DB 15: Length 15:
54 Best Local Similarity 100.0%: Pct. No. 76:
55 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
56
57 CY 4 GKKKK 8
58 DB 1 GKKKK 5
59
60 RESULT 15
61 US-09-858-369-2
62 Sequence 2: Application US/09858-369
63 Patent No. US2002022634A1
64 GENERAL INFORMATION:
65 APPLICANT: Merck & Co., Inc.
66 APPLICANT: Suzukawa, Masahiro
67 APPLICANT: Anthony W. Shaw
68 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
69 FILE REFERENCE: 20001
70
71 PUBLIC:om No. US2004012524A1
72 GENERAL INFORMATION:
73 APPLICANT: ROSENBERG, JOSEPH
74 APPLICANT: RITTER, WOLFGANG
75 APPLICANT: KUDOLPH, CARSTEN
76 APPLICANT: PLANK, CHRISTIAN
77 TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIPLES OF NUCLEAR
78 TITLE OF INVENTION: LOCALIZATION SIGNALS OF A PROTEIN TRANSDUCTION DOMAINS
79 TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
80 TITLE OF INVENTION: INTO CELLS
81 FILE REFERENCE: WO-05-45
82 CURRENT APPLICATION NUMBER: US/09/156,522
83 PRIOR FILING DATE: 2002-05-24
84 PRIOR APPLICATION NUMBER: PCT/EP/01/060
85 NUMBER OF SEQ ID NOS: 32
86 SOFTWARE: PatentIn Ver. 2.1
87 SEQ ID NO 1
88 TYPE: PRT
89 ORGANISM: Artificial Sequence
90 FEATURE:
91 OTHER INFORMATION: Description of Artificial Sequences and/or Gene IV
92 OTHER INFORMATION: nuclear localization sequence
93 US 10-156-570A 12
94
95 Query Match 45.5% Score 5: DB 15: Length 12:
96 Best Local Similarity 100.0%: Pct. No. 76:
97 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
98
99 CY 5 KKKKK 9
100 DB 5 KKKKK 10
101
102 RESULT 14
103 US 09-770-467-2
104 Sequence 2: Application US/09770-067
105 Patent No. US2002010184A1
106 GENERAL INFORMATION:
107 APPLICANT: Merck & Co., Inc.
108 APPLICANT: Teismore, Christopher J.
109 APPLICANT: Bequith, Jeffrey M.
110 TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferrase
111 FILE REFERENCE: 20495
112 CURRENT APPLICATION NUMBER: US/09/770-067
113 PRIOR FILING DATE: 2001-01-26
114 PRIOR APPLICATION NUMBER: 09/180,000
115 NUMBER OF SEQ ID NOS: 21
116 SOFTWARE: FastSeq for Windows Version 4.0
117 SEQ ID NO 1
118 LENGTH: 15
119 TYPE: PRT
120 ORGANISM: Homosapien
121 US 09-770-467-2
122
123 Query Match 45.5% Score 5: DB 15: Length 15:
124 Best Local Similarity 100.0%: Pct. No. 76:
125 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
126
127 CY 4 GKKKK 8
128 DB 1 GKKKK 5
129
130 RESULT 15
131 US-09-858-369-2
132 Sequence 2: Application US/09858-369
133 Patent No. US2002022634A1
134 GENERAL INFORMATION:
135 APPLICANT: Merck & Co., Inc.
136 APPLICANT: Suzukawa, Masahiro
137 APPLICANT: Anthony W. Shaw
138 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
139 FILE REFERENCE: 20001

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1 APPLICANT: Stump, Craig A.
2 TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferrase
3 FILE REFERENCE: 20673
4 CURRENT APPLICATION NUMBER: US/09/858,369
5 CURRENT FILING DATE: 2001-05-16
6 PRIOR APPLICATION NUMBER: 60/215,655
7 PRIOR FILING DATE: 2000/06/30
8 NUMBER OF SEQ ID NOS: 21
9 SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 2
11 LENGTH: 15
12 TYPE: PRT
13 ORGANISM: Homosapien
14 US-09-858-369-2
15
16 Query Match 45.5% Score 5: DB 9: Length 15:
17 Best Local Similarity 100.0%: Pct. No. 93:
18 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
19
20 CY 4 GKKKK 8
21 DB 1 GKKKK 5
22
23 RESULT 16
24 US 09-819-522-2
25 Sequence 2: Application US/09819522
26 Patent No. US2002037889A1
27 GENERAL INFORMATION:
28 APPLICANT: desolins, S. Jane
29 APPLICANT: Graham, Samuel L.
30 APPLICANT: Shaw, Anthony W.
31 APPLICANT: Ciccarone, Terrence M.
32 APPLICANT: Storker, Gerald E.
33 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN
34 TITLE OF INVENTION: TRANSFERASE
35 FILE REFERENCE: 20312Y
36 CURRENT APPLICATION NUMBER: US/09/819,522
37 PRIOR FILING DATE: 2001-03-28
38 PRIOR APPLICATION NUMBER: 09/456,153
39 PRIOR FILING DATE: 1999-12-07
40 PRIOR APPLICATION NUMBER: US 60/111,416
41 PRIOR FILING DATE: 1998-12-06
42 PRIOR APPLICATION NUMBER: US 60/129,282
43 PRIOR FILING DATE: 1999-04-14
44 NUMBER OF SEQ ID NOS: 21
45 SOFTWARE: FastSeq for Windows Version 4.0
46 SEQ ID NO 2
47 LENGTH: 15
48 TYPE: PRT
49 ORGANISM: Homosapien
50 US-09-819-522-2
51
52 Query Match 45.5% Score 5: DB 9: Length 15:
53 Best Local Similarity 100.0%: Pct. No. 93:
54 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
55
56 CY 4 GKKKK 8
57 DB 1 GKKKK 5
58
59 RESULT 17
60 US-09-757-251-3
61 Sequence 2: Application US/09757251
62 Patent No. US2002004217A1
63 GENERAL INFORMATION:
64 APPLICANT: Merck & Co., Inc.
65 APPLICANT: S. Jane desolins
66 APPLICANT: Suzukawa, Masahiro
67 APPLICANT: Anthony W. Shaw
68 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
69 FILE REFERENCE: 20001

```

: CURRENT APPLICATION NUMBER: US/09/757,251  
 : PRIOR FILING DATE: 2001-01-09  
 : PRIOR APPLICATION NUMBER: 60/175,784  
 : PRIOR FILING DATE: 2000-01-12  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO: 3  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely Synthetic Amino Acid  
 US-09-757-251-3

Query Match 45.5% Score 5; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 III I  
 Db 1 GKKKK 5

RESULT 14  
 US-09-784-897A-2  
 : Sequence 2; Application US/09/784897A  
 : Patent No. US20020052363A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Dinsmore, Christopher J.  
 : APPLICANT: Bergman, Jeffrey M.  
 : TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS  
 : FILE REFERENCE: 20497  
 : CURRENT APPLICATION NUMBER: US/09/784,897A  
 : PRIOR FILING DATE: 2001-06-20  
 : PRIOR APPLICATION NUMBER: 60/283,449  
 : PRIOR FILING DATE: 2000-02-18  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO: 2  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
 US-09-784-897A-2

Query Match 45.5% Score 5; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 III I  
 Db 1 GKKKK 5

RESULT 19  
 US-09-770-983-2  
 : Sequence 2; Application US/09/770,983  
 : Patent No. US2002052380A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Dinsmore, Christopher J.  
 : APPLICANT: Bergman, Jeffrey M.  
 : TITLE OF INVENTION: Inhibitors of Prenyl Protein Transferase  
 : FILE REFERENCE: 20309  
 : CURRENT APPLICATION NUMBER: US/09/770,983  
 : PRIOR FILING DATE: 2001-01-26  
 : PRIOR APPLICATION NUMBER: 60/183,656  
 : PRIOR FILING DATE: 2000-2-18  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO: 2

: LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Homosapien  
 US-09-770-983-2

Query Match 45.5% Score 5; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 III I  
 Db 1 GKKKK 5

RESULT 20  
 US-09-828-325A-3  
 : Sequence 3; Application US/09/828325A  
 : Patent No. US2002068747A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Craig A. Stump  
 : APPLICANT: Theresa M. Williams  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20646Y  
 : CURRENT APPLICATION NUMBER: US/09/828,325A  
 : PRIOR FILING DATE: 2001-08-17  
 : PRIOR APPLICATION NUMBER: 60/196,244  
 : PRIOR FILING DATE: 2000-04-10  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO: 3  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
 US-09-828-325A-3

Query Match 45.5% Score 5; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 III I  
 Db 1 GKKKK 5

RESULT 21  
 US-09-757-217A-4  
 : Sequence 3; Application US/09/757217A  
 : Patent No. US2002054903A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: S. Jang doSoms  
 : APPLICANT: Gerald F. Stokker  
 : APPLICANT: Anthony W. Shaw  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20603Y  
 : CURRENT APPLICATION NUMBER: US/09/757,217A  
 : CURRENT FILING DATE: 2001-06-25  
 : PRIOR APPLICATION NUMBER: 60/175,901  
 : PRIOR FILING DATE: 2000-01-12  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO: 3  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely Synthetic Amino Acid  
 US-09-757-217A-3

Query Match 45.5% Score 5; DB 9; Length 15;

```

Query Match      45.5%; Score 5; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8
DB 1 GKXXX 5

RESULT 22
US-09-828-259A-3
: Sequence 1: Application US/09824259A
: Patent No. US2002013497A1
: GENERAL INFORMATION:
: APPLICANT: Merck & Co., Inc.
: APPLICANT: Genom N. Nguyen
: APPLICANT: Gracia A. Stamp
: APPLICANT: Theresa M. Williams
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
: FILE REFERENCE: 26637Y
: CURRENT APPLICATION NUMBER: US/09/828-259A
: CURRENT FILING DATE: 2001-04-09
: PRIOR APPLICATION NUMBER: 60/195,951
: PRIOR FILING DATE: 2000-04-10
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Completely Synthetic Analog Amino Acid
US-09-828-259A-3

Query Match      45.5%; Score 5; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8
DB 1 GKXXX 5

RESULT 23
US-09-945-249-84
: Sequence 84: Application US/09945249
: Patent No. US20020168748A1
: GENERAL INFORMATION:
: APPLICANT: BERLIN, VIVIAN
: APPLICANT: LAMAGNEZ, VERENIQUE
: APPLICANT: SMITH, SUSAN E.
: TITLE OF INVENTION: ASSAYS AND REAGENTS FOR MEASURING AND PREDICTING AGENTS.
: FILE REFERENCE: MIV-074.06
: CURRENT APPLICATION NUMBER: US/99/945-249
: CURRENT FILING DATE: 2001-06-31
: PRIOR APPLICATION NUMBER: 09/041,993
: PRIOR FILING DATE: 2001-01-13
: PRIOR APPLICATION NUMBER: 08/771,212
: PRIOR FILING DATE: 1996-12-20
: PRIOR APPLICATION NUMBER: 08/631,311
: PRIOR FILING DATE: 1996-04-11
: NUMBER OF SEQ ID NOS: 89
: SOFTWARE: Patentio Ver. 2.1
: SEQ ID NO 84
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Peptide that corresponds to the C-terminal of Phase 1 of Olfase
: OTHER INFORMATION: substrates
US-09-945-249-84

Query Match      45.5%; Score 5; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8
DB 1 GKXXX 5

RESULT 24
US-09-784-818-2
: Sequence 2: Application US/09/84818
: Publication No. US2002019328A1
: GENERAL INFORMATION:
: APPLICANT: Merck & Co., Inc.
: APPLICANT: Bismore, Christopher J.
: APPLICANT: Bergman, Jeffrey M.
: TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
: FILE REFERENCE: 20496
: CURRENT APPLICATION NUMBER: US/09/784-818
: CURRENT FILING DATE: 2001-02-16
: PRIOR APPLICATION NUMBER: 60/183,451
: PRIOR FILING DATE: 2000-02-18
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: completely synthetic sequence
US-09-784-818-2

Query Match      45.5%; Score 5; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8
DB 1 GKXXX 5

RESULT 25
US-09-756-248-2
: Sequence 2: Application US/09756248
: Publication No. US2002014460A1
: GENERAL INFORMATION:
: APPLICANT: Merck & Co., Inc.
: APPLICANT: Bismore, Christopher J.
: TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase
: FILE REFERENCE: 26341
: CURRENT APPLICATION NUMBER: US/09/756-248
: CURRENT FILING DATE: 2001-01-08
: PRIOR APPLICATION NUMBER: 60/175,706
: PRIOR FILING DATE: 2000-01-12
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Homosapien
US-09-756-248-2

Query Match      45.5%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8
DB 1 GKXXX 5

RESULT 26

```

```
US-09-813-653-5
: Sequence 5, Application US/09813653
: Patent No. US20020064770A1
: GENERAL INFORMATION:
: APPLICANT: Nestor, John
: APPLICANT: Wilson, Carol
: APPLICANT: See, Raymond
: APPLICANT: Tan, Heir, Christina
: TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
: FILE REFERENCE: CNS-005
: CURRENT APPLICATION NUMBER: US/09/813,653
: PRIOR FILING DATE: 2000-03-20
: PRIOR APPLICATION NUMBER: US 60/190,446
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/190,996
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/191,299
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: preferred peptide for pdz binding domain
US-09-813-653-5
Query Match 36.4% Score 4; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKKK 8
DB 1 KKKK 4
RESULT 27
US-09-997-579-46
: Sequence 46, Application US/09997579
: Patent No. US20020113203A1
: GENERAL INFORMATION:
: APPLICANT: Cambridge University Technical Services
: TITLE OF INVENTION: A novel family of beta sub unit proteins from a voltage gated sod
: TITLE OF INVENTION: channel
: TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
: FILE REFERENCE: 674558-2001
: CURRENT APPLICATION NUMBER: US/09/997,579
: CURRENT FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: PCT/EP00/01364
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: 60,129,479
: PRIOR FILING DATE: 2000-02-24
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 46
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-997-579-46
Query Match 36.4% Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EGGK 5
DB 1 EGGK 4
RESULT 28
US-09-380-323-1
: Sequence 1, Application US/09380323
: Sequence 46, Application US/09997579
: Patent No. US20020113203A1
: GENERAL INFORMATION:
: APPLICANT: Cambridge University Technical Services
: TITLE OF INVENTION: A novel family of beta sub unit proteins from a voltage gated sod
: TITLE OF INVENTION: channel
: TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
: FILE REFERENCE: 674558-2001
: CURRENT APPLICATION NUMBER: US/09/997,579
: CURRENT FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: PCT/EP00/01364
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: 60,129,479
: PRIOR FILING DATE: 2000-02-24
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 46
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-997-579-46
Query Match 36.4% Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EGGK 5
DB 1 EGGK 4
RESULT 28
US-09-380-323-1
: Sequence 1, Application US/09380323
```

```
: Patent No. US20020123471A1
: GENERAL INFORMATION:
: APPLICANT: Bavarian No. US20020123471A1dic Research Institute A/S
: APPLICANT: Uberla, Klaus
: TITLE OF INVENTION: LENTIVIRUS BASED VECTOR AND VECTOR
: TITLE OF INVENTION: SYSTEM
: FILE REFERENCE: 20239-705
: CURRENT APPLICATION NUMBER: US/09/380,323
: PRIOR FILING DATE: 1999-11-22
: PRIOR APPLICATION NUMBER: PCT/EP98/01191
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: DK 6238/97
: PRIOR FILING DATE: 1997-03-06
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Vector mutant
US-09-380-323-1
Query Match 36.4% Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GKKK 7
DB 1 GKKK 4
RESULT 29
US-09-380-323-4
: Sequence 4, Application US/09380323
: Patent No. US20020123471A1
: GENERAL INFORMATION:
: APPLICANT: Bavarian No. US20020123471A1dic Research Institute A/S
: APPLICANT: Uberla, Klaus
: TITLE OF INVENTION: LENTIVIRUS BASED VECTOR AND VECTOR
: TITLE OF INVENTION: SYSTEM
: FILE REFERENCE: 20239-705
: CURRENT APPLICATION NUMBER: US/09/380,323
: CURRENT FILING DATE: 1999-11-22
: PRIOR APPLICATION NUMBER: PCT/EP98/01191
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: DK 6238/97
: PRIOR FILING DATE: 1997-03-06
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Vector mutant
US-09-380-323-4
Query Match 36.4% Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GKKK 7
DB 1 GKKK 4
RESULT 30
US-09-813-448-2
: Sequence 2, Application US/09813448
: Patent No. US20020142346A1
: GENERAL INFORMATION:
: APPLICANT: Nestor, John
: APPLICANT: Wilson, Carol
: TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou
: FILE REFERENCE: CNS-006
: CURRENT APPLICATION NUMBER: US/09/813,448
```

? CURRENT FILING DATE: 2001-03-20  
 ? PRIOR APPLICATION NUMBER: US 60/190,946  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: US 60/190,996  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: US 60/141,299  
 ? PRIOR FILING DATE: 2000-03-21  
 ? NUMBER OF SEQ ID NOS: 8  
 ? SOFTWARE: PatentIn version 3.0  
 ? SEQ ID NO 2  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: preferred amino acids for HLE binding domain  
 US-09-813 448-2

Query Match 36.4% Score 4: DB 16, Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
 LB 1 KKKK 4

RESULT 33  
 US-09-142 043-2  
 ? Sequence 2: Application US/09142043  
 ? Patent No. US20020142372A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: MOSSAKOWSKA, Danuta Eva Irene  
 ? APPLICANT: EDGE, Colin Michael  
 ? APPLICANT: SMITH, Richard Anthony Jackson  
 ? TITLE OF INVENTION: FRAGMENTS OF PRC AND THEIR USE  
 ? FILE REFERENCE: 86362/104  
 ? CURRENT APPLICATION NUMBER: US/09/142,043  
 ? CURRENT FILING DATE: 1998-12-01  
 ? EARLIER APPLICATION NUMBER: WO PCT/EP97/00,994  
 ? EARLIER FILING DATE: 1997-02-26  
 ? EARLIER APPLICATION NUMBER: GB 96045142.2  
 ? EARLIER FILING DATE: 1996-03-02  
 ? NUMBER OF SEQ ID NOS: 8  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 2  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificially synthesized peptide

Query Match 36.4% Score 4: DB 16, Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
 LB 1 KKKK 4

RESULT 32  
 US-09-843 676-223  
 ? Sequence 24: Application US/09843076  
 ? Patent No. US20020164786A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Cech, Thomas R.  
 ? APPLICANT: Lingner, Joachim  
 ? APPLICANT: Nakamura, Toru  
 ? APPLICANT: Chapman, Karen B.  
 ? APPLICANT: Morin, Gregg B.  
 ? APPLICANT: Harley, Calvin  
 ? APPLICANT: Andrews, William H.

? TITLE OF INVENTION: NO. US20020164786A1el Telomerase  
 ? NUMBER OF SEQUENCES: 225  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Townsend and Townsend and Crew LLP  
 ? STREET: Two Embarcadero Center, 8th Floor  
 ? CITY: San Francisco  
 ? STATE: California  
 ? COUNTRY: United States of America  
 ? ZIP: 94111

? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/09/843,676  
 ? FILING DATE: 26-APR-2001  
 ? CLASSIFICATION: 536

? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/854,050  
 ? FILING DATE: 09-MAY-1997  
 ? APPLICATION NUMBER: US 08/846,017  
 ? FILING DATE: 25-APR-1997  
 ? APPLICATION NUMBER: US 08/844,419  
 ? FILING DATE: 18-APR-1997  
 ? APPLICATION NUMBER: US 08/724,643  
 ? FILING DATE: 01-OCT-1996

? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Apple, Randolph L.  
 ? REGISTRATION NUMBER: 36,429  
 ? REFERENCE/DOCKET NUMBER: 015389-0029300S  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (415) 576-0200  
 ? TELEFAX: (415) 576-0300

? INFORMATION FOR SEQ ID NO: 223:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 8 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: <Unknown>  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 223:  
 US 09-843-676-223

Query Match 36.4% Score 4: DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5, 10-05;  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
 LB 1 KKKK 4

RESULT 33  
 US-09-945-249-82  
 ? Sequence 82: Application US/09945249  
 ? Patent No. US20020168748A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: BERLIN, VIVIAN  
 ? APPLICANT: DAMAGNEZ, VERONIQUE  
 ? APPLICANT: SMITH, SUSAN F.  
 ? TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,  
 ? FILE REFERENCE: MIV-074.06  
 ? CURRENT APPLICATION NUMBER: US/09/945,249  
 ? CURRENT FILING DATE: 2001-08-31  
 ? PRIOR APPLICATION NUMBER: 09/041,990  
 ? PRIOR FILING DATE: 2001-01-13  
 ? PRIOR APPLICATION NUMBER: 08/771,212  
 ? PRIOR FILING DATE: 1996-12-20  
 ? PRIOR APPLICATION NUMBER: 08/631,319  
 ? PRIOR FILING DATE: 1996-04-11  
 ? NUMBER OF SEQ ID NOS: 89



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1 SOFTWARE: PatentIn Ver. 2.1
2 SEQ ID NO: 82
3 LENGTH: 8
4 TYPE: PRF
5 ORGANISM: Artificial Sequence
6 FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: Peptide that
8 corresponds to the C-terminus of P1ase of GC4ase
9 OTHER INFORMATION: substrates
10 US-09-945 249-82
11
12 Query Match: 36.4%, Score 41, DB NO: 09805401
13 Best Local Similarity: 100.0%, Pred. No. 5.1e+05
14 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
15
16 QY 5 KKKK 8
17 DB 1 KKKK 4
18
19 RESULT 34
20 US-09-805-301-40
21 Sequence 2: Application US/09805401
22 Patent No. US20020173456A1
23 GENERAL INFORMATION:
24 APPLICANT: Smith, Louis C.
25 Sparrow, James T.
26 Hauer, Jochen
27 Mims, Martha P.
28 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
29 MACROMOLECULE DELIVERY
30 NUMBER OF SEQUENCES: 139
31 CORRESPONDENCE ADDRESS:
32 ADDRESSEE: Lyon & Lyon
33 STREET: 633 West Fifth Street
34 Suite 4700
35 CITY: Los Angeles
36 STATE: California
37 COUNTRY: U.S.A.
38 ZIP: 90071-2066
39 COMPUTER READABLE FORM:
40 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
41
42 COMPUTER: IBM Compatible
43 OPERATING SYSTEM: IBM P.C. DOS 6.0
44 SOFTWARE: Word Perfect 6.1
45 CURRENT APPLICATION DATA:
46 APPLICATION NUMBER: US/09-805,301
47 FILING DATE: 12-Mar-2001
48 CLASSIFICATION: <unknown>
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: 08/584,043
51 FILING DATE: <unknown>
52 ATTORNEY/AGENT INFORMATION:
53 NAME: Warburg, Richard J.
54 REGISTRATION NUMBER: 32,427
55 REFERENCE/DOCKET NUMBER: 217/189
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (213) 489-1600
58 TELEFAX: (213) 955-0440
59 TELEX: 67-3510
60 INFORMATION FOR SEQ ID NO: 21:
61 SEQUENCE CHARACTERISTICS:
62 LENGTH: 8 amino acids
63 TYPE: amino acid
64 STRANDEDNESS: single
65 TOPOLOGY: linear
66 MOLECULE TYPE: peptide
67 OTHER INFORMATION: "Xaa" stands for any naturally
68 occurring amino acid and
69 analogues thereof
70 SEQUENCE DESCRIPTION: SEQ ID NO: 21
71 US-09-805-301-40
72
73 Query Match: 36.4%, Score 41, DB NO: 09805401
74 Best Local Similarity: 100.0%, Pred. No. 5.1e+05
75 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
76
77 QY 5 KKKK 8
78 DB 1 KKKK 4
79
80 RESULT 35
81 US-09-805-301-40
82 Sequence 40: Application US/09805401
83 Patent No. US20020173456A1
84 GENERAL INFORMATION:
85 APPLICANT: Smith, Louis C.
86 Sparrow, James T.
87 Hauer, Jochen
88 Mims, Martha P.
89 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
90 MACROMOLECULE DELIVERY
91 NUMBER OF SEQUENCES: 139
92 CORRESPONDENCE ADDRESS:
93 ADDRESSEE: Lyon & Lyon
94 STREET: 633 West Fifth Street
95 Suite 4700
96 CITY: Los Angeles
97 STATE: California
98 COUNTRY: U.S.A.
99 ZIP: 90071-2066
100 COMPUTER READABLE FORM:
101 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
102
103 COMPUTER: IBM Compatible
104 OPERATING SYSTEM: IBM P.C. DOS 6.0
105 SOFTWARE: Word Perfect 6.1
106 CURRENT APPLICATION DATA:
107 APPLICATION NUMBER: US/09-805,301
108 FILING DATE: 12-Mar-2001
109 CLASSIFICATION: <unknown>
110 PRIOR APPLICATION DATA:
111 APPLICATION NUMBER: 08/584,043
112 FILING DATE: <unknown>
113 ATTORNEY/AGENT INFORMATION:
114 NAME: Warburg, Richard J.
115 REGISTRATION NUMBER: 32,427
116 REFERENCE/DOCKET NUMBER: 217/189
117 TELECOMMUNICATION INFORMATION:
118 TELEPHONE: (213) 489-1600
119 TELEFAX: (213) 955-0440
120 TELEX: 67-3510
121 INFORMATION FOR SEQ ID NO: 40:
122 SEQUENCE CHARACTERISTICS:
123 LENGTH: 8 amino acids
124 TYPE: amino acid
125 STRANDEDNESS: single
126 TOPOLOGY: linear
127 MOLECULE TYPE: peptide
128 OTHER INFORMATION: "Xaa" stands for any naturally
129 occurring amino acid and
130 analogues thereof
131 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
132 US-09-805-301-40
133
134 Query Match: 36.4%, Score 41, DB NO: 09805401
135 Best Local Similarity: 100.0%, Pred. No. 5.1e+05
136 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
137
138 QY 5 KKKK 8
139 DB 1 KKKK 4
140
141 RESULT 36
142 US-09-805-301-40
```

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1 Sequence 46, Application US/0985540;
2 Patent No. US20020173436A1
3 GENERAL INFORMATION:
4 APPLICANT: Smith, Louis C.
5 Sparrow, James E.
6 Hauser, Jocheu
7 Mams, Martha F.
8 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
9 MATERNAL-FETAL DELIVERY
10 NUMBER OF SEQUENCES: 139
11 C) RESIDENT/ADDRESS:
12 ADDRESSEE: Lyon & Lyon
13 STREET: 633 West Fifth Street
14 CITY: Suite 4700
15 Los Angeles
16 STATE: California
17 COUNTRY: U.S.A.
18 ZIP: 90071-2064
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5" diskette, 1.44 MB
21 storage
22 COMPUTER: IBM Compatible
23 OPERATING SYSTEM: IBM P.C. DOS 6.0
24 SOFTWARE: Word Perfect 5.1
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/09/805,441
27 FILING DATE: 12 Mar 2001
28 CLASSIFICATION: <Unknown>
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/064,044
31 FILING DATE: <Unknown>
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Warburg, Richard J.
34 REGISTRATION NUMBER: 32,427
35 REFERENCE/DOCKET NUMBER: 217/149
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (213) 489-163
38 TELEFAX: (213) 965-5440
39 TELEX: 67-3510
40 INFORMATION FOR SEQ ID NO: 96:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 8 amino acids
43 TYPE: amino acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: peptide
47 SEQUENCE DESCRIPTION: SEQ ID NO: 96:
48
49 US-09 805,401-96
50
51 Query Match 36.4% Sequences 4
52 Best Local Similarity 100.0% First Match 1
53 Matches 4; Conservative 0; Mismatches 0
54
55 QY 5 KKKK R
56 11
57 1b 1 KKKK K
58
59 RESULT 47
60 US 09-813,214A 2
61 Sequence 2, Application US/09813214A
62 Patent No. US20020177200A1
63 GENERAL INFORMATION:
64 APPLICANT: Tucker, Kenneth
65 Piosilla, Laura
66 TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
67 PROTEIN EXPRESSION, SEQUENCE AND USES THEREOF
68 FILE REFERENCE: 7969-089-999
69 CURRENT APPLICATION NUMBER: US/09/713,214A
70 CURRENT FILING DATE: 2000-03-20
71 PRIOR APPLICATION NUMBER: 08/956,195
72 PRIOR FILING DATE: 1997-11-12
73 NUMBER OF SEQ ID NOS: 20

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1 SOFTWARE: Patentlin version 3.0
2 SEQ ID NO 2
3 LENGTH: 8
4 TYPE: PRT
5 ORGANISM: Moraxella catarrhalis
6 US-9-813-214A 2
7
8 Query Match 46.4% Score 41 DB 10. Length 87
9 Best Local Similarity 100.0% Pctd Nbr 5 1e+05;
10 Matches 43 Conservative 0 Mismatches 0 Indels
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17 3 GKKK 5
18 11
19 5 GKKK 5
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1 SURANDEDNESS:  
2 TOPOLOGY: linear  
3 MOLECULE TYPE: peptide  
4 US 09-438-486-223

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 40  
US 09-999-724 1  
Sequence 1, Application US/0999724  
Publication No. US20030040472A1  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: KOVESDI, IMRE  
APPLICANT: BROUGHT, DOUGLAS E.  
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER  
FILE REFERENCE: 212960  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US 09/101,175  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: WO 96/0519160  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 08/730,846  
PRIOR FILING DATE: 1996-08-21  
PRIOR APPLICATION NUMBER: US 06/701,124  
PRIOR FILING DATE: 1996-08-21  
PRIOR APPLICATION NUMBER: US 08/463,468  
PRIOR FILING DATE: 1995-11-28  
NUMBER OF SEQ ID NOS: 94  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-999-724 1

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 40  
US 09-882-291-63  
Sequence 63, Application US/09882291  
Publication No. US20030040472A1  
GENERAL INFORMATION:  
APPLICANT: Zealand Pharmaceuticals A/S  
TITLE OF INVENTION: 007-2001  
FILE REFERENCE: 007-2001  
CURRENT APPLICATION NUMBER: US/09/882,291  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 63  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence

US-09-882-291-63

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 41  
US-09-882-291-73  
Sequence 73, Application US/09882291  
Publication No. US20030040472A1  
GENERAL INFORMATION:  
APPLICANT: Zealand Pharmaceuticals A/S  
TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates  
FILE REFERENCE: 007-2001  
CURRENT APPLICATION NUMBER: US/09/882,291  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 73  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-882-291-73

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 42  
US-09-911-569-3  
Sequence 3, Application US/09911569  
Publication No. US20030069173A1  
GENERAL INFORMATION:  
APPLICANT: HARLEY-NEELSON, PAMELA  
LAN, JIANGJING  
SETH, POJEN  
JENSE, JOEL A.  
SCHIFFER, KEVIN P.  
GEHEBER, GILGAT  
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GREENLEE, WINNER & SULLIVAN  
STREET: 5370 MANHATTAN CIRCLE, SUITE 201  
CITY: BOULDER  
STATE: CO  
COUNTRY: US  
Zip: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/911,569  
FILING DATE: 23-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/039,780  
FILING DATE: 16-MAR-1998  
ATTORNEY/AGENT INFORMATION:

NAME: SULLIVAN, SALLY A.  
 REGISTRATION NUMBER: 32,064  
 REFERENCE/DOCKET NUMBER: 32,950  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303)499-8080  
 TELEFAX: (303)499-8089  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US 09/911-569-3

Query Match 36.4% Score 4; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8

Db 2 KKKK 5

#### RESULT 43

US-09-876-904A-53

Sequence 53, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

FILE REFERENCE: TB-2002.00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 53

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus 5 Cap

US-09-876-904A-53

Query Match

36.4% Score 4; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8

Db 2 KKKK 5

#### RESULT 44

US-09-876-904A-394

Sequence 394, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

FILE REFERENCE: TB-2002.00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 485

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 394

LENGTH: 8

TYPE: PRT

ORGANISM: Xenopus sp.

FEATURE:

OTHER INFORMATION: Xenopus KAR (retinoic acid receptor)

US-09-876-904A-394

Query Match

36.4% Score 4; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8

Db 4 KKKK 7

#### RESULT 45

US-09-876-904A-405

Sequence 405, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

FILE REFERENCE: TB-2002.00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 405

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human TFIIIE-beta (general transcription initiation

OTHER INFORMATION: protein factor; forms tetramer alpha 2 beta 2 with

OTHER INFORMATION: TFIIIE-alpha).

US-09-876-904A-405

Query Match

36.4% Score 4; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8

Db 2 KKKK 5

#### RESULT 46

US-09-876-904A-485

Sequence 485, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

FILE REFERENCE: TB-2002.00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 485

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? LENGTH: 8
? TYPE: PRT
? ORGANISM: Mus sp.
? FEATURE:
? OTHER INFORMATION: Murine HNF-1beta
US 09-876 904A-465

Query Match 36.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKKK 8
DB 2 KKKK 5

RESULT 47
US-09-791-524-139
? Sequence 139, Application US/09791524
? Publication No. US20030143209A1
? GENERAL INFORMATION:
? APPLICANT: Aventis Pharmaceuticals Products Inc.
? TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
? FILE REFERENCE: A3319A
? CURRENT APPLICATION NUMBER: US/09/791-524
? CURRENT FILING DATE: 2001-02-22
? PRIOR APPLICATION NUMBER: 60/09928
? PRIOR FILING DATE: 1998-08-27
? NUMBER OF SEQ ID NOS: 150
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 139
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Adenovirus
US-09-791-524-139

Query Match 36.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 1 KKKK 4

RESULT 48
US 10-073-333A-26
? Sequence 26, Application US/1007333A
? Publication No. US20030134788A1
? GENERAL INFORMATION:
? APPLICANT: Kevin Baker et al.
? TITLE OF INVENTION: HUMAN TUMOR NEURONAL FACTOR RECEPTOR TR16
? FILE REFERENCE: PF514P1
? CURRENT APPLICATION NUMBER: US/10/073-333A
? CURRENT FILING DATE: 2002-06-18
? PRIOR APPLICATION NUMBER: 60/268,364
? PRIOR FILING DATE: 2001-02-14
? PRIOR APPLICATION NUMBER: 09/637,856
? PRIOR FILING DATE: 2000-08-10
? PRIOR APPLICATION NUMBER: 60/148,348
? PRIOR FILING DATE: 1999-08-12
? PRIOR APPLICATION NUMBER: 60/148,683
? PRIOR FILING DATE: 1999-08-13
? PRIOR APPLICATION NUMBER: 60/148,758
? PRIOR FILING DATE: 1999-08-16
? PRIOR APPLICATION NUMBER: 60/148,870
? PRIOR FILING DATE: 1999-08-13
? PRIOR APPLICATION NUMBER: 60/149,181
? PRIOR FILING DATE: 1999-08-17
? PRIOR APPLICATION NUMBER: 60/149,453
? PRIOR FILING DATE: 1999-08-18
? PRIOR APPLICATION NUMBER: 60/149,498
? PRIOR FILING DATE: 1999-08-18
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? NUMBER OF SEQ ID NOS: 43
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 26
? LENGTH: 8
? TYPE: PRT
? ORGANISM: human
US-10-073-333A-26

Query Match 46.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 4 KKKK 7

RESULT 49
US-10-200-879-3
? Sequence 3, Application US/0200879
? Publication No. US20030144230A1
? GENERAL INFORMATION:
? APPLICANT: HANLEY-NELSON, PAMELA
? INVENTOR: SHIH, PO-JEN
? TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
? NUMBER OF SEQ ID NOS: 120
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: GREENLEE, WINNER & SULLIVAN
? STREET: 5370 MANHATTAN CIRCLE, SUITE 201
? CITY: BOULDER
? STATE: CO
? COUNTRY: US
? ZIP: 80303
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION NUMBER: US/10/200,879
? FILING DATE: 23-Jul-2002
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 09/911,569
? FILING DATE: 23-JUL-2001
? APPLICATION NUMBER: US 09/039,780
? FILING DATE: 16-MAR-1998
? APPLICATION NUMBER: US 08/818,200
? FILING DATE: 14-MAR-1997
? APPLICATION NUMBER: US 08/658,130
? FILING DATE: 04-JUN-1996
? APPLICATION NUMBER: US 08/477,354
? FILING DATE: 07-JUN-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: SULLIVAN, SALLY A.
? REGISTRATION NUMBER: 32,064
? REFERENCE/DOCKET NUMBER: 32-95E
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303)499-8080
? TELEFAX: (303)499-8089
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-200-879-3

Query Match 36.4% Score 4: 68 125 160 187  
Best Local Similarity 100.0% Pref. No. 5: 100.0%  
Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 5 KKKK 8  
111  
1b 2 KKKK 5

RESULT 50  
US-10-014-322A-02  
Sequence 12: Application US/10014322A  
Publication No. US20030167129A1  
GENERAL INFORMATION:  
APPLICANT: Nestor, Jr., John  
APPLICANT: Wilson, Carol  
APPLICANT: Fan, Hahir, Christina  
APPLICANT: Kates, Steven  
APPLICANT: Krstenansky, John  
TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds  
FILE REFERENCE: CNS-008  
CURRENT APPLICATION NUMBER: US/10/014-322A  
CURRENT FILING DATE: 2002-07-08  
PRIOR APPLICATION NUMBER: US 60/243,587  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 09/813,651  
PRIOR FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: US 09/813,651  
PRIOR FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: US 09/813,446  
PRIOR FILING DATE: 2001-03-20  
NUMBER OF SEQ ID NOS: 126  
SEQ ID NO 62  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURES:  
OTHER INFORMATION: Preferred peptide for HIV binding domain  
US-10-014-322A-02

Query Match 36.4% Score 4: 68 125 160 187  
Best Local Similarity 100.0% Pref. No. 5: 100.0%  
Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 5 KKKK 8  
111  
1b 1 KKKK 4

Search completed: September 30, 2003, 11:07:01  
Job time: 23.5 secs